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The term "protein tyrosine kinase," or PTK, refers to an enzyme that transfers the high energy phosphate of adenosine triphosphate to a tyrosine residue located on a protein target.

A protein tyrosine kinase catalytic domain of the invention can originate from receptor protein tyrosine kinases that bind fibroblast growth factor (FGF). These protein tyrosine kinases are known as "FGFR" herein, and can relate to one member of the FGFR family, such as FGFR1.

The term "catalytic domain" refers to the region of a protein that can exist as a separate entity from the protein. The catalytic domain of a protein tyrosine kinase is characterized as having considerable amino acid identity to the catalytic domain of other protein tyrosine kinases. Considerable amino acid identity preferably refers to at least 30% identity, more preferably at least 35% identity, and most preferably at least 40% identity. These degrees of amino acid identity refer to the identity between different protein tyrosine kinase families. Amino acid identity for members of a given protein tyrosine kinase family range from 55% to 90%. The catalytic domain may be functional as a separate entity. The catalytic domain of a protein tyrosine kinase is also characterized as a polypeptide that is soluble in solution.

The term "identity" identity as used herein refers to a property of sequences that measures their similarity or relationship. Identity is measured by dividing the number of identical residues in the two sequences by the total number of residues and

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multiplying the product by 100. Thus, two copies of exactly the same sequence have 100% identity, but sequences that are less highly conserved and have deletions, additions, or replacements have a lower degree of identity. Those skilled in the art will recognize that several computer programs are available for determining sequence identity.

The term "functional" refers to the ability of a catalytic domain to convert a substrate into a product by phosphorylating the substrate. The term "functional" also relates to the ability of a catalytic domain to bind natural binding partners. The catalytic region may comprise an N-terminal tail, a catalytic core, and a C-terminal tail. The catalytic core is a polypeptide that can be functional in terms of catalysis. N- and C-terminal tails are polypeptide regions that may not confer appreciable functionality in terms of catalysis, but may confer functionality in terms of modulator specificity.

A polypeptide can exist as a catalytic domain eventhough it is not functional. For example, a polypeptide corresponding to a catalytic domain may not be functional if it does not harbor phosphate moieties in key areas. Multiple examples of phosphorylation
25 state dependent function are well documented in the art. Therefore, a catalytic domain can also exist without being functional. A measure of a protein kinase catalytic domain is a polypeptide that is homologous to other protein kinase catalytic domains.

The term "polypeptide" refers to an amino acid chain representing a portion of, or the entire sequence

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of, amino acids comprising a protein.

A preferred embodiment of the invention includes a crystalline form of a PTK that is a receptor PTK.

Receptors are proteins that straddle the inside and outside of the cell membrane. Receptor PTKs comprise an extracellular region, a transmembrane region, and an intracellular region comprising a catalytic domain.

Another preferred embodiment of the invention is the crystalline form of a receptor PTK selected from the group consisting of FGF-R, PDGF-R, FLK, CCK4, MET, TRKA, AXL, TIE, EPH, RYK, DDR, ROS, RET, LTK, ROR1, and MUSK.

Yet another preferred embodiment of the invention is the crystalline form of a PTK that is a non-receptor PTK. Non-receptor PTKs are located inside the cell and do not harbor extracellular or membrane-spanning polypeptides attached to the polypeptide corresponding to the catalytic domain. Non-receptor PTKs may harbor fatty acids or lipids, which can impart a membrane associated character to a PTK. In preferred embodiments of the invention, crystalline forms of non-receptor PTKs are selected from the group consisting of SRC, BRK, BTK, CSK, ABL, ZAP70, FES, FAK, JAK, and ACK.

In still another preferred embodiment, the invention features a crystalline form of a PTK that comprises a heavy metal atom. These types of crystals can be referred to as derivative crystals.

The term "derivative crystal" refers to a crystal where the polypeptide is in association with one or more heavy-metal atoms.

The term "association" refers to a condition of proximity between a chemical entity or compound, or

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portions or fragments thereof, and tyrosine kinase domain protein, or portions or fragments thereof. The association may be non-covalent, i.e., where the juxtaposition is energetically favored by, e.g., hydrogen-bonding, van der Waals, electrostatic or hydrophobic interactions, or it may be covalent.

The term "heavy metal atom" refers to an atom that is a transition element, a lanthanide metal, or an actinide metal. Lanthanide metals include elements with atomic numbers between 57 and 71, inclusive. Actinide metals include elements with atomic numbers between 89 and 103, inclusive.

In a preferred embodiment, the invention features a crystal of an FGF receptor tyrosine kinase domain protein. The FGF receptor tyrosine kinase domain protein can relate to FGFR1

The term "FGFR1" refers to one member of multiple receptor PTKs that are homologous to one another and bind FGF. In this context, the term "homologous" refers to at least 70% amino acid identity between two members of the FGFR family.

The term "FGFR1" can also refer to a mutant of human FGFR1 which is characterized by the amino acid sequence of SEQ ID NO:2. As compared to human FGFR1, FGFR1 contains the following amino acid substitutions: Cys-488 - Ala, Cys-584 - Ser, Leu-457 - Val, and has an additional five amino acid residues at the N-terminus (Ser-Ala-Ala-Gly-Thr).

The term "human FGFR1" refers to the tyrosine

kinase domain of human fibroblast growth factor receptor

("FGFR1") having the amino acid sequence of SEQ ID

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NO:1. Generally, human FGFR1 comprises a 310 amino acid residue fragment (residues 456 to 765) of human FGFR1.

The term "mutant" refers to a polypeptide which is obtained by replacing at least one amino acid residue in a native tyrosine kinase domain with a different amino acid residue. Mutation can be accomplished by adding and/or deleting amino acid residues within the native polypeptide or at the N- and/or C-terminus of a polypeptide corresponding to a native tyrosine kinase domain having substantially the same three-dimensional structure as the native tyrosine kinase domain from which it is derived. By having substantially the same three-dimensional structure is meant having a set of atomic structure coordinates that have a root mean square deviation (r.m.s.d.) of less than or equal to about 2 Å when superimposed with the atomic structure coordinates of the native tyrosine kinase domain from which the mutant is derived when at least about 50% to 100% of the Cα atoms of the native tyrosine kinase are included in the superposition. A mutant may have, but need not have, PTK activity.

In another preferred embodiment, the invention relates to a crystalline form defined by the structural coordinates set forth in Table 1.

25 The term "atomic structural coordinates" as used herein refers to a data set that defines the three dimensional structure of a molecule or molecules.

Structural coordinates can be slightly modified and still render nearly identical three dimensional

30 structures. A measure of a unique set of structural coordinates is the root-mean-square deviation of the

resulting structure. Structural coordinates that render three dimensional structures that deviate from one another by a root-mean-square deviation of less than 1.5 Å may be viewed by a person of ordinary skill in the art as identical. Hence, the structural coordinates set forth in Table 1, Table 2, Table 3, and Table 4 are not limited to the values defined therein.

In other preferred embodiments, the invention features a crystalline form of the polypeptide in

association with a compound. These types of crystalline forms can be referred to as co-crystals. The compound may be a cofactor, substrate, substrate analog, inhibitor, or allosteric effector.

The term "compound" refers to an organic molecule.

The term "organic molecule" refers to a molecule which has at least one carbon atom in its structure. The compound can have a molecular weight of less than 6kDa. Both the geometry of the compound and the interactions formed between the compound and the polypeptide

preferably govern high affinity binding between the two molecules. High affinity binding is preferably governed by a dissociation equilibrium constant on the order of 10-6 M or less. The compound is preferably a modulator that alters the function of a PTK.

The term "function," in reference to the effect of a modulator on PTK function, refers to the ability of a modulator to enhance or inhibit the catalytic activity of a PTK.

The term "catalytic activity", in the context of the invention, defines the ability of a PTK to phosphorylate a substrate polypeptide. Catalytic

activity can be measured, for example, by determining the amount of a substrate converted to a product as a function of time. The conversion of the substrate to a product occurs at the active-site of the PTK.

The term "active-site" refers to a cavity located in the PTK in which one or more substrate molecules may bind. Addition of a modulator to cells expressing a PTK may enhance (activate) or lower (inhibit) the catalytic activity of the PTK.

A small number of inhibitors of PTK catalytic activity are known in the art. Small molecule inhibitors may modulate PTK function by blocking the binding of substrates. Indolinone compounds, for example, may bind to the active-site of PTK catalytic domains and inhibit them effectively, as measured by inhibition constants on the order of 10⁻⁶ M or less.

Activators of PTK intracellular regions can enhance PTK function by interacting with both the PTK catalytic domain and the substrate. Activators may also promote dimerization of PTKs and thus activate them by bringing them into close proximity with one another. In addition, activators may operate by promoting a conformational change in the intracellular region of the PTK such that the catalytic region modifies substrates at a faster rate in the presence of the activator.

The term "function" can also refer to the ability of a modulator to enhance or inhibit the association between a PTK and a natural binding partner.

The term "natural binding partner" refers to a polypeptide that normally binds to a PTK in a cell.

These natural binding partners can play a role in

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propagating a signal in a PTK signal transduction process. The natural binding partner can bind to a PTK with high affinity. High affinity represents an equilibrium binding constant on the order of 10-6 M or less. However, a natural binding partner can also transiently interact with a PTK and chemically modify it. PTK natural binding partners are chosen from a group consisting of, but not limited to, src homology 2 (SH2) or 3 (SH3) domains, other phosphoryl tyrosine binding (PTB) domains, nucleotide exchange factors, and other protein kinases or protein phosphatases.

The term "interactions" refers to hydrophobic, aromatic, and ionic forces and hydrogen bonds formed between atoms in the modulator and the enzyme activesite.

The term "cofactor" refers to a compound that may, in addition to the substrate, bind to a protein and undergo a chemical reaction. Multiple co-factors are nucleotides or nucleotide derivatives, such as phosphate and nicotinamide derivatives of adenosine.

The term "substrate" refers to a compound that reacts with an enzyme. Enzymes can catalyze a specific reaction on a specific substrate. For example, PTKs can phosphorylate specific protein and peptide substrates on tyrosine moieties. In addition, nucleotides can act as substrates for protein kinases.

The term "substrate analog" refers to a compound that is structurally similar, but not identical, to a substrate. The substrate analog may be a nucleotide analog. Examples of nucleotide analogs are described below.

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The term "inhibitor" refers to a compound that decreases the cellular function of a protein kinase. The protein kinase function is preferably the interaction with a natural binding partner and more preferably catalytic activity.

The term "allosteric effector" refers to a compound that causes allosteric interactions in a protein. The term "allosteric interactions" refers to interactions between separate sites on a protein. The sites can be different from the active site. The allosteric effector can enhance or inhibit catalytic activity by binding to a site that may be different than the active site.

The term "co-crystal" refers to a crystal where the polypeptide is in association with one or more compounds.

In preferred embodiments, a co-crystal of the invention can be in association with a heavy metal atom. Examples of heavy metal atoms are described above.

In other preferred embodiments, the invention features a co-crystal comprising the crystalline form of the polypeptide in association with a compound, where the compound is a non-hydrolyzable analog of ATP. These analogs can be referred to as nucleotide analogs.

The term "ATP" refers to the chemical compound adenosine triphosphate.

The term "non-hydrolyzable" refers to a compound having a covalent bond that does not readily react with water. Examples of non-hydrolyzable analogs of ATP are AMP-PNP and AMP-PCP, whose structures are well known to those skilled in the art.

The term "AMP-PNP" refers to adenylyl

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imidodiphosphate, a non-hydrolyzable analog of ATP.

The term "AMP-PCP" refers to adenylyl diphosphonate, a non-hydrolyzable analogue of ATP.

In another preferred embodiment, the invention relates to a crystalline form defined by the structural coordinates set forth in Table 2.

In preferred embodiments, the invention relates to crystalline forms, where the compound in association with the polypeptide is an indolinone.

Certain indolinones are specific modulators of PTK function. A preferred embodiment of the invention is the crystalline form of a PTK complexed with an indolinone of formula I or II:

$$R_{5}$$
 R_{4}
 R_{5}
 R_{6}
 R_{7}
 R_{1}
 R_{4}
 R_{6}
 R_{6}
 R_{7}
 R_{1}
 R_{4}
 R_{4}
 R_{5}
 R_{6}
 R_{6}

$$R_5$$
 A_2
 A_1
 R_6
 A_3
 A_4
 R_7
 R_1
 R_1
 R_2
 R_1
 R_1
 R_2
 R_1
 R_1
 R_2

or a pharmaceutically acceptable salt, isomer,

metabolite, ester, amide, or prodrug thereof, where:

- (a) A_1 , A_2 , A_3 , and A_4 are independently carbon or nitrogen;
 - (b) R₁ is hydrogen or alkyl;
- (c) R_2 is oxygen in the case of an oxindolinone or sulfur in the case of a thiolindolinone;
 - (d) R₃ is hydrogen;
- (e) R₄, R₅, R₆, and R₇ are optionally present, and are either (i) independently selected from the group consisting of alkyl, alkoxy, aryl, aryloxy, alkaryl, alkaryloxy, halogen, trihalomethyl, S(O)R, SO₂NRR', SO₃R, SR, NO₂, NRR', OH, CN, C(O)R, OC(O)R, NHC(O)R, (CH₂)_nCO₂R, and CONRR' or (ii) any two adjacent R₄, R₅, R₆, and R₇ taken together form a fused ring with the aryl portion of the indole-based portion of the indolinone;
- (f) R₂', R₃', R₄', R₅', and R₆' are each
 independently selected from the group consisting of
 hydrogen, alkyl, alkoxy, aryl, aryloxy, alkaryl,
 alkaryloxy, halogen, trihalomethyl, S(O)R, SO₂NRR', SO₃R,
 SR, NO₂, NRR', OH, CN, C(O)R, OC(O)R, NHC(O)R, (CH₂)_nCO₂R,

and CONRR';

- (g) n is 0, 1, 2, or 3;
- (h) R is hydrogen, alkyl or aryl;
- (i) R' is hydrogen, alkyl or aryl; and
- 5 (j) A is a five membered heteroaryl ring selected from the group consisting of thiophene, pyrrole, pyrazole, imidazole, 1,2,3-triazole, 1,2,4-triazole, oxazole, isoxazole, thiazole, isothiazole, furan, 1,2,3oxadiazole, 1,2,4-oxadiazole, 1,2,5-oxadiazole, 1,3,4oxadiazole, 1,2,3,4-oxatriazole, 1,2,3,5-oxatriazole, 10 1,2,3-thiadiazole, 1,2,4-thiadiazole, 1,2,5-thiadiazole, 1,3,4-thiadiazole, 1,2,3,4-thiatriazole, 1,2,3,5thiatriazole, and tetrazole, optionally substituted at one or more positions with alkyl, alkoxy, aryl, aryloxy, alkaryl, alkaryloxy, halogen, trihalomethyl, S(O)R, 15 SO_2NRR' , SO_3R , SR, NO_2 , NRR', OH, CN, C(O)R, OC(O)R, NHC(O)R, $(CH_2)_nCO_2R$ or CONRR'.

The term "pharmaceutically acceptable salt" refers to those salts which retain the biological activity and properties of the free bases. Pharmaceutically acceptable salts can be obtained by reaction with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like.

The term "prodrug" refers to an agent that is converted into the parent drug in vivo. Prodrugs may be easier to administer than the parent drug in some situations. For example, the prodrug may be

bioavailable by oral administration but the parent is not, or the prodrug may improve solubility to allow for

intravenous administration.

"Alkyl" refers to a straight-chain, branched or cyclic saturated aliphatic hydrocarbon. Preferably, the alkyl group has 1 to 12 carbons. More preferably, it is a lower alkyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. Typical alkyl groups include methyl, ethyl, propyl, isopropyl, butyl, isobutyl, tertiary butyl, pentyl, hexyl and the like. The alkyl group may be optionally substituted with one or more substituents are selected from the group consisting of hydroxyl, cyano, alkoxy, =0, =S, NO₂, halogen, N(CH₃)₂ amino, and SH.

"Alkenyl" refers to a straight-chain, branched or cyclic unsaturated hydrocarbon group containing at least one carbon-carbon double bond. Preferably, the alkenyl group has 2 to 12 carbons. More preferably it is a lower alkenyl of from 2 to 7 carbons, more preferably 2 to 4 carbons. The alkenyl group may be optionally substituted with one or more substituents selected from the group consisting of hydroxyl, cyano, alkoxy, =0, =S, NO_2 , halogen, $N(CH_3)_2$ amino, and SH.

"Alkynyl" refers to a straight-chain, branched or cyclic unsaturated hydrocarbon containing at least one carbon-carbon triple bond. Preferably, the alkynyl group has 2 to 12 carbons. More preferably it is a lower alkynyl of from 2 to 7 carbons, more preferably 2 to 4 carbons. The alkynyl group may be optionally substituted with one or more substituents selected from the group consisting of hydroxyl, cyano, alkoxy, =0, =S, NO₂, halogen, N(CH₃)₂ amino, and SH.

"Alkoxy" refers to an "O-alkyl" group.

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"Aryl" refers to an aromatic group which has at least one ring having a conjugated pi-electron system and includes carbocyclic aryl, heterocyclic aryl and biaryl groups. The aryl group may be optionally substituted with one or more substituents selected from the group consisting of halogen, trihalomethyl, hydroxyl, SH, OH, NO₂, amine, thioether, cyano, alkoxy, alkyl, and amino.

"Alkaryl" refers to an alkyl that is covalently
joined to an aryl group. Preferably, the alkyl is a
lower alkyl.

"Carbocyclic aryl" refers to an aryl group wherein the ring atoms are carbon.

"Heterocyclic aryl" refers to an aryl group having

from 1 to 3 heteroatoms as ring atoms, the remainder of
the ring atoms being carbon. Heteroatoms include
oxygen, sulfur, and nitrogen. Thus, heterocyclic aryl
groups include furanyl, thienyl, pyridyl, pyrrolyl, Nlower alkyl pyrrolo, pyrimidyl, pyrazinyl, imidazolyl
and the like.

"Amide" refers to -C(0)-NH-R, where R is alkyl, aryl, alkylaryl or hydrogen.

"Thioamide" refers to -C(S)-NH-R, where R is alkyl, aryl, alkylaryl or hydrogen.

"Amine" refers to a -N(R')R'' group, where R' and R'' are independently selected from the group consisting of alkyl, aryl, and alkylaryl.

"Thioether" refers to -S-R, where R is alkyl, aryl, or alkylaryl.

"Sulfonyl" refers to $-S(O)_2-R$, where R is aryl, C(CN)=C-aryl, CH_2CN , alkyaryl, sulfonamide, NH-alkyl, NH-

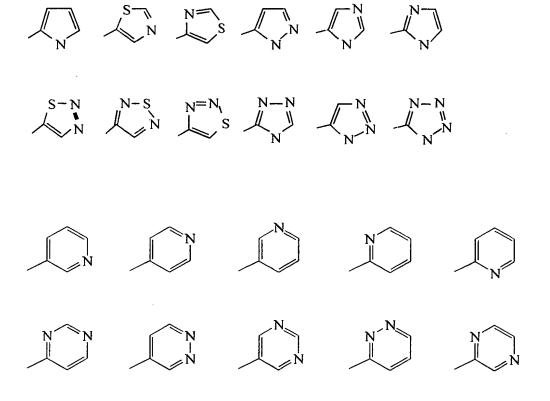
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alkylaryl, or NH-aryl.

The term "acyl" denotes groups -C(O)R, where R is alkyl as defined above, such as formyl, acetyl, propionyl, or butyryl.

It is understood by those skilled in the art that when A_1 , A_2 , A_3 , and A_4 are nitrogen or sulfur that the corresponding R_4 , R_5 , R_6 , and R_7 , as well as the corresponding bond, do not exist.

Examples of indoles having such fused rings (as described in (e) (ii) above include the following:



The six membered rings shown above exemplify possible A rings in compound II.

Other preferred embodiments of the invention are crystalline forms comprising 3-[(3-(2-carboxyethyl)-4-methylpyrrol-5-yl)methylene]-2-indolinone as well as 3-[4-(4-formylpiperazine-1-yl-)benzylidenyl]-2-indolinone. The polypeptide of these crystalline forms can be FGFR, and specifically, FGFR1.

In preferred embodiments, the crystalline forms of the invention can be defined by the structural coordinates set forth in Table 3 or Table 4.

The use of X-ray crystallography can elucidate the three dimensional structure of crystalline forms of the invention. The first characterization of crystalline forms by X-ray crystallography can determine the unit cell shape and its orientation in the crystal.

In other preferred embodiments, the invention features a crystal of an FGF receptor tyrosine kinase domain protein, where the crystal is characterized by having monoclinic unit cells. The crystal may also be characterized by having space group symmetry C2.

The term "unit cell" refers to the smallest and simplest volume element (i.e., parallelpiped-shaped block) of a crystal that is completely representative of the unit of pattern of the crystal. The dimensions of the unit cell are defined by six numbers: dimensions a, b and c and angles α, β and γ. A crystal can be viewed as an efficiently packed array of multiple unit cells. Detailed descriptions of crystallographic terms are described in, which is hereby incorporated herein by reference in its entirety, including any drawings,

The term "monoclinic unit cell" refers to a unit

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cell where a \neq b \neq c; $\alpha = \gamma = 90^{\circ}$; and $\beta > 90^{\circ}$.

The term "space group" refers to the symmetry of a unit cell. In a space group designation (e.g., C2) the capital letter indicates the lattice type and the other symbols represent symmetry operations that can be carried out on the unit cell without changing its appearance.

The term "lattice" in reference to crystal structures refers to the array of points defined by the vertices of packed unit cells.

The term "symmetry operations" refers to geometrically defined ways of exchanging equivalent parts of a unit cell, or exchanging equivalent molecules between two different unit cells. Examples of symmetry operations are screw axes, centers of inversion, and mirror planes.

In a preferred embodiment, the invention features a crystalline form, where the monoclinic unit cells have dimensions of about a=208.3 Å, b=57.8 Å, c=65.5 Å and β =107.2°.

In a preferred embodiment, the invention features a FGFR1 crystal, where the monoclinic unit cells have dimensions of about a=211.6 Å, b=51.3 Å, c=66.1 Å and β =107.7°.

In another aspect the invention features a polypeptide corresponding to the catalytic domain of a protein tyrosine kinase, containing at least about 20 amino acid residues upstream of the first glycine in the conserved glycine-rich region of the catalytic domain, and at least about 17 amino acid residues downstream of the conserved arginine located at the C-terminal

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boundary of the catalytic domain.

The polypeptides of the invention can be isolated, enriched or purified. In addition, the crystalline forms of the invention can be formed from polypeptides that are isolated, enriched, or purified.

By "isolated" in reference to a polypeptide is meant a polymer of 6, 12, 18 or more amino acids conjugated to each other, including polypeptides that are isolated from a natural source or that are synthesized. The isolated polypeptides of the present invention are unique in the sense that they are not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only amino acid chain present, but that it is essentially free (about 90 - 95% pure at least) of material naturally associated with it.

By the use of the term "enriched" in reference to a polypeptide it is meant that the specific amino acid sequence constitutes a significantly higher fraction (2 - 5 fold) of the total of amino acids present in the cells or solution of interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other amino acids present, or by a preferential increase in the amount of the specific amino acid sequence of interest, or by a combination of the two. However, it should be noted that "enriched"

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does not imply that there are no other amino acid sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term significant here is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other amino acids of about at least 2 fold, more preferably at least 5 to 10 fold or even more. The term also does not imply that there are no amino acids from other sources. The other source amino acids may, for example, comprise amino acids encoded by a yeast or bacterial genome, or a cloning vector such as pUC19. The term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

It is also advantageous for some purposes that an amino acid sequence be in purified form. The term "purified" in reference to a polypeptide does not require absolute purity (such as a homogeneous preparation); instead, it represents an indication that the sequence is relatively purer than in the natural environment (compared to the natural level this level should be at least 2-5 fold greater, e.g., in terms of mg/ml). Purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. The substance is preferably free of contamination at a functionally significant level, for example 90%, 95%, or 99% pure.

In a preferred embodiment, the invention features a polypeptide corresponding to the catalytic domain of a

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receptor PTK. The receptor PTK may have a three-dimensional structure substantially similar to that of the insulin receptor, even though the amino acid content may be different.

In a preferred embodiment, the invention features a polypeptide corresponding to the catalytic domain of a non-receptor PTK, where the non-insulin receptor tyrosine kinase is a cytoplasmic tyrosine kinase.

In a preferred embodiment, the invention features a polypeptide corresponding to the catalytic domain of a receptor PTK, selected from the group consisting of FGF-R, PDGF-R, KDR, CCK4, MET, TRKA, AXL, TIE, EPH, RYK, DDR, ROS, RET, LTK, ROR1, or MUSK.

In a preferred embodiment, the invention features a polypeptide corresponding to the catalytic domain of a non-receptor PTK, selected from the group consisting of SRC, BRK, BTK, CSK, ABL, ZAP70, FES, FAK, JAK, or ACK.

In a preferred embodiment, the invention features a polypeptide corresponding to the catalytic domain of a PTK, having the amino acid sequence shown in Table 1 or Table 2.

In another aspect, the invention features a method for creating crystalline forms described herein. The method may utilize the polypeptides described herein to form a crystal. The method comprises the steps of:

- (a) mixing a volume of polypeptide solution with a reservoir solution; and
- (b) incubating the mixture obtained in step
 (a) over the reservoir solution in a closed container,
 under conditions suitable for crystallization.

These processes are described in detail in the

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section entitled "Detailed Description of the Invention."

In another aspect, the invention features a method of obtaining FGF receptor tyrosine kinase domain polypeptide in crystalline form, comprising the steps of: (a) mixing a volume of polypeptide solution with an equal volume of reservoir solution, where the polypeptide solution comprises 1 mg/mL to 60 mg/mL FGFtype tyrosine kinase domain protein, 10 mM to 200 mM buffering agent, 0 mM to 20 mM dithiothreitol and has a pH of about 5.5 to about 7.5, and where the reservoir solution comprises 10% to 30% (w/v) polyethylene glycol, 0.1 M to 0.5 M ammonium sulfate, 0% to 20% (w/v) ethylene glycol or glycerol, 10 mM to 200 mM buffering agent and has a pH of about 5.5 to about 7.5; and (b) incubating the mixture obtained in step (a) over said reservoir solution in a closed container at a temperature between 0° and 25°C until crystals form.

In a preferred embodiment, the invention features a method of obtaining FGF receptor tyrosine kinase domain polypeptide in crystalline form, where the polypeptide solution comprises about 10 mg/mL FGF receptor tyrosine kinase domain, about 10 mM sodium chloride, about 2 mM dithiothreitol, about 10 mM Tris-HCl and has a pH of about 8; the reservoir buffer comprises about 16% (w/v) polyethylene glycol (MW 10000), about 0.3 M ammonium sulfate, about 5% ethylene glycol or glycerol, about 100 mM bis-Tris and has a pH of about 6.5; and the temperature is about 4°C.

In another preferred embodiment, the invention features a method of obtaining FGF receptor tyrosine

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kinase domain polypeptide in crystalline form, where the polypeptide solution includes a compound such as a cofactor, substrate, substrate analog, inhibitor or allosteric effector.

In still another preferred embodiment, the invention features a method of obtaining FGF receptor tyrosine kinase domain polypeptide in crystalline form, where the compound is a nucleotide analog, such as a non-hydrolyzable analog of ATP, or an indolinone.

Indolinone compounds have the general structural formula as described herein.

In another aspect, the invention features a cDNA encoding an FGF receptor tyrosine kinase domain protein, where a coding strand of the cDNA has the nucleotide sequence of SEQ ID NO:5.

Another aspect of the invention relates to a method of determining three dimensional structures of PTKs with unknown structure by utilizing the structural coordinates of Table 1, Table 2, Table 3, and Table 4. These methods can relate to homology modeling, molecular replacement, and nuclear magnetic resonance methods.

In a preferred embodiment, the invention relates to a method of determining three dimensional structures of PTKs with unknown structures by utilizing the coordinates of Table 1, Table 2, Table 3, or Table 4 in conjunction with the amino acid sequences of PTKs. This method of homology modeling comprises the steps of: (a) aligning the computer representation of an amino acid sequence of a PTK with unknown structure with that of a PTK with known structure, where alignment is achieved by matching homologous regions of the amino acid sequences;

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(b) transferring the computer representation of an amino acid structure in the PTK sequence of known structure to a computer representation of a structure of the corresponding amino acid in the PTK sequence with unknown structure; and (c) determining low energy conformations of the resulting PTK structure.

The term "amino acid sequence" describes the order of amino acids in the amino acid chain comprising a polypeptide corresponding to the catalytic domain of a PTK.

The term "aligning" describes matching the beginning and the end of two or more amino acid sequences. Homologous amino acid sequences are placed on top of one another during the alignment process.

The term "homologous" describes amino acids in two sequences that are identical or have similar side-chain chemical groups (e.g., aliphatic, aromatic, polar, negatively charged, or positively charged).

The term "corresponding" refers to an amino acid that is aligned with another in the sequence alignment mentioned above.

The term "determining the low energy conformation" describes a process of changing the conformation of the PTK structure such that the structure is of low free energy. The PTK structure may or may not have molecules, such as modulators bound to it.

The term "low free energy" describes a state where the molecules are in a stable state as measured by the process. A stable state is achieved when favorable interactions are formed within the complex.

The term "favorable interactions" refers to

hydrophobic, aromatic, and ionic forces, and hydrogen bonds.

Another preferred embodiment of the invention relates to a method of determining three dimensional structures of PTKs with unknown structure. This method is accomplished by applying the structural coordinates of Table 1, Table 2, Table 3, or Table 4 to an incomplete X-ray crystallographic data set for a PTK. The method comprises the steps of: (a) aligning the positions of atoms in the unit cell by matching electron diffraction data from two crystals, where one data set is complete and the other is incomplete; and (b) determining a low energy conformation of the resulting PTK structure.

The term "incomplete data set" relates to a X-ray crystallographic data set that does not have enough information to give rise to a three dimensional structure.

In another preferred embodiment, the invention relates to a method of determining three dimensional structures of PTKs with unknown structure by applying the structural coordinates of Table 1, Table 2, Table 3, or Table 4 to nuclear magnetic resonance (NMR) data of a PTK. This method comprises the steps of: (a)

determining the secondary structure of a PTK structure using NMR data; and (b) simplifying the assignment of through-space interactions of amino acids. The PTK structure may not be complexed with compounds or modulators.

The term "secondary structure" describes the arrangement of amino acids in a three dimensional

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structure, such as in α -helix or β -sheet elements.

The term "through-space interactions" defines the orientation of the secondary structural elements in the three dimensional structure and the distances between amino acids from different portions of the amino acid sequence.

The term "assignment" defines a method of analyzing NMR data and identifying which amino acids give rise to signals in the NMR spectrum.

In another aspect, the invention features a method of identifying potential modulators of PTK function.

These modulators are identified by docking a computer representation of a structure of a compound with a computer representation of a cavity formed by the active-site of a PTK. The computer representation of the PTK active-site structure can be defined by structural coordinates.

The term "chemical group" refers to moieties that can form hydrogen bonds, hydrophobic, aromatic, or ionic interactions.

The term "docking" refers to a process of placing a compound in close proximity with a PTK. The term can also refer to a process of finding low energy conformations of the compound/PTK complex.

A preferred embodiment of the invention is a method of identifying potential modulators of PTK function.

The method involves utilizing the structural coordinates or a PTK three dimensional structure. The structural coordinates set forth in Table 1, Table 2, Table 3, and Table 4 can be utilized. The method comprises the steps of: (a) removing a computer representation of a PTK

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structure and docking a computer representation of a compound from a computer data base with a computer representation of the active-site of the PTK; (b) determining a conformation of the complex with a favorable geometric fit and favorable complementary interactions; and (c) identifying compounds that best fit the PTK active-site as potential modulators of PTK function. The initial PTK structure may or may not have compounds bound to it.

The term "favorable geometric fit" refers to a conformation of the compound-PTK complex where the surface area of the compound is in close proximity with the surface area of the active-site without forming unfavorable interactions. Unfavorable interactions can be steric hindrances between atoms in the compound and atoms in the PTK active-site

The term "favorable complementary interactions" relates to hydrophobic, aromatic, ionic, and hydrogen bond donating, and hydrogen bond accepting forces formed between the compound and the PTK active-site.

The term "potential" qualifies the term "modulator of PTK function" because the potential modulator or PTK function has not yet been tested for activity in vitro or in vivo.

The term "best fit" describes compounds that complexed the most surface area in the complex and/or form the most favorable complementary interactions with the PTK in the screen in a given experiment.

Another preferred embodiment of the invention is a method of identifying potential modulators of PTK function. The method involves utilizing a three

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dimensional structure of a PTK, with or without compounds bound to it. The method comprises the steps of: (a) modifying a computer representation of a PTK having one or more compounds bound to it, where the computer representations of the compound or compounds and PTK are defined by structural coordinates; (b) determining a conformation of the complex with a favorable geometric fit and favorable complementary interactions; and (c) identifying the compounds that best fit the PTK active-site as potential modulators of PTK function.

The term "modifying" relates to deleting a chemical group or groups or adding a chemical group or groups.

Computer representations of the chemical groups can be selected from a computer data base.

Yet another preferred embodiment of the invention is a method of identifying potential modulators of PTK function by operating modulator construction or modulator searching computer programs on the compounds complexed with the PTK. The method comprises the steps of: (a) removing a computer representation of one or more compounds complexed with a PTK; and (b) searching a data base for compounds similar to the removed compounds using a compound searching computer program, or replacing portions of the compounds complexed with the PTK with similar chemical structures from a data base using a compound construction computer program, where the representations of the compounds are defined by structural coordinates.

The term "operating" as used herein refers to utilizing the three-dimensional conformation of

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molecules defined by the processes described herein in various computer programs.

The term "similar compound" refers to a compound in a computer data base that has a similar geometric structure as compounds that can bind to a PTK. The similar compound can also have similar chemical groups as the compounds that are either bound to the PTK or once bound to the PTK. The similar chemical groups can form complementary interactions with the PTK.

The term "compound searching computer program"

describes a computer program that searches computer
representations of compounds from a computer data base
that have similar three dimensional structures and
similar chemical groups as a compound of interest. The
compound of interest is preferably an indolinone
compound.

The term "similar chemical structures" refers to chemical groups that share similar geometry as portions of the compounds in complex with the PTK or compounds removed from the PTK structure. Similar chemical structures can also refer to chemical groups that may form similar complementary interactions as portions of the compounds in complex with the PTK or compounds removed from the PTK structure.

The term "replacing structures" refers to removing a portion of the compounds in complex with the PTK or compounds removed from the PTK structure and connecting the broken bonds to a similar chemical structure.

The term "compound construction computer program"

describes a computer program that replaces computer representations of chemical groups in a compound with

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groups from a computer data base. The compound is preferably an indolinone compound.

The term "similar three dimensional structure" describes two molecules with nearly identical shape and volume.

In another preferred embodiment of the invention, the PTK structures used in the modulator design or identification method of the invention are defined by the structural coordinates of Table 1, Table 2, Table 3, or Table 4.

The methods for using the crystalline forms and three dimensional structures of the invention can relate to a broad range of protein kinases. Thus, in preferred embodiments, the invention relates to a receptor PTK. The receptor PTK can be selected form the group consisting of FGF-R, PDGF-R, FLK, CCK4, MET, TRKA, AXL, TIE, EPH, RYK, DDR, ROS, RET, LTK, ROR1, and MUSK. The PTK may also exist as a non-receptor PTK. The non-receptor PTK can be selected from the group consisting of SRC, BRK, BTK, CSK, ABL, ZAP70, FES, FAK, JAK, and

In another aspect, the invention features a potential modulator of PTK function identified by methods disclosed in the invention.

A preferred embodiment of the invention is that the potential modulator of PTK function is an oxindolinone or a thiolindolinone of formula I or II disclosed above.

Another aspect of the invention is a method for synthesizing a potential modulator of PTK function or its pharmaceutically acceptable salts, isomers, metabolites, esters, amides, or prodrugs by a standard

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synthetic method known in the art. Synthetic procedures are discussed below.

In another aspect, the invention features a method of identifying a potential modulator of PTK function as a modulator of PTK function. The method comprises the steps of: (a) administering a potential modulator of PTK function to cells; (b) comparing the level of PTK phosphorylation between cells not administered the potential modulator and cells administered the potential modulator; and (c) identifying the potential modulator as a modulator of PTK function based on the difference in the level of PTK phosphorylation.

The term "cells" refers to any type of cells either primary or cultured. Primary cells can be extracted directly from an organism while cultured cells rapidly divide and can be cultured in many successive rounds. Cells can be grown in a variety of containers including, but not limited to flasks, dishes, and well plates.

The term "administer" refers to a method of

delivering a compound to cells. The compound can be

prepared using a carrier such as dimethyl sulfoxide

(DMSO) in an aqueous solution. The aqueous solution

comprising the compound, also termed an "aqueous

preparation", can be simply mixed into the medium

bathing the layer of cells or microinjected into the

cells themselves. The compounds may be administered to

the cells using a suitable buffered solution.

The term "suitable buffered solution" refers to an aqueous preparation of the compound that comprises a salt that can control the pH of the solution at low concentrations. Because the salt exists at low

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concentrations, the salt preferably does not alter the function of the cells.

The term "PTK phosphorylation" refers to the presence of phosphate on the PTK. Phosphates on PTKs can be identified by antibodies that bind them specifically with high affinity.

In another aspect, the invention features a method of identifying a potential modulator of PTK function as a modulator of PTK function. The method comprises the steps of: (a) administering a potential modulator of PTK function to cells; (b) comparing the level of cell growth between cells not administered the potential modulator and cells administered the potential modulator; and (c) identifying the potential modulator as a modulator of PTK function based on the difference in cell growth.

The term "cell growth" refers to the rate at which a group of cells divides. Cell division rates can be readily measured by methods utilized by those skilled in the art.

Another aspect of the invention features a method of diagnosing a disease by identifying cells harboring a PTK with inappropriate activity. The method comprises the steps of: (a) administering a modulator of PTK function to cells; (b) comparing the rate of cell growth between cells not administered the modulator and cells administered the modulator; and (c) diagnosing a disease by characterizing cells harboring a PTK with inappropriate activity from the effect of the modulator on the difference in the rate of cell growth. The modulator can be identified by the methods of the

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invention.

The term "inappropriate activity" refers to a PTK that regulates a step in a signal transduction process at a higher or lower rate than normal cells.

Aberrations in the rate of signal transduction can be caused by alterations in the stimulation of a receptor PTK by a growth factor, alterations in the activity of PTK-specific phosphatase, over-expression of a PTK in a cell, or mutations in the catalytic region of the PTK itself.

The term "signal transduction process" describes the steps in a cascade of events where an extracellular signal is transmitted into an intracellular signal.

The term "PTK-specific phosphatase" describes an enzyme that dephosphorylates a particular PTK and thereby regulates that PTK's activity.

Another aspect of the invention is a method of treating a disease associated with a PTK with inappropriate activity in a cellular organism, where the method comprises the steps of: (a) administering the modulator of PTK function to the organism, where the modulator is in an acceptable pharmaceutical preparation; and (b) activating or inhibiting the PTK function to treat the disease.

The term "organism" relates to any living being comprised of at least one cell. An organism can be as simple as one eukaryotic cell or as complex as a mammal.

The term "administering", in reference to an organism, refers to a method of introducing the compound to the organism. The compound can be administered when the cells or tissues of the organism exist within the

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organism or outside of the organism. Cells existing outside the organism can be maintained or grown in cell culture dishes. For cells harbored within the organism, many techniques exist in the art to administer compounds, including (but not limited to) oral, parenteral, dermal, and injection applications. For cells outside of the patient, multiple techniques exist in the art to administer the compounds, including (but not limited to) cell microinjection techniques,

10 transformation techniques, and carrier techniques.

The term "pharmaceutically acceptable composition" refers to a preparation comprising the modulator of PTK activity. The composition is acceptable if it does not appreciably cause irritations to the organism administered the compound.

Preferred embodiments of the of the invention are that the PTK is a receptor PTK selected from the group consisting of FGF-R, PDGF-R, FLK-1, CCK4, MET, TRKA, AXL, TIE, EPH, RYK, DDR, ROS, RET, LTK, ROR1, and MUSK. Other preferred embodiments of the invention are that the PTK is a non-receptor PTK selected from the group consisting of SRC, BRK, BTK, CSK, ABL, ZAP70, FES, FAK, JAK, and ACK.

The summary of the invention described above is non-limiting and other features and advantages of the invention will be apparent from the following detailed description, and from the claims.

BRIEF DESCRIPTION OF THE FIGURES

30 FIG. 1 provides a ribbon diagram of the structure of FGFR1 showing the side chains of tyrosines Tyr-653

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and Tyr-654 and the α helical (α C, α D, α E, α EF, α F- α I), β strand (β 1- β 5, β 7, β 8), nucleotide-binding loop, catalytic loop, activation loop and kinase insert regions of the molecule. The termini are denoted by N and C. The loop between β 2 and β 3 is disordered, indicated by a break in the chain in this region.

FIG. 2 provides a stereo view of a C_{α} trace of FGFR1 shown in the same orientation as FIG. 1, with every tenth amino acid residue marked with a filled circle and every twentieth amino acid residue labeled with a residue number.

FIG. 3 provides a structure-based sequence alignment of human fibroblast growth factor receptor 1 (FGFR1), human fibroblast growth factor receptor 2 (FGFR2), human fibroblast growth factor receptor 3 (FGFR3), human fibroblast growth factor receptor 4 (FGFR4), a D. malanogaster homolog (DFGFR1), a C. elegans homolog (EGL-15) and insulin receptor tyrosine kinase (IRK).

FIGS. 4A and 4B provide ribbon diagrams of the N-terminal lobes (4A) and C-terminal lobes (4B) of FGFR1 and IRK in which the C_{α} atoms of the β sheets (4A) or α -helices (4B) of the two proteins have been superimposed.

FIG. 5 illustrates the side-chain positions of the tyrosine autophosphorylation sites of FGFR1 on the backbone representation of FGFR1.

FIGS. 6A and 6B are amino acid sequence alignments of the catalytic domains of PTKs, including receptor and non-receptor type PTKs. FIG. 6A depicts one

representative member from each of the eighteen subfamilies of receptor tyrosine kinases. FIG. 6B

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depicts one representative member from each of the subfamilies of cytoplasmic tyrosine kinases. In FIGS. 6A and 6B highly conserved residues are boxed. The position of the glycine-rich domain, kinase insert, catalytic loop, and activation loop are indicated. The numbering is for human FGF-receptor.

BRIEF DESCRIPTION OF THE CRYSTALLOGRAPHIC ATOMIC STRUCTURAL COORDINATES

10 The crystallographic structural coordinates are located at the end of the section entitled "Examples" and before the claims. Three sets of coordinates can be found in the Protein Data Bank under accession names 1FGK, 1AGW, and 1FGI. The 1FGK coordinates correspond to those listed in Table 1, the 1AGW coordinates correspond to those listed in Table 4, and the 1FGI coodinates correspond to those listed in Table 3. The 1AGW and 1FGI coordinate sets will be publically available in March 1998.

Table 1 provides the atomic structure coordinates of native FGFR1 crystals of the invention as determined by X-ray crystallography; and

Table 2 provides the atomic structure coordinates of FGFR1:AMP-PCP co-crystals of the invention as determined by X-ray crystallography.

Table 3 lists crystallographic coordinates defining the three dimensional structure of FGF-R1 complexed with 3-[(3-(2-carboxyethyl)-4-methylpyrrol-5-yl)methylene]-2-indolinone. The columns (from left to right) are descriptions of the atoms by number and type, amino acid and number containing the atom, the x coordinate, y

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coordinate, z coordinate, bond connectivity, and temperature factor. All of these parameters are well defined in the art.

Table 4 is a file of crystallographic coordinates defining the three dimensional structure of FGF-R1 complexed with 3-[4-(4-formylpiperazine-1-yl) benzylidenyl]-2-indolinone. The columns are as described in Table 3.

10 <u>DETAILED DESCRIPTION OF THE INVENTION</u>

The present invention is directed to the design and identification of modulators of protein tyrosine kinase function that are PTK subfamily specific, non-hydrolyzable under acidic conditions, and highly bioavailable. The three dimensional structures of a PTK optionally complexed with compounds can facilitate design and identification of modulators of PTK function.

Protein tyrosine kinases (PTKs) comprise a large and diverse class of enzymes. Schlessinger and Ullrich, 1992, Neuron 9: 383-391. The PTK family is subdivided into members that are receptors and those that are non-receptors. The PTK receptor family contains multiple subfamilies, one of which is the fibroblast growth factor receptor (FGF-R) PTK which is a molecule implicated in regulating angiogenesis a well as cellular proliferation and differentiation. Givol and Yayon, 1992, FASEB J. 6 (15): 3362-3369.

FGF-R1 can mediates cellular functions by its role in one or more cellular signal transduction processes.

Cellular signal transduction processes comprise multiple steps that convert an extracellular signal into an

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intracellular signal.

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Receptor PTK mediated signal transduction is initiated by binding a specific extracellular ligand, followed by receptor dimerization, and subsequent autophosphorylation of the receptor PTK. The phosphate groups are binding sites for intracellular signal transduction molecules which leads to the formation of protein complexes at the cell membrane. These complexes facilitate an appropriate cellular effect (e.g., cell division, metabolic effects to the extracellular microenvironment) in response to the ligand that began the cascade of events.

Receptor PTKs function as binding sites for several intracellular proteins. Intracellular PTK binding proteins are divided into two principal groups: (1) those which harbor a catalytic domain; and (2) those which lack such a domain but serve as adapters and associate with catalytically active molecules. Songyang et al., 1993, Cell 72:767-778. SH2 (src homology) domains are common adaptors found in proteins which directly bind to the receptor PTK. SH2 domains are harbored by PTK binding proteins of both groups mentioned above. Fantl et al., 1992, Cell 69:413-423; Songyang et al., 1994, Mol. Cell. Biol. 14:2777-2785); Songyang et al., 1993, Cell 72:767-778; and Koch et al., 1991, Science 252:668-678.

The specificity of the interactions between receptor PTKs and the SH2 domains of their binding proteins is determined by the amino acid residues immediately surrounding the phosphorylated tyrosine residue. Differences in the binding affinities of SH2

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domains is correlated with the observed differences in substrate phosphorylation profiles of downstream molecules in the signal transduction process. Songyang et al., 1993, Cell 72:767-778. These observations suggest that the function of each receptor PTK is determined not only by its pattern of expression and ligand availability but also by the array of downstream signal transduction pathways that are activated by a particular receptor. Thus, PTKs provide a controlling regulatory role in signal transduction processes as a consequence of autophosphorylation.

PTK-mediated signal transduction regulates cell proliferative, differentiation, and metabolic responses in cells. Therefore, inappropriate PTK activity can result in a wide array of disorders and diseases. These disorders, which are described below, may be treated by the modulators of PTK function designed or identified by the methods disclosed herein.

The present invention also relates to crystalline polypeptides corresponding to the catalytic domain of 20 receptor tyrosine kinases. Such tyrosine kinases include receptors of a class that are not covalently cross-linked but are understood to undergo ligandinduced dimerization, as well as cytoplasmic tyrosine 25 Preferably, the crystalline catalytic domains are of sufficient quality to allow for the determination of a three-dimensional X-ray diffraction structure to a resolution of about 1.5 Å to about 2.5 Å. The invention also relates to methods for preparing and crystallizing the polypeptides. The polypeptides themselves, as well 30 as information derived from their crystal structures can

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be used to analyze and modify tyrosine kinase activity as well as to identify compounds that interact with the catalytic domain.

The polypeptides of the invention are designed on 5 the basis of the structure of a region in the cytoplasmic domain of the receptor tyrosine kinase that contains the catalytic domain. By way of illustration, FIG. 6A shows the amino acid sequence alignment of the catalytic domains of eighteen human receptor tyrosine 10 kinases; one representative member from each of the eighteen subfamilies is shown. FIG. 6B shows the alignment for cytoplasmic kinases. The applicants have discovered and determined the boundaries of the domain required for crystallization of the resulting 15 polypeptide. Surprisingly, these boundaries differ from that required for catalytic activity. For example, referring to FIG. 6A, the domain required for catalytic activity is generally believed to span about 7 amino acid residues upstream of the first glycine (FIG. 6A 20 residue number 485) of the N-terminal glycine-rich region through about 10 residues beyond the C-terminal conserved arginine (FIG. 6A, residue number 744). However, the additional sequence upstream of the Nterminal glycine-rich region and downstream of the C-25 terminal conserved arginine can be required for crystallization. In particular, at least about 20 amino acid residues (+/- 5 amino acid residues) upstream of the first glycine (i.e., FIG. 6A, residue number 485) in the conserved glycine-rich region of the catalytic 30 domain, and at least about 17 amino acid residues (+/- 5

amino acid residues) downstream of the conserved

arginine (<u>i.e.</u>, FIG. 6A, residue number 744) located at the C-terminal boundary of the catalytic domain can be required to engineer a polypeptide suitable for crystallization.

5 In those situations where the resulting polypeptide contains cysteine residues that interfere with crystallization (e.g., cysteine residue numbers 488 and 584 in the FGF-R1 sequence shown in FIG. 6A), such cysteine residues can be substituted with an appropriate amino acid that does not readily form covalent bonds 10 with other amino acid residues under crystallization conditions; e.g., by substituting the cysteine with Ala, Ser or Gly. Any cysteine located in a non-helical or $non-\beta$ -stranded segment, based on secondary structure 15 assignments, are good candidates for replacement. For example, cysteines located in regions corresponding to the glycine-rich-loop, the kinase insert, the juxtamembrane region or the activation loop are prime candidates for replacement. However, substitutions of cysteine residues that are conserved among the kinases 20 (e.g., FIG. 6A at positions 725 and 736) are preferably avoided.

I. PTK Associated Diseases

Blood vessel proliferative disorders refer to angiogenic and vasculogenic disorders generally resulting in abnormal proliferation of blood vessels. The formation and spreading of blood vessels play important roles in a variety of physiological processes such as embryonic development, corpus luteum formation, wound healing and organ regeneration. They also play a

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pivotal role in cancer development. Other examples of blood vessel proliferation disorders include arthritis, where new capillary blood vessels invade the joint and destroy cartilage, and ocular diseases, like diabetic retinopathy, where new capillaries in the retina invade the vitreous, bleed and cause blindness. Conversely, disorders related to the shrinkage, contraction or closing of blood vessels are implicated in such diseases as restenosis.

Fibrotic disorders refer to the abnormal formation of extracellular matrix. Examples of fibrotic disorders include hepatic cirrhosis and mesangial cell proliferative disorders. Hepatic cirrhosis is characterized by the increase in extracellular matrix constituents resulting in the formation of a hepatic scar. Hepatic cirrhosis can cause diseases such as cirrhosis of the liver. An increased extracellular matrix resulting in a hepatic scar can also be caused by viral infection such as hepatitis.

Mesangial cell proliferative disorders refer to disorders brought about by abnormal proliferation of mesangial cells. Mesangial proliferative disorders include various human renal diseases, such as glomerulonephritis, diabetic nephropathy, malignant nephrosclerosis, thrombotic microangiopathy syndromes, transplant rejection, and glomerulopathies. The PDGF-R has been implicated in the maintenance of mesangial cell proliferation. Floege et al., 1993, Kidney International 43:47S-54S.

PTKs are directly associated with the cell proliferative disorders described above. For example,

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46 some members of the receptor PTK family have been associated with the development of cancer. Some of these receptors, like EGFR (Tuzi et al., 1991, Br. J. Cancer 63:227-233; Torp et al., 1992, APMIS 100:713-719) HER2/neu (Slamon et al., 1989, Science 244:707-712) and PDGF-R (Kumabe et al., 1992, Oncogene 7:627-633) are over-expressed in many tumors and/or persistently activated by autocrine loops. In fact, PTK overexpression (Akbasak and Suner-Akbasak et al., 1992, J. Neurol. Sci. 111:119-133; Dickson et al., 1992, Cancer Treatment Res. 61:249-273; Korc et al., 1992, J. Clin. Invest. 90:1352-1360) and autocrine loop stimulation (Lee and Donoghue, 1992, J. Cell. Biol. 118:1057-1070; Korc et al., supra; Akbasak and Suner-Akbasak et al., supra) account for the most common and severe cancers. For example, EGFR is associated with squamous cell carcinoma, astrocytoma, glioblastoma, head and neck cancer, lung cancer and bladder cancer. HER2 is associated with breast, ovarian, gastric, lung, pancreas and bladder cancer. PDGF-R is associated with glioblastoma, lung, ovarian, melanoma and prostate The receptor PTK c-met is generally associated with hepatocarcinogenesis and thus hepatocellular carcinoma. Additionally, c-met is linked to malignant tumor formation. More specifically, c-met has been associated with, among other cancers, colorectal, thyroid, pancreatic and gastric carcinoma, leukemia and lymphoma. Additionally, over-expression of the c-met gene has been detected in patients with Hodgkins disease, Burkitts disease, and the lymphoma cell line. The IGF-I receptor PTK, in addition to being

implicated in nutritional support and in type-II diabetes, is also associated with several types of cancers. For example, IGF-I has been implicated as an autocrine growth stimulator for several tumor types, e.g. human breast cancer carcinoma cells (Arteaga et al., 1989, J. Clin. Invest. 84:1418-1423) and small lung tumor cells (Macauley et al., 1990, Cancer Res. 50:2511-In addition, IGF-I, integrally involved in the normal growth and differentiation of the nervous system, appears to be an autocrine stimulator of human gliomas. Sandberg-Nordqvist et al., 1993, Cancer Res. 53:2475-The importance of the IGF-IR and its modulators in cell proliferation is further supported by the fact that many cell types in culture (fibroblasts, epithelial cells, smooth muscle cells, T-lymphocytes, myeloid cells, chondrocytes, osteoblasts, the stem cells of the bone marrow) are stimulated to grow by IGF-I. Goldring and Goldring, 1991, Eukaryotic Gene Expression 1:301-In a series of recent publications suggest that IGF-IR plays a central role in the mechanisms of transformation and, as such, could be a preferred target for therapeutic interventions for a broad spectrum of human malignancies. Baserga, 1995, Cancer Res. 55:249-252; Baserga, 1994, Cell 79:927-930; Coppola et al., 1994, Mol. Cell. Biol. 14:4588-4595.

The association between abnormalities in receptor PTKs and disease are not restricted to cancer, however. For example, receptor PTKs are associated with metabolic diseases like psoriasis, diabetes mellitus, wound healing, inflammation, and neurodegenerative diseases. EGF-R is indicated in corneal and dermal wound healing.

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Defects in Insulin-R and IGF-IR are indicated in type-II diabetes mellitus. A more complete correlation between specific receptor PTKs and their therapeutic indications is set forth in Plowman et al., 1994, DN&P 7:334-339.

5 Non-receptor PTKs, including src, abl, fps, yes, fyn, lyn, lck, blk, hck, fgr, yrk (reviewed by Bolen et al., 1992, FASEB J. 6:3403-3409), are involved in the proliferative and metabolic signal transduction pathways also associated with receptor PTKs. Therefore, the 10 present invention is also directed towards designing modulators against this class of PTKs. For example, mutated src (v-src) is an oncoprotein (pp60 $^{v-src}$) in chicken. Moreover, its cellular homolog, the protooncogene pp60 $^{\text{c-src}}$ transmits oncogenic signals of many 15 receptors. For example, over-expression of EGF-R or HER2/neu in tumors leads to the constitutive activation of $pp60^{c-src}$, which is characteristic of the malignant cell but absent in the normal cell. On the other hand, mice deficient for the expression of c-src exhibit an osteopetrotic phenotype, indicating a key participation of c-src in osteoclast function and a possible involvement in related disorders. Similarly, Zap 70 is implicated in T-cell signaling. Both receptor PTKs and non-receptor PTKs are connected to hyperimmune disorders.

The instant invention is directed in part towards designing modulators of PTK function that could indirectly kill tumors by cutting off their source of sustenance. Normal vasculogenesis and angiogenesis play important roles in a variety of physiological processes such as embryonic development, wound healing, organ

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regeneration and female reproductive processes such as follicle development in the corpus luteum during ovulation and placental growth after pregnancy. Folkman and Shing, 1992, J. Biological Chem. 267:10931-34.

However, many diseases are driven by persistent unregulated or inappropriate angiogenesis. For example, in arthritis, new capillary blood vessels invade the joint and destroy the cartilage. In diabetes, new capillaries in the retina invade the vitreous, bleed and cause blindness. Folkman, 1987, in: Congress of Thrombosis and Haemostasis (Verstraete, et. al, eds.), Leuven University Press, Leuven, pp.583-596. Ocular neovascularization is the most common cause of blindness and dominates approximately twenty (20) eye diseases.

Moreover, vasculogenesis and/or angiogenesis can be associated with the growth of malignant solid tumors and metastasis. A tumor must continuously stimulate the growth of new capillary blood vessels for the tumor itself to grow. Furthermore, the new blood vessels embedded in a tumor provide a gateway for tumor cells to enter the circulation and to metastasize to distant sites in the body. Folkman, 1990, J. Natl. Cancer Inst. 82:4-6; Klagsbrunn and Soker, 1993, Current Biology 3:699-702; Folkman, 1991, J. Natl., Cancer Inst. 82:4-6; Weidner et al., 1991, New Engl. J. Med. 324:1-5.

Several polypeptides with in vitro endothelial cell growth promoting activity have been identified. Examples include acidic and basic fibroblastic growth factor (α FGF, β FGF), vascular endothelial growth factor (VEGF) and placental growth factor. Unlike α FGF and β FGF, VEGF has recently been reported to be an

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endothelial cell specific mitogen. Ferrara and Henzel, 1989, Biochem. Biophys. Res. Comm. 161:851-858; Vaisman et al., 1990, J. Biol. Chem. 265:19461-19566.

Thus, identifying the specific receptors that bind 5 FGF or VEGF is important for understanding endothelial cell proliferation regulation. Two structurally related receptor PTKs that bind VEGF with high affinity are identified: the flt-1 receptor (Shibuya et al., 1990, Oncogene 5:519-524; De Vries et al., 1992, Science

255:989-991) and the KDR/FLK-1 receptor, discussed in 10 the U.S. Patent Application No. 08/193,829. addition, a receptor that binds αFGF and βFGF is identified. Jaye et al., 1992, Biochem. Biophys. Acta 1135:185-199). Consequently, these receptor PTKs most

likely regulate endothelial cell proliferation. 15

FGFRs play important roles in angiogenesis, wound healing, embryonic development, and malignant transformation. Basilico and Moscatelli, 1992, Adv. Cancer Res. 59:115-165. Four mammalian FGFR (FGFR1-4)

- have been described and additional diversity is 20 generated by alternative RNA splicing within the extracellular domains. Jaye et al., 1992, Biochem. Biophys. Acta 1135:185-199. Like other receptor PTKs, dimerization of FGF receptors is essential for their
- activation. Soluble or cell surface-bound heparin 25 sulfate proteoglycans act in concert with FGF to induce dimerization (Schlessinger et al., 1995, Cell 83:357-360), which leads to autophosphorylation of specific tyrosine residues in the cytoplasmic domain. 30 et al., 1996, Mol. Cell Biol. 16:977-989.

Mutations in three human FGF receptor genes, FGFR1,

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FGFR2, and FGFR3, have been implicated in a variety of human genetic skeletal disorders. Mutations in FGFR1 and FGFR2 result in the premature fusion of the flat bones of the skull and cause the craniosynostosis syndromes, such as Apert (FGFR2) (Wilkie et al., 1994, Nat. Genet. 8:269-274), Pfeiffer (FGFR1 and FGFR2) (Muenke et al., 1994, Nat. Genet. 8:269-274), Jackson-Weiss (FGFR2) (Jabs et al., 1994, Nat. Genet. 8:275-279) and Crouzon (FGFR2) (Jabs et al., 1994, Nat. Genet. 8:275-279) syndromes. In contrast mutations in FGFR3 are implicated in long bone disorders and cause several clinically related forms of dwarfism including achondroplasia (Shiang et al., 1994, Cell 78:335-342), hypochondroplasia (Bellus et al., 1995, Nat. Genet. 10:357-359) and the neonatal lethal thanatophoric dysplasia (Tavormina et al., 1995, Nat. Genet. 9:321-328). It has been shown that these mutations lead to constitutive activation of the tyrosine kinase activity of FGFR3 (Webster et al., 1996, EMBO J. 15:520-527). Furthermore gene-targeting experiments in mice have revealed an essential role for FGFR3 in developmental bone formation (Deng et al., 1996, Cell 84:911-921).

Another major role proposed for FGFs in vivo is the induction of angiogenesis (Folkman and Klagsbrun, 1987, Science 236:442). Therefore, inappropriate expression of FGFs or of their receptors or aberrant function of the tyrosine kinase activity could contribute to several human angiogenic pathologies such as diabetic retinopathy, rheumatoid arthritis, atherosclerosis and tumor neovascularization (Klagsbrun and Edelman, 1989, Arteriosclerosis 9:269). Moreover, FGFs are thought to

be involved in malignant transformation. Indeed, the genes coding for the three FGF homologues int-2, FGF-5 and hst-1/K-fgf were originally isolated as oncogenes. Furthermore, the cDNA encoding FGFR1 and FGFR2 are amplified in a population of breast cancers (Adnane et al., 1991, Oncogene 6:659-663). Over-expression of FGF receptors has been also detected in human pancreatic cancers, astrocytomas, salivary gland adenosarcomas, Kaposi sarcomas, ovarian cancers and prostate cancers.

10 Evidence, such as the disclosure set forth in copending U.S. Application Serial No. 08/193,829, strongly suggests that VEGF is not only responsible for endothelial cell proliferation, but also is a prime regulator of normal and pathological angiogenesis. See 15 generally, Klagsburn and Soker, 1993, Current Biology 3:699-702; Houck et al., 1992, J. Biol. Chem. 267:26031-26037. Moreover, it has been shown that KDR/FLK-1 and flt-1 are abundantly expressed in the proliferating endothelial cells of a growing tumor, but not in the surrounding quiescent endothelial cells. 20 Plate et al., 1992, Nature 359:845-848; Shweiki et al., 1992, Nature 359:843-845.

The invention is directed to designing and identifying modulators of receptor and non-receptor PTK functions that could modify the inappropriate activity of a PTK involved with a clinical disorder. The rational design and identification of modulators of PTK functions can be accomplished by utilizing the structural coordinates that define a PTK three

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II. <u>Modulators of PTK functions as Therapeutics for</u> Disease

As a consequence of the disorders discussed above, scientists in the biomedical community are searching for modulators of PTK functions that down-regulate signal transduction pathways associated with inappropriate PTK activity.

In particular, small molecule modulators of PTK functions are sought as some can traverse the cell membrane and do not hydrolyze in acidic environments. Some compounds have already been discovered. For example, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642), vinylene-azaindole derivatives (PCT WO 94/14808) 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427), tricyclic polyhydroxylic compounds (PCT WO 92/21660), and benzylphosphonic acid compounds (PCT WO 91/15495) are described as PTK inhibitors.

Although some modulators of PTK function are known, many of these are not specific for PTK subfamilies and will therefore cause multiple side-effects as therapeutics. Compounds of the oxindolinone/ thiolindolinone family, however, are specific for the FGF receptor subfamily (U.S. Patent Application Serial No. 08/702,232, filed August 23, 1996, invented by Tang et al., entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of

Disease," Attorney Docket No. 221/187). In addition, compounds of the oxindolinone/thiolindolinone family are non-hydrolyzable in acidic conditions and can be highly bioavailable.

5 The invention provides information regarding the specific interactions between a PTK and compounds of the oxindolinone/thiolindolinone family. Although the use of X-ray crystallography has provided three dimensional structures of other PTKs, the PTKs in these structures are not complexed with PTK subfamily specific, 10 hydrolysis resistant, highly bioavailable small molecules. The X-ray crystallography techniques used in the current invention resolve interactions between a PTK and compounds in complex with it at the atomic level, which provides detailed information regarding the 15 orientation of chemical groups defining an effective modulator of PTK function.

III. Crystalline Tyrosine Kinases

Crystalline PTKs of the invention include native crystals, derivative crystals and co-crystals. The native crystals of the invention generally comprise substantially pure polypeptides corresponding to the tyrosine kinase domain in crystalline form.

It is to be understood that the crystalline tyrosine kinase domains of the invention are not limited to naturally occurring or native tyrosine kinase domains. Indeed, the crystals of the invention include mutants of native tyrosine kinase domains. Mutants of native tyrosine kinase domains are obtained by replacing at least one amino acid residue in a native tyrosine

kinase domain with a different amino acid residue, or by adding or deleting amino acid residues within the native polypeptide or at the N- or C-terminus of the native polypeptide, and have substantially the same three-dimensional structure as the native tyrosine kinase domain from which the mutant is derived.

By having substantially the same three-dimensional structure is meant having a set of atomic structure coordinates that have a root-mean-square deviation of less than or equal to about 2\AA when superimposed with the atomic structure coordinates of the native tyrosine kinase domain from which the mutant is derived when at least about 50% to 100% of the $C\alpha$ atoms of the native tyrosine kinase domain are included in the superposition.

Amino acid substitutions, deletions and additions which do not significantly interfere with the three-dimensional structure of the tyrosine kinase domain will depend, in part, on the region of the tyrosine kinase domain where the substitution, addition or deletion occurs. In highly variable regions of the molecule, such as those shown in FIG. 6, non-conservative substitutions as well as conservative substitutions may be tolerated without significantly disrupting the three-dimensional structure of the molecule. In highly conserved regions, or regions containing significant secondary structure, such as those regions shown in FIG. 6, conservative amino acid substitutions are preferred.

Conservative amino acid substitutions are wellknown in the art, and include substitutions made on the basis of similarity in polarity, charge, solubility,

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hydrophobicity, hydrophilicity and/or the amphipathic nature of the amino acid residues involved. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; amino acids with uncharged polar head groups having similar hydrophilicity values include the following: leucine, isoleucine, valine; glycine, alanine; asparagine, glutamine; serine, threonine; phenylalanine, tyrosine. Other conservative amino acid substitutions are well known in the art.

For tyrosine kinase domains obtained in whole or in part by chemical synthesis, the selection of amino acids available for substitution or addition is not limited to the genetically encoded amino acids. Indeed, the mutants described herein may contain non-genetically encoded amino acids. Conservative amino acid substitutions for many of the commonly known non-genetically encoded amino acids are well known in the art. Conservative substitutions for other amino acids can be determined based on their physical properties as compared to the properties of the genetically encoded amino acids.

In some instances, it may be particularly advantageous or convenient to substitute, delete and/or add amino acid residues to a native tyrosine kinase domain in order to provide convenient cloning sites in cDNA encoding the polypeptide, to aid in purification of the polypeptide, and for crystallization of the polypeptide. Such substitutions, deletions and/or additions which do not substantially alter the three dimensional structure of the native tyrosine kinase

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domain will be apparent to those of ordinary skill in the art.

It should be noted that the mutants contemplated herein need not exhibit PTK activity. Indeed, amino acid substitutions, additions or deletions that interfere with the kinase activity of the tyrosine kinase domain but which do not significantly alter the three-dimensional structure of the domain are specifically contemplated by the invention. Such crystalline polypeptides, or the atomic structure coordinates obtained therefrom, can be used to identify compounds that bind to the native domain. These compounds may affect the activity or the native domain.

The derivative crystals of the invention generally comprise a crystalline tyrosine kinase domain polypeptide in covalent association with one or more heavy metal atoms. The polypeptide may correspond to a native or a mutated tyrosine kinase domain. Heavy metal atoms useful for providing derivative crystals include, by way of example and not limitation, gold, mercury, etc.

The co-crystals of the invention generally comprise a crystalline tyrosine kinase domain polypeptide in association with one or more compounds. The association may be covalent or non-covalent. Such compounds include, but are not limited to, cofactors, substrates, substrate analogues, inhibitors, allosteric effectors, etc.

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IV. Three Dimensional Structure Determination Using X-ray Crystallography

X-ray crystallography is a method of solving the three dimensional structures of molecules. The structure of a molecule is calculated from X-ray diffraction patterns using a crystal as a diffraction grating. Three dimensional structures of protein molecules arise from crystals grown from a concentrated aqueous solution of that protein. The process of X-ray crystallography can include the following steps:

- (a) synthesizing and isolating a polypeptide;
- (b) growing a crystal from an aqueous solution comprising the polypeptide with or without a modulator; and
- (c) collecting X-ray diffraction patterns from the crystals, determining unit cell dimensions and symmetry, determining electron density, fitting the amino acid sequence of the polypeptide to the electron density, and refining the structure.

Production of Polypeptides

The native and mutated tyrosine kinase domain

polypeptides described herein may be chemically
synthesized in whole or part using techniques that are
well-known in the art (see, e.g., Creighton, 1983).

Alternatively, methods which are well known to those
skilled in the art can be used to construct expression
vectors containing the native or mutated tyrosine kinase
domain polypeptide coding sequence and appropriate

transcriptional/translational control signals. These methods include in vitro recombinant DNA techniques, synthetic techniques and in vivo recombination/genetic recombination. See, for example, the techniques described in Maniatis et al., 1989 and Ausubel et al.,

A variety of host-expression vector systems may be 1989. utilized to express the tyrosine kinase domain coding These include but are not limited to sequence. microorganisms such as bacteria transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing the tyrosine kinase domain coding sequence; yeast transformed with recombinant yeast expression vectors containing the tyrosine kinase domain coding sequence; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing the tyrosine kinase domain coding sequence; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing the tyrosine kinase domain coding sequence; or animal cell systems. The expression elements of these systems vary in their strength and specificities.

Depending on the host/vector system utilized, any of a number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used in the expression vector. For example, when cloning in bacterial systems, inducible promoters such as pL of bacteriophage λ , plac, ptrp,

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ptac (ptrp-lac hybrid promoter) and the like may be used; when cloning in insect cell systems, promoters such as the baculovirus polyhedrin promoter may be used; when cloning in plant cell systems, promoters derived from the genome of plant cells (e.g., heat shock promoters; the promoter for the small subunit of RUBISCO; the promoter for the chlorophyll a/b binding protein) or from plant viruses (e.g., the 35S RNA promoter of CaMV; the coat protein promoter of TMV) may be used; when cloning in mammalian cell systems, promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter) may be used; when

generating cell lines that contain multiple copies of 15 the tyrosine kinase domain DNA, SV40-, BPV- and EBVbased vectors may be used with an appropriate selectable

Methods describing methods of DNA manipulation, vectors, various types of cells used, methods of 20 incorporating the vectors into the cells, expression techniques, protein purification and isolation methods, and protein concentration methods are disclosed in detail with respect to the protein PYK-2 in PCT 25 publication WO 96/18738. This publication is incorporated herein by reference in its entirety, including any drawings. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

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Crystal Growth

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Crystals are grown from an aqueous solution containing the purified and concentrated polypeptide by a variety of techniques. These techniques include batch, liquid, bridge, dialysis, vapor diffusion, and hanging drop methods. McPherson, 1982, John Wiley, New York; McPherson, 1990, Eur. J. Biochem. 189:1-23; Webber, 1991, Adv. Protein Chem. 41:1-36, incorporated by reference herein in its entirety, including all figures, tables, and drawings.

Generally, the native crystals of the invention are grown by adding precipitants to the concentrated solution of the polypeptide corresponding to the PTK catalytic domain. The precipitants are added at a concentration just below that necessary to precipitate the protein. Water is removed by controlled evaporation to produce precipitating conditions, which are maintained until crystal growth ceases.

For crystals of the invention, it has been found that hanging drops containing about 2.0 μ L of tyrosine kinase domain polypeptide (10 mg/mL in 10mM Tris-HCl, pH 8.0, 10 mM NaCl and 2 mM dithiothreitol) and 2.0 μ L reservoir solution (16% w/v polyethylene glycol MW 10000, 0.3 M (NH₄)₂SO₄, 5% v/v ethylene glycol or glycerol and 100 mM bis-Tris, pH 6.5) suspended over 0.5 mL reservoir buffer for about 3-4 weeks at 4°C provide crystals suitable for high resolution X-ray structure determination.

Those of ordinary skill in the art will recognize
that the above-described crystallization conditions can
be varied. Such variations may be used alone or in

combination, and include polypeptide solutions containing polypeptide concentrations between about 1 mg/mL and about 60 mg/mL, Tris-HCl concentrations between about 10 mM and about 200 mM, dithiothreitol concentrations between about 0 mM and about 20 mM, pH $\,$ 5 ranges between about 5.5 and about 7.5; and reservoir solutions containing polyethylene glycol concentrations between about 10% and about 30% (w/v), polyethylene glycol molecular weights between about 1000 and about 20,000, $(NH_4)_2SO_4$ concentrations between about 0.1 M and 10 about 0.5 M, ethylene glycol or glycerol concentrations between about 0% and about 20% (v/v), bis-Tris concentrations between about 10 mM and about 200 mM, pH ranges between about 5.5 and about 7.5 and temperature ranges between about 0° C and about 25°C. Other buffer solutions may be used such as HEPES buffer, so long as the desired pH range is maintained.

Derivative crystals of the invention can be obtained by soaking native crystals in mother liquor containing salts of heavy metal atoms. It has been found that soaking a native crystal in a solution containing about 0.1 mM to about 5 mM thimerosal, 4chloromeruribenzoic acid or $\mathrm{KAu}\left(\mathrm{CN}\right)_2$ for about 2 hr to about 72 hr provides derivative crystals suitable for use as isomorphous replacements in determining the X-ray crystal structure of the tyrosine kinase domain polypeptide.

Co-crystals of the invention can be obtained by soaking a native crystal in mother liquor containing compound that bind the kinase domain, or described 30 above, or can be obtained by co-crystallizing the kinase

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domain polypeptide in the presence of one or more binding compounds.

For co-crystals of tyrosine kinase domain polypeptide in co-complex with AMP-PCP, it has been found that co-crystallizing the kinase domain polypeptide in the presence of AMP-PCP using the abovedescribed crystallization conditions for obtaining native crystals with a polypeptide solution additionally containing 10 mM AMP-PCP and 20 mM MgCl₂ yields cocrystals suitable for the high resolution structure determination by X-ray crystallography. Of course, those having skill in the art will recognize that the concentrations of AMP-PCP and $MgCl_2$ in the polypeptide solution can be varied, alone or in combination with the variations described above for native crystals. Such variations include polypeptide solutions containing AMP-1.5 PCP concentrations between 0.1 mM and 50 mM and MgCl $_{\scriptscriptstyle 2}$ concentrations between 0 mM and 50 mM.

Crystals comprising a polypeptide corresponding to a PTK catalytic domain complexed with a compound can be grown by one of two methods. In the first method, the modulator is added to the aqueous solution containing the polypeptide corresponding to the PTK catalytic domain before the crystal is grown. In the second method, the modulator is soaked into an already existing crystal of a polypeptide corresponding to a PTK catalytic domain.

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Crystalline FGFR

In one illustrative embodiment, the invention provides crystals of FGFR1. The crystals were obtained by the methods provided in the Examples. The FGFR1 crystals, which may be native crystals, derivative crystals or co-crystals, have monoclinic unit cells (i.e., unit cells wherein $a\neq b\neq c$; $\alpha=\gamma=90^\circ$; and $\beta>90^\circ$) and space group symmetry C2. There are two FGFR1 molecules in the asymmetric unit, related by an approximate two-fold axis.

Two forms of crystalline FGFR1 were obtained. In one form (designated "C2-A form"), the unit cell has dimensions of a=208.3 Å, b=57.2 Å, c=65.5 Å and β =107.2°. In another form (designated "C2-B form"), the unit cell has dimensions of a=211.6 Å, b=51.3 Å, c=66.1 Å and β =107.7°.

Three distinct two-fold related FGFR1 dimers are observed in both the C2-A and C2-B forms of the FGFR1 crystal, one non-crystallographically related dimer and two crystallographically related dimers. The non-crystallographically related dimer comprises the two molecules in the asymmetric unit. The residues making up the dimer interface are located in C-terminal lobe. In this dimer, the C-terminal lobes abut with the N-terminal lobes distal to one another. The total amount of surface area buried in the surface is about 950 Å². Very few of the interactions in the interface are of a specific nature, e.g., hydrogen-bonding or close packing of hydrophobic residues.

There are two crystallographically-related dimers in the C2 lattice. In the first dimer, the residues

that constitute the dimer interface are limited to those in the β -sheet of the N-terminal lobe (amino acid residues 477, 479, 498, 506, 508 and 496). The total surface area buried in this interface is about 670 Å^2 . The interactions are rather specific. Three hydrophobic residues which are partially solvent-exposed in the monomer, Val-479, Ile-498 and Val-508, come together with their two-fold-related residues to form a compact hydrophobic plug. This plug is capped on either side by a salt bridge between Arg-477 and Glu-496. In addition, two main-chain hydrogen-bonds connect the β -sheets of the two monomers at the start of \$3 (amino acid residues 506 and 508). The residues in this dimer interface, or their residue character, are generally conserved in the mammalian FGF receptors, but not in the invertebrate homologues.

The other crystallographically-related dimer buries about 1650 Ų in its interface. In this dimer, the αC helices of the two monomers are nearly parallel and contact each other at their C-terminal ends. Met-534 and Met-537 are in van der Waals contact with their two-fold-related residues. Other hydrophobic contacts involve Pro-466 with Ile-648 and Pro-469 with Ile-676 and Thr-678. In addition, hydrogen bonds (side-chain to main-chain) are made between Arg-470 and Lys-618 and between His-649 and Glu-464, and there are several water molecules that bridge the two monomers through hydrogen bonding.

In the C2-B form of the crystal, the monomers of this second crystallographically-related dimer are shifted slightly with respect to one another (6°

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rotation), indicating that this interface is somewhat fluid.

In both of the crystallographically-related dimers, the N-termini of the two molecules comprising the dimer point in the same direction and are reasonably close to one another.

Determining Unit Cell Dimensions and the Three
Dimensional Structure of a Polypeptide or Polypeptide
Complex

Once the crystal is grown, it can be placed in a glass capillary tube and mounted onto a holding device connected to an X-ray generator and an X-ray detection 15 device. Collection of X-ray diffraction patterns are well documented by those in the art. Ducruix and Geige, 1992, IRL Press, Oxford, England, and references cited therein. A beam of X-rays enter the crystal and then diffract from the crystal. An X-ray detection device can be utilized to record the diffraction patterns 20 emanating from the crystal. Although the X-ray detection device on older models of these instruments is a piece of film, modern instruments digitally record Xray diffraction scattering.

Methods for obtaining the three dimensional structure of the crystalline form of a peptide molecule or molecule complex are well known in the art. Ducruix and Geige, 1992, IRL Press, Oxford, England, and references cited therein. The following are steps in the process of determining the three dimensional structure of a molecule or complex from X-ray diffraction data.

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After the X-ray diffraction patterns are collected from the crystal, the unit cell dimensions and orientation in the crystal can be determined. They can be determined from the spacing between the diffraction emissions as well as the patterns made from these emissions. The unit cell dimensions are characterized in three dimensions in units of Angstroms (one $\mathring{A}=10^{-10}$ meters) and by angles at each vertices. The symmetry of the unit cell in the crystals is also characterized at this stage. The symmetry of the unit cell in the crystal simplifies the complexity of the collected data by identifying repeating patterns. Application of the symmetry and dimensions of the unit cell is described below.

Each diffraction pattern emission is characterized as a vector and the data collected at this stage of the method determines the amplitude of each vector. phases of the vectors can be determined using multiple techniques. In one method, heavy atoms can be soaked into a crystal, a method called isomorphous replacement, and the phases of the vectors can be determined by using these heavy atoms as reference points in the X-ray analysis. Otwinowski, 1991, Daresbury, United Kingdom, 80-86. The isomorphous replacement method usually requires more than one heavy atom derivative. another method, the amplitudes and phases of vectors from a crystalline polypeptide with an already determined structure can be applied to the amplitudes of the vectors from a crystalline polypeptide of unknown structure and consequently determine the phases of these This second method is known as molecular vectors.

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replacement and the protein structure which is used as a reference must have a closely related structure to the protein of interest. Naraza, 1994, Proteins 11:281-296. Thus, the vector information from a PTK of known structure, such as those reported herein, are useful for the molecular replacement analysis of another PTK with unknown structure.

Once the phases of the vectors describing the unit cell of a crystal are determined, the vector amplitudes and phases, unit cell dimensions, and unit cell symmetry 10 can be used as terms in a Fourier transform function. The Fourier transform function calculates the electron density in the unit cell from these measurements. electron density that describes one of the molecules or one of the molecule complexes in the unit cell can be 15 referred to as an electron density map. The amino acid structures of the sequence or the molecular structures of compounds complexed with the crystalline polypeptide may then fit to the electron density using a variety of 20 computer programs. This step of the process is sometimes referred to as model building and can be accomplished by using computer programs such as TOM/FRODO. Jones, 1985, Methods in Enzymology 115:157-

A theoretical electron density map can then be calculated from the amino acid structures fit to the experimentally determined electron density. The theoretical and experimental electron density maps can be compared to one another and the agreement between these two maps can be described by a parameter called an R-factor. A low value for an R-factor describes a high

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degree of overlapping electron density between a theoretical and experimental electron density map.

The R-factor is then minimized by using computer programs that refine the theoretical electron density map. A computer program such as X-PLOR can be used for model refinement by those skilled in the art. Brünger, 1992, Nature 355:472-475. Refinement may be achieved in an iterative process. A first step can entail altering the conformation of atoms defined in an electron density The conformations of the atoms can be altered by simulating a rise in temperature which will increase the vibrational frequency of the bonds and modify positions of atoms in the structure. At a particular point in the atomic perturbation process, a force field, which typically defines interactions between atoms in terms of allowed bond angles and bond lengths, Van der Waals interactions, hydrogen bonds, ionic interactions, and hydrophobic interactions, can be applied to the system of atoms. Favorable interactions may be described in terms of free energy and the atoms can be moved over many iterations until a free energy minimum is achieved. The refinement process can be iterated until the Rfactor reaches a minimum value.

The three dimensional structure of the molecule or molecule complex is described by atoms that fit the theoretical electron density characterized by a minimum R-value. A file can then be created for the three dimensional structure that defines each atom by coordinates in three dimensions. Examples of such structural coordinate files are defined in Table 1, Table 2, Table 3, and Table 4.

V. <u>Structures of FGFR1</u>

The present invention provides high-resolution three-dimensional structures and atomic structure coordinates of crystalline FGFR1 and crystalline FGFR1:AMP-PCP co-complex as determined by X-ray crystallography. The specific methods used to obtain the structure coordinates are provided in the examples. The atomic structure coordinates of crystalline FGFR1, obtained from the C2-A form of the crystal to 2.0 Å resolution, are listed in Table 3; the coordinates of crystalline FGFR1:AMP-PCP co-complex, obtained from the C2-A form of the crystal to 2.3 Å resolution are listed in Table 4.

15 Those having skill in the art will recognize that atomic structure coordinates as determined by X-ray crystallography are not without error. Thus, it is to be understood that any set of structure coordinates obtained for crystals of FGFR1, whether native crystals, 20 derivative crystals or co-crystals, that have a root mean square deviation ("r.m.s.d.") of less than or equal to about 1.5 Å when superimposed, using backbone atoms (N, $C_{\alpha},$ C and O), on the structure coordinates listed in Table 3 or Table 4 are considered to be identical with the structure coordinates listed in the Tables when at 25 least about 50% to 100% of the backbone atoms of FGFR1 are included in the superposition.

Referring now to FIG. 1, the overall structure of FGFR1 is bi-lobate. The N-terminal lobe of FGFR1 spans amino acid residues 456-567 (FIG. 3) and comprises a curled β -sheet of five anti-parallel strands (β 1- β 5) and

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one α -helix (α C). The C-terminal lobe spans amino acid residues 568-765 (FIG. 3) and comprises two β -strands (β 7, β 8) and seven α -helices (α D, α E, α EF, α F- α I). The secondary structure nomenclature follows that used for IRK (Hubbard et al., 1994) which in turn is based on the assignments for cAPK (Knighton et al., 1991). FIG. 2 shows a stereo view of a C $_{\alpha}$ trace of FGFR1 in the same orientation as FIG. 1.

A structure-based sequence alignment of the tyrosine kinase domains of human fibroblast growth factor receptor 1 (human FGFR1; labelled FGFR1), human 10 fibroblast growth factor receptors 2, 3 and 4 (labelled FGFR2, FGFR3 and FGFR4, respectively), a D. melanogaster homologue (labelled DFDFR1), a C elegans homologue (labelled EGL-15) and insulin receptor kinase (labelled IRK), is shown in FIG. 3. The sequence of FGFR1, which 15 is not shown in FIG. 3 is identical to the sequence of FGFR1 except that FGFR1 has the following amino acid substitutions and additions: Cys-488 → Ala, Cys-584 → Ser, Leu-457 \rightarrow Val and an additional five N-terminal amino acids (Ser-Ala-Ala-Gly-Thr). The secondary 20 structure assignments for FGFR1 and IRK were obtained using the Kabsch and Sander algorithm (Kabsch and Sander, 1983) as implemented in PROCHECK (Laskowski et al., 1993). In the FGF receptor sequences, a period represents sequence identity to FGFR1. In the IRK 25 sequence, residues that are identical to FGFR1 are highlighted. A hyphen denotes an insertion.

The numbers under the EGL-15 sequence represent the fractional solvent accessibility (FSA2) of the residue in the FGFR1 structure. The FSA ratio is the ratio of

asymmetric unit.

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the solvent-accessible surface area of a residue in a Gly-X-Gly tripeptide compared to that in the FGFR1 structure. A value of 0 represents an FSA between 0.00 and 0.09; 1 represents an FSA between 0.10 and 0.19, The higher the value, the more solvent-exposed the residue. An asterisk or pound sign in the FSA line indicates that the residue (asterisk) or side chain (pound sign) is not included in the atom model due to disorder. The numbers below the FSA line are the FSAs

for those residues that form part of a dimer interface. The amino acid residue numbers for FGFR1, and hence FGFR1, and IRK provided in FIG. 3 are used in the discussion that follows. Significant differences in the N-terminal lobe of FGFR1 as compared to IRK are found in the loops between β strands and in $\alpha C.$ Residues from the 15 end of $\beta1$ through the beginning of $\beta2$ (amino acid residues 485-490) form the nucleotide-binding loop, named because of its role in ATP coordination. residue stretch contains the protein kinase-conserved GXGXXG sequence motif, where X is any amino acid. This 20 loop is poorly ordered in one FGFR1 molecule in the asymmetric unit and disordered (i.e., not included in the atomic model) in the other FGFR1 molecule in the asymmetric unit. The loop between $\beta1$ and $\beta3$ is disordered in both FGFR1 molecules comprising the 25

Referring now to FIG. 4A, which provides a ribbon diagram of the N-terminal lobes of FGFR1 and IRK in which the C_{α} atoms of the $\beta\text{-sheets}$ have been superimposed, it can be seen that in FGFR1 αC is longer by one helical turn than in IRK and is oriented such

that residues Lys-514 and Glu-531, which are conserved in protein kinases, form a salt bridge (represented by a black line). While not intending to be bound by theory, this salt bridge is believed to be important for proper positioning of the conserved lysine side chain, which coordinates two phosphate oxygens of ATP. The salt bridge is observed in the structures of cAPK (Knighton et al., 1991) and mitogen-activated protein kinase (MAPK) (Zhang et al., 1994).

Referring now to FIG. 4B, which provides a ribbon diagram of the C-terminal lobes of FGFR1 and IRK in which the C_{α} atoms of the α -helices have been superimposed, a significant difference is found in the C-terminal helix of FGFR1 when compared to IRK; helix α I of FGFR1 is longer by seven residues (two helical turns) than its counterpart in IRK. The extended length of α I is presumably important in the biological functioning of FGF receptors, since the tyrosine autophosphorylation site to which an SH2 domain of PLCy binds is six residues C-terminal to this helix.

The structure of FGFR1 displays an open disposition of the N- and C-terminal lobes. Despite having different sets of lattice contacts, the two FGFR1 molecules in the asymmetric unit have only a 2° difference in relative lobe orientation. It appears as though the stearic interaction between residues in α C (Glu-531 and Met-534) with Phe-642 and Gly-643 of the protein kinase-conserved DFG sequence at the beginning of the activation loop accounts for the open conformation of FGFR1.

The active site of FGFR1 is characterized by at

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least amino acid residues spanning the catalytic loop, activation loop and nucleotide binding loop. Unlike the structure of IRK, in which Tyr-1162 occupies the active site of the molecule, the active sites of both FGFR1 molecules in the asymmetric unit are unoccupied.

The activation loop, which regulates phosphorylation, is characterized by at least resides 640 to 663. Quite surprisingly, while the activation loops of FGFR1 and IRK contain the same number of amino

acid residues and share greater than 50% sequence homology, the paths of the polypeptide chains are strikingly dissimilar, diverging at Ala-640 (Gly-1149 in IRK) and reconverging at Val-664 (Val-1173 in IRK).

Tyr-653 and Tyr 564 are not bound in the active site.

Instead, these residues point away from it. Tyr-653 is in van der Waals contact with several hydrophobic residues (Val-664, Leu-672 and Phe-710) and is hydrogen-bonded via its hydroxyl group to a backbone carbonyl oxygen (Leu-672). Tyr-654 is more solvent exposed than Tyr-653, and its only van der Waals contact is with Val-

706. Temperature factor data suggest that the activation loop is relatively mobile and adopts multiple conformations.

The catalytic loop of protein kinases lies between secondary structure elements αE and β7 and contains an invariant aspartic acid residue (Asp-623 in FGFR1) which serves as the catalytic base in the phosphotransfer reaction, abstracting the proton from the hydroxyl group of the substrate tyrosine, serine or threonine. The catalytic loop sequence of FGFR1 comprises at least residues His-621 to Asn-628 (amino acid sequence

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HRDLAARN), and is identical to that for IRK and most receptor and non-receptor PTKs.

In addition to the two tyrosine autophosphorylation sites in the activation loop (Tyr-653 and Tyr-654), there are four other autophosphorylation sites present in the FGFR1 crystals of the invention: one in the juxtamembrane region (Tyr-463), two in the kinase insert (Tyr-583 and Tyr-585) and one in the C-terminal lobe (Tyr-730) (Mohammadi et al., 1996). They exhibit varying degrees of conservation in mammalian FGF varying degrees of conservation in FGFR1 and 2; Tyr-583 in FGFR1, 2 and 3; and Tyr-730 in FGFR 1, 2, 3 and 4 (FIG. 3).

Referring now to FIG. 5, the positions of the autophosphorylation sites are mapped onto the FGFR1 structure. The juxtamembrane site (Tyr-463) and the residues N-terminal to it are disordered in one of the FGFR1 molecules in the asymmetric unit. In the other molecule in the asymmetric unit Tyr-463 is involved in a lattice contact.

The kinase insert region (the region between helices αD and αE) contains autophosphorylation sites Tyr-583 and Tyr-585 and is disordered in both FGFR1 molecules in the asymmetric unit of the C2-A form of the crystal. In the C2-B form, several lattice contacts partially pin down this region in one of the two FGFR1 molecules in the asymmetric unit, allowing a trace of the polypeptide chain to be made. There is no well-defined secondary structure for these residues. Tyr-730, situated in αH in the C-terminal lobe, is nearly buried and the side-chain hydroxyl group makes two

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hydrogen-bonds. The side chains of neighboring Met-732 and Met-733 are both buried. Therefore, phosphorylation of Tyr-730 would presumably require prior unfolding of $\alpha_{\rm H}$.

- Aside from Tyr-730, the five other
 autophosphorylation sites (including Tyr-653 and Tyr654) are found in relatively mobile segments of the
 FGFR1 molecule. While not intending to be bound by
 theory, the spatial positions of the autophosphorylation
 sites relative to the active site suggest that
 autophosphorylation occurs by a trans mechanism between
 two kinase domains, supporting the hypothesis that
 ligand-induced receptor dimerization is critical for the
 initiation of autophosphorylation events.
- The structure of crystalline FGFR1:AMP-PCP cocomplex is essentially similar to that observed for
 crystalline FGFR1. There are no significant changes in
 the structure of FGFR1 induced by AMP-PCP binding. In
 particular, binding of AMP-PCP, and by extension ATP,
 does not by itself promote lobe closure under the
 crystallization conditions used. Furthermore,
 complexation did not result in any noticeable changes in
 the conformations of the activation and nucleotidebinding loops.
- The crystalline FGFR1:AMP-PCP co-complex contains hydrogen bonds that are present between N1 of adenine and the amide nitrogen of Ala-564 and between N6 of adenine and the carbonyl oxygen of Glu-562. The adenine ring is flanked on one side by Leu-484 and Val-492 (N-terminal lobe) and on the other side by Leu-630 (C-terminal lobe). The ribose hydroxyl groups make no

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direct hydrogen bonds with protein atoms. Lys-514 is hydrogen-bonded to oxygens of the β - and γ -phosphates. There is no unambiguous electron density that would indicate the positions of Mg²+ ions. Generally, AMP-PCP appears to be coordinated rather loosely to unphosphorylated FGFR1, being bound to the "roof" of the cleft rather than being tightly sandwiched between the two kinase lobes.

10 Structural Differences Between FGF-R and IRK

Several features distinguish the FGF-receptor structure from that of the insulin-receptor tyrosine kinase. These distinctions are likely to be important in signaling by FGF-receptors, and other monomeric receptors that are believed to undergo ligand-induced dimerization.

The most significant difference between the structures of FGFR1 and IRK is the conformation of the activation loop. In FGFR1, the activation loop is disposed such that the binding site for substrate peptides is blocked not by an activation loop tyrosine, as in IRK, but by Arg-661 and PTK-invariant Pro-663, while the ATP binding site is accessible. This represents another molecular mechanism by which a receptor PTK may be autoinhibited. The observed autoinhibition in FGFR1 would appear to be weaker than that in IRK because of fewer specific interactions made by residues in the FGFR1 activation loop (manifested in the relatively higher B-values) and the accessibility of the ATP site. One obvious distinction between the insulin and FGF receptor families is that in the former,

receptors are covalently linked heterotetramers $(\alpha_2\beta_2)$, whereas in the latter, receptor dimerization is ligand dependent. Receptors whose kinase domains are always in close proximity may require a stronger autoinhibition mechanism than those receptors that associate only upon ligand binding (Taylor et al., 1995). Since most growth factor receptors undergo ligand-dependent dimerization and activation, the FGF receptor autoinhibition mechanism appears to be a more general one.

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Uses of the Crystals and Atomic Structure

The crystals of the invention, and particularly the atomic structure coordinates obtained therefrom, have a wide variety of uses. For example, the crystals 15 described herein can be used as a starting material in any of the art-known methods of use for receptor and non-receptor tyrosine kinases. Such methods of use include, for example, identifying molecules that bind to the native or mutated catalytic domain of tyrosine 20 kinases. The crystals and structure coordinates are particularly useful for identifying compounds that inhibit receptor and non-receptor tyrosine kinases as an approach towards developing new therapeutic agents (see, e.g., Levitzki and Gazit, 1995).

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The structure coordinates described herein can be used as phasing models for determining the crystal structures of additional native or mutated tyrosine kinase domains, as well as the structures of co-crystals of such domains with ligands such as inhibitors, agonists, antagonists, and other molecules.

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structure coordinates, as well as models of the three-dimensional structures obtained therefrom, can also be used to aid the elucidation of solution-based structures of native or mutated tyrosine kinase domains, such as those obtained via NMR. Thus, the crystals and atomic structure coordinates of the invention provide a convenient means for elucidating the structures and functions of receptor and non-receptor tyrosine kinases.

For purposes of clarity and discussion, the crystals of the invention will be described by reference to specific FGFR1 exemplary crystals. Those skilled in the art will appreciate that the principles described herein are generally applicable to crystals of the tyrosine kinase domain of any cytoplasmic tyrosine kinase that undergoes ligand-induced dimerization or receptor tyrosine kinase, including but not limited to the tyrosine kinases of FIG. 6.

VII. Structure Determination for PTKs with Unknown
Structure Using Structural Coordinates

Structural coordinates, such as those set forth in Table 1, Table 2, Table 3, and Table 4, can be used to determine the three dimensional structures of PTKs with unknown structure. The methods described below can apply structural coordinates of a polypeptide with known structure to another data set, such as an amino acid sequence, X-ray crystallographic diffraction data, or nuclear magnetic resonance (NMR) data. Preferred embodiments of the invention relate to determining the three dimensional structures of PTKs and related polypeptides. These include receptor PTKs such as FGF-

R, PDGF-R, KDR, CCK4, MET, TRKA, AXL, TIE, EPH, RYK, DDR, ROS, RET, LTK, ROR1, and MUSK. Non-receptor PTKs such as SRC, BRK, BTK, CSK, ABL, ZAP70, FES, FAK, JAK, and ACK can also be used in the methods described herein.

Structures Using Amino Acid Homology

Homology modeling is a method of applying structural coordinates of a polypeptide of known structure to the amino acid sequence of a polypeptide of 10 unknown structure. This method is accomplished using a computer representation of the three dimensional structure of a polypeptide or polypeptide complex, the computer representation of amino acid sequences of the polypeptides with known and unknown structures, and 15 standard computer representations of the structures of amino acids. Homology modeling comprises the steps of (a) aligning the amino acid sequences of the polypeptides with and without known structure; (b) 20 transferring the coordinates of the conserved amino acids in the known structure to the corresponding amino acids of the polypeptide of unknown structure; refining the subsequent three dimensional structure; and (d) constructing structures of the rest of the polypeptide. One skilled in the art recognizes that conserved amino 25 acids between two proteins can be determined from the sequence alignment step in step (a).

The above method is well known to those skilled in the art. Greer, 1985, Science 228, 1055. Blundell et al., 1988, Eur. J. Biochem. 172, 513. A computer program currently utilized for homology modeling by

those skilled in the art is the Homology module in the Insight II modeling package distributed by Molecular Simulations Inc.

Alignment of the amino acid sequence is accomplished by first placing the computer representation of the amino acid sequence of a polypeptide with known structure above the amino acid sequence of the polypeptide of unknown structure. Amino sequence of the polypeptide of unknown structure. Amino acids in the sequences are then compared and groups of amino acids that are homologous (e.g., amino acid side chains that are similar in chemical nature - aliphatic, chains that are similar in chemical nature. This aromatic, polar, or charged) are grouped together. This method will detect conserved regions of the polypeptides and account for amino acid insertions or deletions.

Once the amino acid sequences of the polypeptides with known and unknown structures are aligned, the structures of the conserved amino acids in the computer representation of the polypeptide with known structure are transferred to the corresponding amino acids of the polypeptide whose structure is unknown. For example, a polypeptide whose structure is unknown structure tyrosine in the amino acid sequence of known structure may be replaced by a phenylalanine, the corresponding homologous amino acid in the amino acid sequence of unknown structure.

The structures of amino acids located in nonconserved regions are to be assigned manually by either
using standard peptide geometries or molecular
simulation techniques, such as molecular dynamics. The
final step in the process is accomplished by refining
the entire structure using molecular dynamics and/or
energy minimization.

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The homology modeling method is well known to those skilled in the art and has been practiced using different protein molecules. The three dimensional structure of the polypeptide corresponding to the catalytic domain of a serine/threonine protein kinase, 5 myosin light chain protein kinase, was homology modeled from the cAMP-dependent protein kinase catalytic subunit. Knighton et al., 1992, Science 258:130-135.

Structures Using Molecular Replacement 10

Molecular replacement is a method of applying the X-ray diffraction data of a polypeptide of known structure to the X-ray diffraction data of a polypeptide of unknown sequence. This method can be utilized to define the phases describing the X-ray diffraction data 15 of a polypeptide of unknown structure when only the amplitudes are known. X-PLOR is a commonly utilized computer software package used for molecular replacement. Brünger, 1992, Nature 355:472-475. AMORE is another program used for molecular replacement. 20 Navaza, 1994, Acta Crystallogr. A50:157-163. Preferably, the resulting structure does not exhibit a

root-mean-square deviation of more than 3 Å. A goal of molecular replacement is to align the positions of atoms in the unit cell by matching electron 25 diffraction data from two crystals. A program such as X-PLOR can involve four steps. A first step can be to determine the number of molecules in the unit cell and define the angles between them. A second step can involve rotating the diffraction data to define the 30

orientation of the molecules in the unit cell. A third

step can be to translate the electron density in three dimensions to correctly position the molecules in the unit cell. Once the amplitudes and phases of the X-ray diffraction data is determined, an R-factor can be calculated by comparing electron diffraction maps calculated experimentally from the reference data set and calculated from the new data set. An R-factor between 30-50% indicates that the orientations of the atoms in the unit cell are reasonably determined by this method. A fourth step in the process can be to decrease the R-factor to roughly 20% by refining the new electron density map using iterative refinement techniques described herein and known to those or ordinary skill in the art.

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Structures Using NMR Data

Structural coordinates of a polypeptide or polypeptide complex derived from X-ray crystallographic techniques can be applied towards the elucidation of 20 three dimensional structures of polypeptides from nuclear magnetic resonance (NMR) data. This method is used by those skilled in the art. Wuthrich, 1986, John Wiley and Sons, New York: 176-199; Pflugrath et al., 1986, J. Molecular Biology 189:383-386; Kline et al., 25 1986, J. Molecular Biology 189:377-382. While the secondary structure of a polypeptide is often readily determined by utilizing two-dimensional NMR data, the spatial connections between individual pieces of secondary structure are not as readily determinable. 30 The coordinates defining a three-dimensional structure of a polypeptide derived from X-ray crystallographic

techniques can guide the NMR spectroscopist to an understanding of these spatial interactions between secondary structural elements in a polypeptide of related structure.

5 The knowledge of spatial interactions between secondary structural elements can greatly simplify Nuclear Overhauser Effect (NOE) data from twodimensional NMR experiments. Additionally, applying the crystallographic coordinates after the determination of secondary structure by NMR techniques only simplifies 10 the assignment of NOEs relating to particular amino acids in the polypeptide sequence and does not greatly bias the NMR analysis of polypeptide structure. Conversely, using the crystallographic coordinates to simplify NOE data while determining secondary structure 15 of the polypeptide would bias the NMR analysis of protein structure.

As the analysis of polypeptide structure by NMR methods is a relatively new technique, the use of structural coordinates defining a PTK structure will most likely be utilized more frequently in the near future. As the method progresses, the three dimensional structure analysis of polypeptides of the same size as a PTK catalytic domain will become more frequent.

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VIII. Structure-Based Design of Modulators of PTK
Function Utilizing Structural Coordinates
Structure-based modulator design and identification
methods are powerful techniques that can involve
searches of computer data bases containing a wide
variety of potential modulators and chemical functional

groups. The computerized design and identification of modulators is useful as the computer data bases contain more compounds than the chemical libraries, often by an order of magnitude. For reviews of structure-based drug design and identification see Kuntz et al., 1994, Acc. Chem. Res. 27:117; Guida, 1994, Current Opinion in Struc. Biol. 4: 777; Colman, 1994, Current Opinion in Struc. Biol. 4: 868.

The three dimensional structure of a polypeptide defined by structural coordinates can be utilized by these design methods. The structural coordinates of Table 1, Table 2, Table 3, and Table 4 can be utilized by this method. In addition, the three dimensional structures of receptor and non-receptor PTKs determined by the homology, molecular replacement, and NMR techniques described herein can also be applied to modulator design and identification methods. Thus, the structures of receptor PTKs, FGF-R, PDGF-R, FLK, CCK4, MET, TRKA, AXL, TIE, EPH, RYK, DDR, ROS, RET, LTK, ROR1, and MUSK, can be utilized by the methods described herein. The structures of non-receptor PTKs, SRC, BRK, BTK, CSK, ABL, ZAP70, FES, FAK, JAK, and ACK, can also be utilized by the rational modulator design method.

25 <u>Design by Searching Molecular Data Bases</u>

One method of rational modulator design searches for modulators by docking the computer representation of compounds from a data base of molecules. Publicly available data bases include:

a) ACD from Molecular Designs Limited

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- NCI from National Cancer Institute b) C)
- CCDC from Cambridge Crystallographic Data Center d)
- CAST from Chemical Abstract Service
- Derwent from Derwent Information Limited e) f)
- 5 Maybridge from Maybridge Chemical Company LTD g)
 - Aldrich from Aldrich Chemical Company h)
 - Directory of Natural Products from Chapman & Hall

One such data base (ACD distributed by Molecular Designs Limited Information Systems) contains, for example, 10 200,000 compounds that are synthetically derived or are natural products. Methods available to those skilled in the art can convert a data set represented in two dimensions to one represented in three dimensions.

These methods are enabled by such computer programs as 15 CONCORD from Tripos Associates or DB-Converter from Molecular Simulations Limited.

Multiple methods of structure-based modulator design are known to those in the art. Kuntz et al., 1982, J. Mol. Biol. 162: 269; Kuntz et al., 1994, 20 Acc. Chem. Res. 27: 117; Meng et al., 1992, J. Compt. Chem. 13: 505; Bohm, 1994, J. Comp. Aided Molec. Design 8: 623.

A computer program widely utilized by those skilled in the art of rational modulator design is DOCK from the 25 University of California in San Francisco. The general methods utilized by this computer program and programs like it are described in three applications below. More detailed information regarding some of these techniques 30 can be found in the Molecular Simulations User Guide,

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A typical computer program used for this purpose can comprise the following steps:

- (a) remove the existing compound from the protein;
- (b) dock the structure of another compound into the active-site using the computer program (such as DOCK) or by interactively moving the compound into the active-site;
- (c) characterize the space between the compound and the active-site atoms;
- (d) search libraries for molecular fragments which (i)can fit into the empty space between the compound and the active-site, and (ii) can be linked to the compound; and
 - (e) link the fragments found above to the compound and evaluate the new modified compound.

Part (c) refers to characterizing the geometry and the complementary interactions formed between the atoms of the active-site and the compounds. A favorable geometric fit is attained when a significant surface area is shared between the compound and active-site atoms without forming unfavorable steric interactions.

One skilled in the art would note that the method can be performed by skipping parts (d) and (e) and screening a data base of many compounds.

Structure-based design and identification of modulators of PTK function can be used in conjunction with assay screening. As large computer data base of compounds (around 10,000 compounds) can be searched in a matter of hours, the computer based method can narrow the compounds tested as potential modulators of PTK function in cellular assays.

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The above descriptions of structure-based modulator design are not all encompassing and other methods are reported in the literature:

- (1) CAVEAT: Bartlett et al.,1989, in "Chemical and Biological Problems in Molecular, Recognition", Roberts, S.M.; Ley, S.V.; Campbell, M.M. eds.; Royal Society of Chemistry: Cambridge, ppl82-196.
- (2) FLOG: Miller et al., 1994, J. Comp. Aided Molec. Design 8:153.
- 10 (3) PRO Modulator: Clark et al., 1995, J. Comp. Aided Molec. Design 9:13.
 - (4) MCSS: Miranker and Karplus, 1991, Proteins: Structure, Function, and Genetics 11:29.
 - (5) AUTODOCK: Goodsell and Olson, 1990, Proteins: Structure, Function, and Genetics 8:195.
 - (6) GRID: Goodford, 1985, J. Med. Chem. 28:849.

Design by Modifying Compounds in Complex with PTKs
Another way of identifying compounds as potential

modulators is to modify an existing modulator in the polypeptide active-site. For example, the computer representation of modulators can be modified within the computer representation of a PTK active-site. Detailed instructions for this technique can be found in the

Molecular Simulations User Manual, 1995 in LUDI. The computer representation of the modulator is modified by the deletion of a chemical group or groups or by the addition of a chemical group or groups.

Upon each modification to the compound, the atoms
of the modified compound and active-site can be shifted
in conformation and the distance between the modulator

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and the active-site atoms may be scored along with any complimentary interactions formed between the two molecules. Scoring can be complete when a favorable geometric fit and favorable complementary interactions are attained. Compounds that have favorable scores are potential modulators of PTK function.

Design by Modifying the Structure of Compounds that Bind PTKs

A third method of structure-based modulator design is to screen compounds designed by a modulator building or modulator searching computer program. Examples of these types of programs can be found in the Molecular Simulations Package, Catalyst. Descriptions for using this program are documented in the Molecular Simulations User Guide (1995). Other computer programs used in this application are ISIS/HOST, ISIS/BASE, ISIS/DRAW) from Molecular Designs Limited and UNITY from Tripos Associates.

These programs can be operated on the structure of a compound that has been removed from the active-site of the three dimensional structure of a compound-PTK complex. Operating the program on such a compound is preferable since it is in a biologically active conformation.

A modulator construction computer program is a computer program that may be used to replace computer representations of chemical groups in a compound complexed with a PTK with groups from a computer data base. A modulator searching computer program is a computer program that may be used to search computer

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representations of compounds from a computer data base that have similar three dimensional structures and similar chemical groups as compound bound to a PTK.

A typical program can operate by using the following general steps:

- (a) map the compounds by chemical features such as by hydrogen bond donors or acceptors, hydrophobic/lipophilic sites, positively ionizable sites, or negatively ionizable sites.
- (b) add geometric constraints to the mapped features; and
 - (c) search data bases with the model generated in (b).

Those skilled in the art recognize that for
indolinones, the important chemical features include,
but are not limited to, a hydrogen bond donor, a
hydrogen bond acceptor, and two hydrophobic points of
contact. Those skilled in the art also recognize that
not all of the possible chemical features of the
compound need be present in the model of (b). One can
use any subset of the model to generate different models
for data base searches.

IX. Organic Synthetic Techniques

The versatility of computer-based modulator design and identification lies in the diversity of structures screened by the computer programs. The computer programs can search data bases that contain 200,000 molecules and can modify modulators already complexed with the enzyme with a wide variety of chemical

functional groups. A consequence of this chemical diversity is that a potential modulator of PTK function may take a chemical form that is not predictable. A wide array of organic synthetic techniques exist in the 5 art to meet the challenge of constructing these potential modulators of PTK function. Many of these organic synthetic methods are described in detail in standard reference sources utilized by those skilled in the art. One example of such a reference is March, 10 1994, Advanced Organic Chemistry; Reactions, Mechanisms, and Structure, New York, McGraw Hill. Thus, the techniques required to synthesize a potential modulator of PTK function identified by computer-based methods are readily available to those skilled in the art of organic 15 chemical synthesis.

X. <u>Cellular Assays Measuring the Effect of a PTK</u> <u>Modulator in Signal Transduction Pathways</u>

20 Cellular assays can be used to test the activity of a potential modulator of PTK function as well as diagnose a disease associated with inappropriate PTK activity. A potential modulator of PTK function can be tested for activity in vitro by assays that measure the 25 effect of a potential modulator on the autophosphorylation of a particular PTK over-expressed in a cell line. Thus, a modulator that acts as a potent inhibitor of the catalytic domain corresponding to a PTK would decrease the amount of autophosphorylation 30 catalyzed by that PTK. Potential modulators could also be tested for activity in cell growth assays in vitro as well as in animal model assays in vivo.

In vivo assays are also useful for testing the bioactivity of a potential modulator designed by the methods of the invention.

Materials, methods, and experimental data for these assays are fully described in WO 96/40116 published on December 19, 1996, entitled "Indolinone Compounds for the Treatment of Disease". This application is incorporated herein by reference in its entirety, including all drawings, figures, and tables.

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Administration of Modulators of PTK Function as Therapeutics for Disease

Methods of administering compounds to organisms as therapeutics for disease are fully described in WO 96/40116 published on December 19, 1996, entitled 15 "Indolinone Compounds for the Treatment of Disease". This application is incorporated herein by reference in its entirety, including all drawings, figures, and tables.

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EXAMPLES

The examples below are non-limiting and are merely representative of various aspects and features of the present invention. The examples provide illustrative methods for obtaining crystalline forms of protein 25 kinase polypeptides, methods for determining three dimensional structures of these protein kinase polypeptides, and methods for identifying modulators of protein kinases using the three dimensional structures 30 of the protein kinases.

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EXAMPLE 1: X-ray Crystallographic Structure

Determination of FGFR1

Polypeptide Synthesis and Isolation

A recombinant baculovirus was engineered to encode residues 456-765 of human FGFR1. A cleavable N-terminal histidine tag was incorporated to aid in protein purification. Three amino acid substitutions were introduced: Cys-488 to Ala, Cys-584 to Ser and Leu-457 to Val. The two cysteine substitutions were made to prevent the formation of disulfide-linked oligomers, which occurs for the native protein. The substitution Leu-457 to Val introduced a Ncol cloning site near Met-The codon for Tyr-766 (TAC) was changed to a stop codon (TAG) and a HindIII-cloning site was generated following this stop codon. These substitutions were introduced into the full length human cDNA of FGFR1 in m13MPI9 by site-directed mutagenesis according to the manufacturer's protocol (Amersham).

The resulting construct was digested with *Ncol* and *HindIII* and was ligated into appropriately digested pBlueBac HistagB (Invitrogen). Transfection of insect cells (Sf9) was performed with the BaculoGold transfection system according to the manufacturer's protocol (Pharmingen). Following identification of positive plaques, the recombinant baculovirus was amplified to high titer (5x10⁷ virus particles/ml). Sf9 cells were grown in 175-cm² flasks to a density of 2-3x10⁷ per flask and infected with recombinant baculovirus with a multiplicity of infection (MOI) of 10.

After 48 hr, cells were harvested by centrifugation

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at 3,000g for 35 min at 4°C and then lysed in 25 mM HEPES (pH 7.5), 150 mM NaCl, 10% glycerol, 1.5 mM MgCl₂, 1 % Triton X-100, 10 µg/ml aprotonin, 10 µg/ml leupeptin, and 1 mM phenylmethylsulfonyl fluoride (PMSF). Lysates were centrifuged in a Sorval RC 5C (Dupont) for 1 hr at 4°C at 40,000g followed by ultracentrifugation in an XL-80 (Beckman) at 100,000g for 1 hr. After centrifugation, the clarified lysate was passed over a Ni²⁺ -chelating column (Pharmacia), and the bound histidine-tagged fusion protein was eluted with 100 mM imidazole (pH 7.5). Pooled fractions were loaded onto a Mono Q anion exchange column (Pharmacia) and eluted with a NaCl gradient from 0 to 500 mM.

The fractions containing the fusion protein were concentrated in a Centricon-30 (Amicon), and the 15 histidine tag was removed by overnight digestion with enterokinase (Biozyme) at 20°C. The digestion was terminated by the addition of aprotonin, leupeptin, PMSF, TPCK, and bovine pancreatic trypsin inhibitor 20 The cleaved kinase domain was then separated from the histidine tag on a Superose 12 size-exclusion column (Pharmacia). The eluted kinase domain was further purified on a Mono Q column. The purified kinase domain was analyzed by N-terminal sequencing and mass spectrometry. Five amino acids (SAAGT) remained 25 from the histidine tag. The predicted molecular mass was confirmed by mass spectrometry.

Crystal Growth

Purified FGFR1 was concentrated to 20-50 mg/ml and exchanged into 10 mM Tris-HCl (pH 8.0), 10 mM NaCl, and

2 mM DTT using a Centricon-30. Crystals were grown at $4\,^{\circ}$ C by vapor diffusion in hanging drops containing 2.0 μ l of 10 mg/ml protein solution and 2.0 μ l of reservoir solution: 16% polyethylene glycol (PEG) 10000, 0.3 M (NH₄),SO₄, 5% ethylene glycol, and 100 mM bis-Tris (pH 6.5).

Crystals of native FGFR1 were soaked in 500 ml stabilizing solution [25% PEG 10000, 0.3 M (NH4)₂SO₄, 0.1 M Bis-Tris (pH 6.5), 5% ethylene glycol] containing 3-[(3-(2-carboxyethyl)-4-methylpyrrol-5-yl)methylene]-2-indolinone (1-5 mM) or 3-[4-(4-formylpiperazine-1-yl)-benzylidenyl]-2-indolinone (1 mM) at 4°C for 24 to 48 hours. The final soaking concentration of DMSO was between 1 to 5%. The crystals cracked at higher concentrations of DMSO.

Co-crystals of FGFR1 with the inhibitors could also be obtained by vapor diffusion in hanging drops containing 2.0 μ l of 10 mg/ml protein solution and 2.0 μ l of reservoir solution containing 1 mM 3-[(3-(2-carboxyethyl)-4-methylpyrrol-5-yl)methylene]-2-indolinone and 3-[4-(4-formylpiperazine-1-yl-)benzylidenyl]-2-indolinone.

Co-crystals of FGFR1 complexed with AMP-PCP were obtained as described for the creation of native crystals, except that the protein solution additionally contained 10 mM AMP-PCP and 20 mM MgCl₂.

Preparation Of Heavy Atom Derivative Crystals

Heavy atom derivative crystals were obtained by soaking FGFR1 native crystals (C2-A form) in a solution containing ethylmercurithiosalicylic acid (thimerosal),

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 ${\rm KAu}\left({\rm CN}\right)_2$ or 4-chloromercuribenzoic acid, as provided in Table 1, infra,, and containing 25% PEG 10000, 0.3M ${\rm (NH_4)_2SO_4}$, 5% ethylene glycol or glycerol, and 100 mM bis-Tris (pH 6.5), and were flash-cooled either in liquid nitrogen directly (Synchrotron) or in a dry nitrogen stream at -175°C (rotating anode).

Data Collection and Structure Determination

For native crystals and crystals comprising the nucleotide analog AMP-PCP, data were collected either on 10 a Rigaku RU-200 rotating anode operated at 50 kV and 100 mA (Cu $K\alpha)$ and equipped with double-focusing mirrors and an R-AXIS IIC image plate detector, or at beamline X-4A at the National Synchrotron Light Source, Brookhaven National Laboratory. Synchrotron data (λ =1.07Å) were 15 collected on Fuji image plates and read with a Fuji scanner. One cryo-cooled crystal was used for each of the data sets. To obtain cryo-cooled crystals, crystals were soaked in a cryo-protectant solution containing 25% PEG 10000, 0.3 M $(NH_4)_2SO_4$, 5% ethylene glycol or 20 glycerol and 100 mM bis-Tris (pH 6.5), and were flashcooled either in liquid nitrogen directly (synchrotron data) or in a dry nitrogen stream at -175°C (rotating anode data). All data were processed using DENZO and SCALEPACK. Otwinowski, 1993, "Oscillation data 25 reduction program," Proceedings of the CCP4 Study Weekend, Sawyer et al., eds. (Daresbury, United Kingdom: SERC Daresbury Laboratory), 56-62.

For native crystals and crystals comprising the nucleotide analog AMP-PCP, a molecular replacement solution was found initially for the C2-B crystal form

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using an IRK search model that consisted of polyalanine with the common side chains for residues 993-1263 (FGFR1 residues 475-754), excluding residues 1094-1105 (kinase insert) and 1153-1170 (activation loop). With AMORE (Navaza, 1994, AmoRe: an automated package for molecular replacement," Acta Crystallogr. A50: 157-163), using 80% of the structure factor amplitudes between 15.0 and 3.5 Å, one of the two molecules in the asymmetric unit was The correlation coefficient (c.c.) for the correct 1-molecule solution was 0.23 (versus 0.20 for the highest incorrect solution). This molecule was rigid body-refined in X-PLOR (Brünger, 1992, X-PLOR (Version 3.1) Manual (New Haven, Conneticut: The Howeard Hughes Medical Institute and Department of Molecular Biophysics and Biochemistry, Yale Uiversity)), first as one rigid body unit, then as two units each comprising a lobe of the kinase. Rigid body refinement (12.0-3.5 Å, $F>3\sigma$) resulted in a relative rotation of the two lobes of ~10° and an increase of the c.c. from 0.20 to 0.25. The rigid body-refined molecule was then used as a new search model in AMORE, and this time both molecules in the asymmetric unit were located. The c.c. for the correct 2-molecule solution was 0.35 (versus 0.27 for the highest incorrect solution).

Multiple cycles of model building and refinement against 6.0-2.4 Å data resulted in the addition to the model of many of the side chains and some of the missing polypeptide chain. Model building was performed using TOM/FRODO (Jones, 1985, "Diffraction methods for biological macromolecules. Interactive computer graphics: FRODO," Methods in Enzymology 115: 157-171)

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and conjugate-gradient minimization and simulated annealing were performed using X-PLOR. Brünger, supra. At this stage, the R-value was 30% (free R-value of 36%). To help expedite model building and refinement, experimental phases were obtained. Because crystals grown in the presence of ethylene glycol were easier to manipulate than those grown in glycerol, several heavy-atom derivative data sets were collected from C2-A crystals that had been soaked in various heavy atom solutions. The C2-B structure was subsequently refined against 6.0-2.4 Å data to an R-value of 23.8% (free R-value of 30.4%) with r.m.s.d. values of 0.008 Å for bond distances and 1.4° for bond angles

Molecular replacement was used to locate the two FGFR1 molecules (designated FLGK-A and FLGK-B) in the 15 asymmetric unit of the C2-A crystal form. Using AMORE with 80% of structure factor amplitudes between 15.0 and 3.5 Å and the C2-B model, the c.c. for the correct 2molecule solution was 0.62 (versus 0.35 for the highest incorrect solution). Heavy atom positions were 20 determined from difference Fourier maps using the calculated phases from the partial model. Refinement of heavy atom parameters and phase determination were performed with MLPHARE (Otwinowski, 1991, "Maximum likelihood refinement of heavy atom parameters," 25 Isomorphous replacement and anomolous Ssattering, Evans and Leslie eds. (Darsbury, United Kingdom: SERC Daresbury Laboratory), 56-62)). An initial molecular isomorphous replacement (MIR)-phased electron density map was calculated with data between 2.0. and 2.8 $\mbox{\normalfont\AA}$ 30 resolution. This map was improved by solvent

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flattening, histogram matching, and non-crystallographic symmetry (NCS) averaging using DM (Cowtan, 1994, "Protein Crystallography," CCP4 and ESF-EACBM Newsletter (joint) 31: 34-38).

Refinement of the C2-A FGFR1 structure against 6.0-2.0 Å data proceeded by conjugate-gradient minimization and simulated annealing using X-PLOR. Tight NCS restraints were imposed until data to 2.0 Å resolution were included in the refinement, at which point the restraints were lifted. An overall anisotropic B-value was calculated using X-PLOR and applied to the observed structure factors, reducing the R-value by ~3%. Water molecules whose B-values refined to ≥70 Ų were omitted from the subsequent refinement round. The average Bvalue is 37.5 $Å^2$ for all protein atoms, 35.4 $Å^2$ for protein atoms in FLGK-A, 39.7 Å² for protein atoms in FLGK-B, and 40.2 Å² for water molecules. The side chains for Cys-603 in FLGK-A and FLGK-B and for Met-534 in FLGK-B have been modeled in two different conformations. Residues that are not included in the atomic model due to poor supporting electron density are for FLGK-A: 456-463, 486-490, 501-504, 580-591, 763-765; and for FLG-B: 456-460, 501-504, 578-593, 646-651, 657-659, 762-765.

The positions of the two AMP-PCP molecules (one per FGFR1 molecule) were easily identified in $2F_{\text{obs}(\text{co-complex})}$ - $F_{\text{calc}(\text{FGFR1})}$ difference Fourier maps. The AMP-PCP molecule bound to FLGK-B is less tightly bound and has been modeled with an occupancy of 0.5.

Table A summarizes the X-ray crystallography data sets of FGFR1 derivative crystals that were used to determine the structures of crystalline FGFR1 and



100 crystalline FGFR1:AMP-PCP co-complex of the invention.

TABLE 5

5		Native	Collection and M AMP-PCP	Thi-1°			
	X-ray source	X-4A	RU-200		Thi-2ª	PCMB ^a	KAu(CN)
	Resolution limit (Å)	2.0	2.3	RU-200	RU-200	RU-200	RU-200
	Number of sites		2.3	2.6	2.8	2.8	2.8
	Conc. (mM)/time (h)		-	4	7	2	2
	R _{sym} b(%)	4 9/10 700	~	0.1/24	0.1/48	0.2/2	5.0/72
	Total observations	4.8(19.7)°	4.5(23.3)°	5.5	9.8	6.8	6.8
	Unique reflections	122569	91324	55456	59488	67988	45303
	Completeness (%)	50771	31997	42820 ^d	35538ª	18619	18202
	Signal (%1>3 σ)	97.3(96.3)°	95.5(93.7)°	95.0	96.7	98.0	
	Signal (%1>30)	80.7(50.3)°	79.6(51.7) ^c	69.8	66.8	84.7	97.7 77.6
	$R_{iso}^{e}(\%)$,	//.0
	Phasing power			17.1	31.2	15.4	15.2
	R _{cullis} ^g (%)			1.8	2.0	1.0	0.9
	Overall FOMh		_	0.55	0.50	0.81	0.84

^aThi-1, Thi-2; ethylmercurithiosalicylic acid (thimerosal); PCMB: 4-chloromercuribenzoic acid. ${}^{b}R_{sym} = 100 \times \Sigma_{h}\Sigma_{i} | I_{i}(h) - \langle I(h) \rangle | / \Sigma_{h}\Sigma_{i}I_{i}(h)$

^dI(+h) and I(-h) processed as independent reflections. Anomalous scattering contributions were included.

 $^eR_{iso} = 100 \text{ x } \Sigma_h \mid |F_p(h) \pm F_p(h)| - |F_{PH}(h)| \mid /\Sigma_h |F_p(h)|, \text{ where } F_p \text{ and } F_{PH} \text{ are the native and derivative } F_p(h)| = 100 \text{ m}$ structure factors, respectively.

Phasing power: r.m.s. heavy atom structure factor / r.m.s. lack of closure (for acentric reflections

 ${}^gR_{cullis} = 100 \text{ x } \Sigma_h \mid |F_{PH}(h)| - F_{H(cale)}(h)|/\Sigma_h|F_{PH}(h) \pm F_p(h)| \text{ (for centric reflections from 20.0 to 2.8Å)}.$ 30 ^hFigure of merit: $\int P(\phi)\exp(i\phi)d\phi/\int P(\phi)d(\phi)$, where P is the probability distribution of the phase

^cValue in parentheses is for the highest resolution shell.

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For crystals comprising FGFR1 and compounds 1 and 2, data were collected on a Rigaku RU-200 rotating anode (Cu Kα) operating at 50 kV and 100 mA and equipped with double-focusing mirrors and an R-AXIS IIC image plate detector. One cryo-cooled crystal was used for each of the data sets. Crystals were soaked in a cryo-protectant [25% PEG 10000, 0.3 M (NH,),SO,, 5% ethylene glycol, 100 mM bis-Tris (pH 6.5), and 1 mM: 3-[(3-(2-carboxyethyl)-4-methylpyrrol-5-yl)methylene]-2indolinone (hereafter referred to as compound 1) or 3-[4-(4-formylpiperazine-1-yl-)benzylidenyl]-2-indolinone (hereafter referred to as compound 2) and flash-cooled in a dry nitrogen stream at -175°C. Data were processed using DENZO and SCALEPACK. Otwinowski, 1993, Proceedings of the CCP4 Study Weekend (Daresbury, United Kingdom: SERC Daresbury Laboratory) pp 56-62.

A summary of the data collection parameters are included in the following Table 6:

20 TABLE 6

	Resolution limit (Å)	Observa- tions (N)	Complete- ness (%)	Redundan-	R _{sym} a (%)	Signal (I> σI)
compound	2.5	93535	97.6 (96.1)	2.7	6.8 (23.0)	11.8
compound 2	2.4	94093	99.1 (97.9)	3.3	6.3 (32.2)	11.4

compound 1 structure: 550 residues, 252 water molecules, 2 compound 1 molecules (4589 atoms) compound 2 structure: 550 residues, 248 water molecules, 2 compound 2 molecules (4646 atoms)

30 <u>Structure Analyses</u>

Atomic superpositions were performed with TOSS

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(Hendrickson, 1979). Per residue solvent accessible surface calculations were done with X-PLOR. The surface area buried in a dimer interface was calculated with GRASP (Nicholls et al., 1991) using a probe radius of 1.4 Å. The stereochemical quality of the atomic model was monitored using PROCHECK (Laskowski et al., 1993, PROCHECK: a computer program to check the stereochemical quality of protein structures," J. Appl. Cryst. 26: 283-291). As defined in PROCHECK, 93% of the residues in the model have main-chain torsion angles in the most favored Ramachandran regions. There are no residues in disallowed regions, and three residues in generously allowed regions: Arg-622 in FLGK-A and FLGK-B and Arg-554 in FLGK-A. The overall G-factor score is 0.42.

Table 7 summarizes the X-ray crystallography refinement parameters of the structures of crystalline FGFR1 and crystalline FGFR1:AMP-PCP co-complex of the invention. Table 8 summarizes the X-ray crystallography refinement parameters for the FGFR1/compound complexes.

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TABLE 7

Refinement Parameters								
FGFR1: 550 residues, 252 water molecules (4589 atoms)								
FGFR1:AMP-PCP: 550 residues, 238 water molecules, 2 AMP-PCP molecules (4638 atoms)								
Model	d-spacings	D-d		MP-PCP mo	lecules (463)	8 atoms)		
		Reflection s	R-value ^a	R.m.s.d.				
	(Å)	(N)	(%)	bonds (Å)	angles (°)	B-value		
FGFR1:	6.0-2.0	42548	21.3 (26.2)°			(Ų)		
FGFR1:AMP-PCP:	6.0-2.3			0.008	1.3	1.6		
	0.0-2.3	26729	20.1 (27.5)°	0.009	1.4	1.7		

30 a R-value = 100 x $\Sigma_h ||F_{obs}(h)| - |F_{catc}(h)|| / \Sigma_h |F_{obs}(h)|$ for reflections with $F_{obs} > 2\sigma$.

^bFor bonded protein atoms.

^cValue in parentheses is the free R-value (Brünger, 1993) determined from 5% of the data.

TABLE 8

Rbonds (Å) Model d-spacings (Å) Reflecangles (°) Btions valuei (N) valuesⁱ $(Å^2)$ 6.0 - 2.419.7 0.008 compound 42548 1.3 1.6 $(27.0)^{k}$ compound 6.0 - 2.50.008 1.7 26729 20.0 1.4 2 $(28.0)^{k}$

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ⁱR-value = $100 \times S_h ||F_o(h)|| - |F_c(h)|| / S_h ||F_o(h)||$, where F_o and F_c are the observed and calculated structure factors, respectively $(F_o > 2s)$.

15 For bonded protein atoms.

^kValue in parentheses is the free R-value determined from 5% of the data.

Atomic Structural Coordinates

Tables 1 and 2 provide the atomic structural coordinates of unphosphorylated FGFR1 and unphosphorylated FGFR1:AMP-PCP co-complex, respectively. In the Tables, coordinates for both of the FGFR1 molecules of the dimer comprising the asymmetric unit are provided. The amino acid residue numbers coincide with those used in FIG. 3. In the first FGFR1 molecule of the dimer the residue number is preceded by a 1, i.e., residue number 464 of the first FGFR1 molecule of the dimer is denoted by "1464". Tables 3 and 4 provide the atomic structural coordinates of FGFR1 in complex with indolinone compounds found to inhibit FGFR1 function.

 $^{{}^{}a}R_{sym} = 100 \times S_{h}S_{i} |I_{i}(h) - I(h)^{0}| / S_{h}S_{i} |I_{i}(h)$

^cValue in parentheses is for the highest resolution shell.

The following abbreviations are used in the Tables:

"Atom Type" refers to the element whose coordinates
are provided. The first letter in the column defines
the element.

5 "A.A." refers to amino acid.

"X, Y and Z" provide the Cartesian coordinates of the element.

" \underline{B} " is a thermal factor that measures movement of the atom around its atomic center.

"OCC" refers to occupancy, and represents the percentage of time the atom type occupies the particular coordinate. OCC values range from 0 to 1, with 1 being 100%.

"PRT1" or "PRT2" relate to occupancy, with PRT1

designating the coordinates of the atom when in the first conformation and PRT2 designating the coordinates of the atom when in the second or alternate conformation.

Structural coordinates for FGFR1 may be modified by

20 mathematical manipulation. Such manipulations include,
but are not limited to, crystallographic permutations of
the raw structure coordinates, fractionalization of the
raw structure coordinates, integer additions or
subtractions to sets of the raw structure coordinates,

25 inversion of the raw structure coordinates and any
combination of the above.

In addition, the structural coordinates can be slightly modified and still render nearly identical three dimensional structures. Therefore, a measure of a unique set of structural coordinates is the root-mean-square deviation of the resulting structure. Structural

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coordinates that render three dimensional structures that deviate from one another by a root-mean-square deviation of less than 1.5 Å may be viewed as identical.

5 EXAMPLE 2: Computer-Based Design of Modulators of PTK Function

Potential modulators of PTK function were designed and identified by operating the program Catalyst on the structure of 3-[(3-(2-carboxyethyl)-4-methylpyrrol-5-yl)methylene]-2-indolinone. The chemical features constraining the search model include a hydrogen bond donor, a hydrogen bond acceptor, and two hydrophobic points of contact. Approximately 40 compounds were identified as potential modulators of PTK function using this method.

The compounds identified by the method as potential modulators of PTK function were commercially available. These compounds were then tested for their ability to inhibit the FLK PTK in an enzyme linked immunosorbant assay (ELISA). The method of performing this assay is taught in WO 96/40116, entitled "Indolinone Compounds for the Treatment of Disease," published on December 19, 1996, invented by Tang et al., incorporated by reference herein in its entirety, including all figures, drawings, and tables. Flk-1 specific antibodies can be prepared from the following protocol:

1. Prepare a Tresyl-Activated Agarose/Flk-1-D column
by incubating 10 ml of Tresyl-Activated Agarose
with 20 mg of purified GST-Flk-1-D fusion protein

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in 100mM sodium bicarbonate (pH 9.6) buffer overnight at 4°C.

- Wash the column once with PBS. 2.
- Block the excess sites on the column with 2 $\ensuremath{\text{M}}$ 3. glycine for 2 hours at 4°C.
- Wash the column with PBS. 4.
- 5. Incubate the column with Rabbit anti-Flk-1D production bleed for 2 hours at 4°C.
- Wash the column with PBS. 6.
- 10 Elute antiserum with 100 mM Citric Acid, pH3.0 and 7. neutralize the eluate immediately with 2 M Tris , pH
 - Dialyize the eluate against PBS overnight at 4oC with 3 changes of buffer (sample to buffer ratio is 9.
 - Adjust the dialyized antiserum to 5% glycerol and store at -80°C in small aliquotes.
- The Flk-1 ELISA can include a 2,2-azino-bis(3ethylbenz-thiazoline-6-sulfonic acid (ABTS) solution, 20 which can comprise 100mM citric acid (anhydrous), 250 mM $\mathrm{Na_2HPO_4}$ (pH 4.0), 0.5 mg/ml ABTS (Sigma catalog no. A-1888). The solution is most appropriately stored in dark at 4°C until ready for use.
- 25 The FLK-1 specific antibodies can also be purchased from Santa Cruz Biotechnology (Catalog No. SC-504).

Four of the forty compounds identified as potential modulators of PTK function were potent modulators of FLK function. These molecules have the following structures:

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The modulators inhibit the FLK protein kinase with the following IC50 values:

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TABLE 9

		IADLL		ICE ID	
Compound	FLK kinase IC ₅₀ (μM) compounds	FLK kinase IC ₅₀ (μM) compounds tested at 20μM	EGFR IC ₅₀ (μM)	IGF-1R IC ₅₀ (μM)	
	tested at 100 µM	14	>100	>100	
1	14.8	10.6	>100	>100	
2	21.4	16.6	68	30.9	
3	22.9	16.4	>100	>100	

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The invention illustratively described herein may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. The terms and expressions which have

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been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various 5 modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments and optional features, modification and variation of the concepts 10 herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the appended claims.

Those references not previously incorporated herein by reference, including both patent and non-patent references, are expressly incorporated herein by reference for all purposes. Other embodiments are within the following claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

SUGEN, INCORPORATED 351 Galveston Drive Redwood City, CA 94063

(ii) TITLE OF INVENTION:

CRYSTAL STRUCTURES OF A PROTEIN TYROSINE KINASE

(iii) NUMBER OF SEQUENCES:

5

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STATE: (D)

U.S.A.

COUNTRY: (E) ZIP: (F)

90071-2066

(v) COMPUTER READABLE FORM:

MEDIUM TYPE: (A)

3.5" Diskette, 1.44 Mb

storage

COMPUTER: (B)

IBM Compatible

OPERATING SYSTEM: (C)

IBM P.C. DOS 5.0

(D) SOFTWARE:

FastSEQ for Windows 2.0

CURRENT APPLICATION DATA: (vi)

(A) APPLICATION NUMBER:

To Be Assigned Herewith

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:



(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME:

Warburg, Richard J.

(B) REGISTRATION NUMBER:

(C) REFERENCE/DOCKET NUMBER: 227/088-PCT

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(213) 955-0440

(C) TELEX:

67-3510

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

310 amino acids

(B) TYPE:

amino acid

(C) STRANDEDNESS: (D) TOPOLOGY:

single linear

(ii) MOLECULE TYPE:

protein

(iii) HYPOTHETICAL:

NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Leu Ala Gly Val Ser Glu Tyr Glu Leu Pro Glu Asp Pro Arg Trp 15

Glu Leu Pro Arg Asp Arg Leu Val Leu Gly Lys Pro Leu Gly Glu Gly

Cys Phe Gly Gln Val Val Leu Ala Glu Ala Ile Gly Leu Asp Lys Asp

Lys Pro Asn Arg Val Thr Lys Val Ala Val Lys Met Leu Lys Ser Asp

Ala Thr Glu Lys Asp Leu Ser Asp Leu Ile Ser Glu Met Glu Met Met 75

Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys

Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly

Asn Leu Arg Glu Tyr Leu Gln Ala Arg Arg Pro Pro Gly Leu Glu Tyr

Cys Tyr Asn Pro Ser His Asn Pro Glu Glu Gln Leu Ser Ser Lys Asp

Leu Val Ser Cys Ala Tyr Gln Val Ala Arg Gly Met Glu Tyr Leu Ala 150

Ser Lys Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu Val 165 170

Thr Glu Asp Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp 185

Ile His His Ile Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro 195 200

Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Ile Tyr Thr His 215

Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Thr 230 235

Leu Gly Gly Ser Pro Tyr Pro Gly Val Pro Val Glu Glu Leu Phe Lys 245 250

Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ser Asn Cys Thr Asn 265

Glu Leu Tyr Met Met Met Arg Asp Cys Trp His Ala Val Pro Ser Gln 280

Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Ile Val Ala

Leu Thr Ser Asn Gln Glu 310

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

315 amino acids

(B) TYPE:

amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY:

linear

(ii) MOLECULE TYPE:

protein

(iii) HYPOTHETICAL:

NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Ala Ala Gly Thr Met Val Ala Gly Val Ser Glu Tyr Glu Leu Pro

Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu Val Leu Gly Lys 20 25



- Pro Leu Gly Glu Gly Ala Phe Gly Gln Val Val Leu Ala Glu Ala Ile 35 40 45
- Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys Val Ala Val Lys
 50 55 60
- Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Ile Ser 65 70 75 80
- Glu Met Glu Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn 85 90 95
- Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu
- Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln Ala Arg Arg Pro 115 120 125
- Pro Gly Leu Glu Tyr Ser Tyr Asn Pro Ser His Asn Pro Glu Glu Gln 130 135 140
- Leu Ser Ser Lys Asp Leu Val Ser Cys Ala Tyr Gln Val Ala Arg Gly
 145 150 155 160
- Met Glu Tyr Leu Ala Ser Lys Lys Cys Ile His Arg Asp Leu Ala Ala 165 170 175
- Arg Asn Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala Asp Phe 180 185 190
- Gly Leu Ala Arg Asp Ile His His Ile Asp Tyr Tyr Lys Lys Thr Thr
 195 200 205
- Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp 210 215 220
- Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu 225 230 235 240
- Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Val Pro Val 245 250 255
- Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro 260 265 270
- Ser Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp His 275 280 285
- Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu 290 295 300
- Asp Arg Ile Val Ala Leu Thr Ser Asn Gln Glu 305 310 315

(2)	INFORMATION	FOR	SEQ	ID	NO:3:

(i) SEQUENCE CHARACTERISTICS:

351 amino acids (A) LENGTH: amino acid (B) TYPE:

(C) STRANDEDNESS: single linear (D) TOPOLOGY:

protein (ii) MOLECULE TYPE:

(iii) HYPOTHETICAL:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Arg Gly Ser His His His His His Gly Met Ala Ser Met Thr

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Lys Asp

Pro Ser Ser Arg Ser Ala Ala Gly Thr Met Val Ala Gly Val Ser Glu

Tyr Glu Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu

Val Leu Gly Lys Pro Leu Gly Glu Gly Ala Phe Gly Gln Val Val Leu

Ala Glu Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys

Val Ala Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser 100

Asp Leu Ile Ser Glu Met Glu Met Lys Met Ile Gly Lys His Lys

Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr

Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln 150 145

Ala Arg Arg Pro Pro Gly Leu Glu Tyr Ser Tyr Asn Pro Ser His Asn

Pro Glu Glu Gln Leu Ser Ser Lys Asp Leu Val Ser Cys Ala Tyr Gln 180

Val Ala Arg Gly Met Glu Tyr Leu Ala Ser Lys Lys Cys Ile His Arg

BNSDOCID: <WO___9807835A2_IA>



Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val Met Lys 210 215 220
Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile His His Ile Asp Tyr Tyr 230 235
Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu
Ala Leu Phe Asp Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Phe
Gly Val Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro 275 280
Gly Val Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg
Met Asp Lys Pro Ser Asn Cys Thr Asn Glu Leu Tyr Met Met Arg
Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu
Val Glu Asp Leu Asp Arg Ile Val Ala Leu Thr Ser Asn Gln Glu 340 345 350

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:
(B) TYPE:
(C) STRANDEDNESS:
(D) TOPOLOGY:

933 base pairs nucleic acid double linear

(ii) MOLECULE TYPE:

CDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGCTAGCAG GGGTCTCTGA GTATGAGCTT CCCGAAGACC CTCGCTGGGA GCTGCCTCGG 60
GACAGACTGG TCTTAGGCAA ACCCCTGGGA GAGGGCTGCT TTGGGCAGGT GGTGTTGGCA 120
GAGGCTATCG GGCTGGACAA GGACAAACCC AACCGTGTGA CCAAAGTGGC TGTGAAGATG 180
TTGAAGTCGG ACGCAACAGA GAAAGACTTG TCAGACCTGA TCTCAGAAAT GGAGATGATG 240
AAGATGATCG GGAAGCATAA GAATATCATC AACCTGCTGG GGGCCTGCAC GCAGGATGGT 300
CCCTTGTATG TCATCGTGGA GTATGCCTCC AAGGGCAACC TGCGGGAGTA CCTGCAGGCC 360
CGGAGGCCCC CAGGGCTGGA ATACTGCTAC AACCCCAGCC ACAACCCAGA GGAGCAGCTC 420



TCCTCCAAGG ACCTGGTGTC CTGCGCCTAC CAGGTGGCCC GAGGCATGGA GTATCTGGCC 480 TCCAAGAAGT GCATACACCG AGACCTGGCA GCCAGGAATG TCCTGGTGAC AGAGGACAAT 540 GTGATGAAGA TAGCAGACTT TGGCCTCGCA CGGGACATTC ACCACATCGA CTACTATAAA 600 AAGACAACCA ACGGCCGACT GCCTGTGAAG TGGATGGCAC CCGAGGCATT ATTTGACCGG 660 ATCTACACCC ACCAGAGTGA TGTGTGGTCT TTCGGGGTGC TCCTGTGGGA GATCTTCACT 720 CTGGGCGGCT CCCCATACCC CGGTGTGCCT GTGGAGGAAC TTTTCAAGCT GCTGAAGGAG 780 GGTCACCGCA TGGACAAGCC CAGTAACTGC ACCAACGAGC TGTACATGAT GATGCGGGAC 840 TGCTGGCATG CAGTGCCCTC ACAGAGACCC ACCTTCAAGC AGCTGGTGGA AGACCTGGAC 900 933 CGCATCGTGG CCTTGACCTC CAACCAGGAG TAG

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

1056 base pairs nucleic acid

(B) TYPE: (C) STRANDEDNESS: double

(D) TOPOLOGY:

linear

(ii) MOLECULE TYPE:

cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGCGGGGTT CTCATCATCA TCATCATCAT GGTATGGCTA GCATGACTGG TGGACAGCAA 60 ATGGGTCGGG ATCTGTACGA CGATGACGAT AAGGATCCGA GCTCGAGATC TGCAGCTGGT 120 ACCATGGTAG CAGGGGTCTC TGAGTATGAG CTTCCCGAAG ACCCTCGCTG GGAGCTGCCT 180 CGGGACAGAC TGGTCTTAGG CAAACCCCTG GGAGAGGGCG CCTTTGGGCA GGTGGTGTTG 240 GCAGAGGCTA TCGGGCTGGA CAAGGACAAA CCCAACCGTG TGACCAAAGT GGCTGTGAAG 300 ATGTTGAAGT CGGACGCAAC AGAGAAAGAC TTGTCAGACC TGATCTCAGA AATGGAGATG 360 ATGAAGATGA TCGGGAAGCA TAAGAATATC ATCAACCTGC TGGGGGCCTG CACGCAGGAT 420 GGTCCCTTGT ATGTCATCGT GGAGTATGCC TCCAAGGGCA ACCTGCGGGA GTACCTGCAG 480 GCCCGGAGGC CCCCAGGGCT GGAATACTCC TACAACCCCA GCCACAACCC AGAGGAGCAG 540 CTCTCCTCCA AGGACCTGGT GTCCTGCGCC TACCAGGTGG CCCGAGGCAT GGAGTATCTG 600 GCCTCCAAGA AGTGCATACA CCGAGACCTG GCAGCCAGGA ATGTCCTGGT GACAGAGGAC 660

AATGTGATGA AGATAGCAGA CTTTGGCCTC GCACGGGACA TTCACCACAT CGACTACTAT	
AAAAAGACAA CCAACGGCCC ACTOR	720
AAAAAGACAA CCAACGGCCG ACTGCCTGTG AAGTGGATGG CACCCGAGGC ATTATTTGAC	780
TGATGTGTGG TCTTTCGGGG TGCTCCTCTG	700
ACTCTGGGCG GCTCCCCATA CCCCGGTGTG CCTGTGGAGG AACTTTTCAA GCTGCTGAAG	840
GAGGGTCACC GCATGGACAA GCCCACTAAG	900
GAGGGTCACC GCATGGACAA GCCCAGTAAC TGCACCAACG AGCTGTACAT GATGATGCGG	960
GACTGCTGGC ATGCAGTGCC CTCACAGAGA CCCACCTTCA AGCAGCTGGT GGAAGACCTG	
GACCGCATCG TGGCCTTGAC CTCCAACCAG GAGTAG	1020
	1056



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TABLE 1

Ato No		Atom Type	A.A	A.A No.	x	Y	Z	occ	В	
	•	-750		2.0.						
ATOM	1	N	GLU	1464	-13.639	16.975	8.571	1.00	54.29	-
MOTA	3	CA	GLU	1464	-12.479	17.105	7.695	1.00	52.62	
ATOM	4	CB	GLU	1464	-11.400	17.974	8.349	1.00	54.64	
ATOM	5	, C	GLU	1464	-11.914	15.738	7.319	1.00	49.74	
ATOM	6	0	GLU	1464	-11.845	15.407	6.136	1.00	52.04	
MOTA	7	N	LEU	1465	-11.562	14.925	8.310	1.00	44.95	
ATOM	9	CA	LEU	1465	-11.018	13.599	8.037	1.00	41.04	
MOTA	10	СВ	LEU	1465	-10.236	13.066	9.235	1.00	40.18	
ATOM	11	CG	LEU	1465	-8.719	13.196	9.130	1.00	43.70	
MOTA	12	CD1	LEU	1465	-8.346	14.654	8.891	1.00	46.74	
ATOM	13	CD2	LEU	1465	-8.061	12.671		1.00	40.72	
ATOM	14	C	LEU	1465	-12.092	12.594	7.656	1.00	39.18	
ATOM	15	0	LEU	1465	-13.187	12.590	8.219	1.00	38.05	
MOTA	16	N	PRO	1466	-11.802	11.748	6.657	1.00	37.20	
ATOM	17	CD	PRO	1466	-10.597	11.793	5.810	1.00	36.41	
MOTA	18	CA	PRO	1466	-12.741	10.727	6.189	1.00	36.13	
MOTA	19	СВ	PRO	1466	-12.110	10.262	4.878	1.00	37.50	
MOTA	20	CG	PRO	1466	-10.629	10.459	5.135	1.00	36.20	
ATOM	21	С	PRO	1466	-12.846	9.595	7.201	1.00	35.61	
MOTA	22	0	PRO	1466	-11.847	9.174	7.788	1.00	35.18	
ATOM	23	N	GLU	1467	-14.060	9.121	7.429	1.00	35.38	
ATOM	25	CA	GLU	1467	-14.268	8.053	8.377	1.00	35.43	
ATOM	26	CB	GLU	1467	-15.744	7.965	8.746	1.00	41.10	
ATOM	27	CG	GLU	1467	-16.375	9.280	9.098	1.00	48.25	
ATOM	28	CD	GLU	1467	-17.819	9.145	9.596	1.00	50.24	
ATOM	29	OE1	GLU	1467	-18.446	8.071	9.378	1.00	52.82	
MOTA	30	OE2	GLU	1467	-18.314	10.109	10.230	1.00	51.26	
MOTA	31	C	GLU	1467	-13.838	6.714	7.801	1.00	32.65	
MOTA	32	0	GLU	1467	-13.899	6.511	6.591	1.00	35.06	
MOTA	33	N	ASP	1468	-13.299	5.854	8.659	-1.00	30.46	
MOTA	35	CA	ASP	1468	-12.883	4.516	8.262	1.00	28.85	
ATOM	36	CB	ASP	1468	-11.384	4.424	7.975	1.00	29.34	
ATOM	37	CG	ASP	1468	-10.985	3.072	7.408	1.00	27.57	
ATOM	38	OD1	ASP	1468	-11.833	2.159	7.359	1.00	27.78	
ATOM	39	OD2	ASP	1468	-9.817	2.916	7.003	1.00	30.64	
MOTA	40	C	ASP	1468	-13.252	3.564	9.384	1.00	29.29	
MOTA	41	0	ASP	1468	-12.481	3.364	10.336	1.00	27.76	
ATOM	42	N	PRO	1469	-14.435	2.939	9.268	1.00	28.99	
MOTA	43	CD	PRO	1469	-15.354	3.091	8.120	1.00	28.09	
ATOM	44	CA	PRO	1469	-14.971	1.987	10.244	1.00	30.01	
ATOM	45	CB	PRO	1469	-16.244	1.473	9.553	1.00	33.33	
ATOM	46	CG	PRO	1469	-16.665	2.630	8.690	1.00	30.53	
ATOM	47	С	PRO	1469	-14.012	0.848	10.563	1.00	28.96	
ATOM	48	0	PRO	1469	-14.085	0.251	11.636	1.00	28.52	
ATOM	49	N	ARG	1470	-13.106	0.556	9.631	1.00	27.59	
ATOM	51	CA	ARG	1470	-12.139	-0.520	9.810	1.00	27.37	
ATOM	5 2	CB	ARG	1470	-11.301	-0.707	8.533	1.00	28.84	

ATOM	53	CG	ARG	1470	-12.049	-1.279	7.317	1.00	30.57
ATOM	54	CD	ARG	1470	-11.137	-1.352	6.068	1.00	26.71
ATOM	55	NE	ARG	1470	-10.489	-0.068	5.793	1.00	31.26
ATOM	57	CZ	ARG	1470	-9.603	0.151	4.823	1.00	32.60
ATOM	58	NH1	ARG	1470	-9.241	-0.828	3.999	1.00	33.19
MOTA	61	NH2	ARG	1470	-9.067	1.359	4.686	1.00	28.65
ATOM	64	C	ARG	1470	-11.180	-0.285	10.981	1.00	29.21
ATOM	65	0	ARG	1470	-10.757	-1.230	11.641	1.00	28.47
ATOM	66	N	TRP	1471	-10.909	0.977	11.280	1.00	27.80
ATOM	68	CA	TRP	1471	-9.940	1.314	12.306	1.00	28.62
ATOM	69	CB	TRP	1471	-8.729	1.944	11.609	1.00	24.97
MOTA	70	CG	TRP	1471	-8.044	0.976	10.728	1.00	24.86
ATOM	71	CD2	TRP	1471	-7.156	-0.060	11.144	1.00	28.00
ATOM	72	CE2	TRP	1471	-6.782	-0.776	9.989	1.00	29.23
MOTA	7 3	CE3	TRP	1471	-6.642	-0.460	12.389	1.00	26.59
ATOM	74	CD1	\mathtt{TRP}	1471	-8.166	0.860	9.374	1.00	27.23
MOTA	7 5	NE1	TRP	1471	-7.413	-0.192	8.922	1.00	30.10
MOTA	77	CZ2	TRP	1471	-5.912	-1.866	10.036	1.00	28.70
MOTA	78	CZ3	TRP	1471	-5.778	-1.545	12.435	1.00	27.18
ATOM	79	CH2	TRP	1471	-5.424	-2.237	11.266	1.00	27.23
ATOM	80	C	TRP	1471	-10.371	2.223	13.440	1.00	28.42
ATOM	81	0	TRP	1471	-9.664	2.321	14.442	1.00	26.48
MOTA	82	N	GLU	1472	-11.521	2.874	13.293	1.00	28.62
MOTA	84	CA	GLU	1472	-11.981	3.823	14.297	1.00	27.16
MOTA	85	CB	GLU	1472	-13.245	4.534	13.799	1.00	28.89
MOTA	86	CG	GLU	1472	-13.552	5.869	14.520	1.00	29.09
MOTA	87	CD	GLU	1472	-12.692	7.042	14.054	1.00	26.43
MOTA	88	OE1	GLU	1472	-12.134	7.009	12.938	1.00	28.59
MOTA	89	OE2	GLU	1472	-12.596	8.024	14.801	1.00	27.28
MOTA	90	С	GLU	1472	-12.217	3.269	15.701	1.00	25.10
ATOM	91	0	GLU	1472	-12.763	2.196	15.861	1.00	26.48
ATOM	92	N	LEU	1473	-11.750	3.991	16.711	1.00	24.65
MOTA	94	CA	LEU	1473	-11.962	3.608	18.104	1.00	26.27
MOTA	95	CB	LEU	1473	-10.645	3.266	18.817	1.00	28.24
MOTA	96	CG	LEU	1473	-10.750	3.025	20.337	1.00	27.23
MOTA	97	CD1	LEU	1473	-11.323	1.636	20.642	1.00	25.23
MOTA	98	CD2	LEU	1473	-9.390	3.183	21.000	1.00	26.33
ATOM	99	С	LEU	1473	-12.546	4.856	18.740	1.00	26.52
ATOM	100	0	LEU	1473	-12.122	5.973	18.411	1.00	25.16
MOTA	101	N	PRO	1474	-13.610	4.703	19.554	1.00	28.52
ATOM	102	CD	PRO	1474	-14.435	3.500	19.770	1.00	29.65
MOTA	103	CA	PRO	1474	-14.215	5.870	20.207	1.00	29.18
MOTA	104	CB	PRO	1474	-15.368	5.251	21.003	1.00	28.58
ATOM ·	105	CG	PRO	1474	-15.768	4.097	20.154	1.00	28.17
MOTA	106	C	PRO	1474	-13.173	6.528	21.124	1.00	29.75
MOTA	107	0	PRO	1474	-12.427	5.841	21.828	1.00	31.78
ATOM	108	N	ARG	1475	-13.107	7.849	21.097	1.00	30.76
MOTA	110	CA	ARG	1475	-12.149	8.588	21.900	1.00	32.26
MOTA	111	CB	ARG	1475	-12.362	10.083	21.743	1.00	
MOTA	112	CG	ARG	1475	-12.178	10.536	20.342	1.00	31.58 37.54
ATOM	113	CD	ARG	1475	-12.048	12.027	20.342	1.00	36.96
ATOM	114	NE	ARG	1475	-11.733	12.317	18.813	1.00	
MOTA	116	CZ	ARG	1475	-10.503	12.501	18.352	1.00	40.07
ATOM	117	NH1	ARG	1475	-9.470	12.301			37.59
					J. 7 / U	14.44/	19.186	1.00	34.89

ATOM	120	NH2	ARG	1475	-10.308	12.669	17.049	1.00	34.54
ATOM	123	C	ARG	1475	-12.173	8.261	23.371	1.00	35.58
MOTA	124	0	ARG	1475	-11.135	8.318	24.036	1.00	37.03
MOTA	125	N	ASP	1476	-13.356	7.958	23.889	1.00	36.68
MOTA	127	CA	ASP	1476	-13.498	7.647	25.307	1.00	37.07
MOTA	128	CB	ASP	1476	-14.967	7.759	25.740	1.00	37.87
MOTA	129	CG	ASP	1476	-15.851	6.704	25.115	1.00	38.93
MOTA	130	OD1	ASP	1476	-15.412	6.015	24.179	1.00	43.75
MOTA	131	OD2	ASP	1476	-17.003	6.558	25.563	1.00	45.77
ATOM	132	С	ASP	1476	-12.922	6.292	25.701	1.00	35.86
MOTA	133	0	ASP	1476	-12.923	5.928	26.878	1.00	37.98
MOTA	134	N	ARG	1477	-12.478	5.527	24.711	1.00	33.37
ATOM	136	CA	ARG	1477	-11.889	4.221	24.961	1.00	31.84
ATOM	137	CB	ARG	1477	-12.214	3.262	23.809	1.00	31.84
MOTA	138	CG	ARG	1477	-13.693	2.965	23.580	1.00	29.70
ATOM	139	CD	ARG	1477	-14.366	2.365	24.809	1.00	33.88
ATOM	140	NE	ARG	1477	-14.596	3.372	25.838	1.00	33.86
ATOM	142	cz	ARG	1477	-14.845	3.102	27.113	1.00	34.14
ATOM	143	NH1	ARG	1477	-14.906	1.846	27.542	1.00	30.58
ATOM	146	NH2	ARG	1477	-15.024	4.102	27.961	1.00	33.14
ATOM	149	С	ARG	1477	-10.373	4.338	25.105	1.00	31.30
MOTA	150	0	ARG	1477	-9.679	3.362	25.365	1.00	32.32
MOTA	151	N	LEU	1478	-9.856	5.544	24.978	1.00	32.85
MOTA	153	CA	LEU	1478	-8.426	5.739	25.054	1.00	35.64
MOTA	154	CB	LEU	1478	-7.964	6.360	23.737	1.00	34.96
ATOM	155	CG	LEU	1478	-6.498	6.291	23.331	1.00	36.36
MOTA	156	CD1	LEU	1478	-6.059	4.833	23.192	1.00	30.71
ATOM	157	CD2	LEU	1478	-6.335	7.048	22.020	1.00	33.97
ATOM	158	С	LEU	1478	-8.054	6.625	26.243	1.00	37.60
ATOM	159	0	LEU	1478	-8.366	7.815	26.263	1.00	41.20
ATOM	160	N	VAL	1479	-7.442	6.023	27.257	1.00	36.52
ATOM	162	CA	VAL	1479	-7.008	6.745	28.449	1.00	35.59
MOTA	163	CB	VAL	1479	-7.041	5.829	29.688	1.00	35.92
MOTA	164	CG1	VAL	1479	-6.712	6.627	30.926	1.00	39.40
MOTA	165	CG2	VAL	1479	-8.404	5.163	29.825	1.00	34.46
ATOM	166	С	VAL	1479	-5.577	7.224	28.197	1.00	35.36
MOTA	167	0	VAL	1479	-4.622	6.443	28.269	1.00	32.50
MOTA	168	N	LEU	1480	-5.439	8.506	27.878	1.00	37.77
MOTA	170	CA	LEU	1480	-4.132	9.086	27.572	1.00	42.77
MOTA	171	CB	LEU	1480	-4.298	10.421	26.842	1.00	41.84
MOTA	172	CG	LEU	1480	-4.991	10.369	25.471	1.00	42.45
MOTA	173	CD1	LEU	1480	-5.135	11.774	24.924	1.00	42.58
MOTA	174	CD2	LEU	1480	-4.200	9.508	24.502	1.00	43.09
MOTA	175	C	LEU	1480	-3.211	9.233	28.778	1.00	45.25
MOTA	176	0	LEU	1480	-3.621	9.739	29.822	1.00	45.47
MOTA	177	N	GLY	1481	-1.958	8.816	28.612	1.00	46.82
MOTA	179	CA	GLY	1481	-1.016	8.889	29.708	1.00	50.47
MOTA	180	С	GLY	1481	0.296	9.617	29.472	1.00	52.24
ATOM	181	0	GLY	1481	0.360	10.638	28.781	1.00	53.41
MOTA	182	N	LYS	1482	1.349	9.070	30.068	1.00	53.64
MOTA	184	CA	LYS	1482	2.697	9.627	30.000	1.00	56.19
MOTA	185	CB	LYS	1482	3.636	8.776	30.859	1.00	57.19
MOTA	186	CG	LYS	1482	5.115	9.023	30.628	1.00	61.02
MOTA	187	CD	LYS	1482	5.938	7.831	31.089	1.00	63.12

7.07	1014								
	OM 18	-		YS 1482	5.494	6.54	47 30.39	95 1.00	
				YS 1482		5.36			
					3.297	9.79			
AT		_			0.251	8.86			
AT		_			0.002	10.98	3 28.32		
AT		_			رون. ت	12.19			
ATO						11.25			
ATO						12.71			
ATO					,2,	13.27			58.75
ATO			PR		0.075	10.33	5 26.83		58.79 61.17
ATO			PR		6.509	10.21			61.31
ATC			LE		5.728	9.64	3 25.702		64.31
ATO					6.838	8.73	8 25.408		67.77
ATO					6.349	7.512			67.66
ATO					5.415	6.558			69.00
ATO					4.943	5.457			66.76
ATO					6.126	5.972			67.77
ATO			LEU		7.934	9.431			70.82
ATO		N	LEU		9.117	9.115			71.82
ATO		CA	GLY		7.534	10.357	23.742		73.28
ATO		C	GLY		8.492	11.077	22.922		74.53
ATON		0	GLY		7.819	11.754	21.747		75.19
ATON		и	GLY GLN		6.635	12.090	21.822	1.00	75.61
ATOM		CA	GLN		4.406	14.274	18.638	1.00	50.72
ATOM		CB	GLN		4.042	13.876		1.00	47.33
ATOM		C	GLN		3.033	14.869	20.587	1.00	46.67
ATOM		ō	GLN		3.486	12.449	20.073	1.00	46.66
ATOM		N	VAL	1491	2.581	12.074	19.323	1.00	45.20
ATOM		CA	VAL	1492 1492	4.072	11.650	20.960	1.00	45.41
ATOM		CB	VAL	1492	3.646	10.274	21.184	1.00	43.83
ATOM	226	CG1	VAL	1492	4.680	9.244	20.709	1.00	41.60
ATOM	227	CG2	VAL	1492	4.138	7.849	20.937	1.00	41.35
ATOM	228	C	VAL	1492	5.007	9.445	19.237	1.00	42.72
ATOM	229	0	VAL	1492	3.458	10.084	22.683	1.00	44.45
ATOM	230	N	VAL	1493	4.335	10.437	23.482	1.00	43.86
ATOM	232	CA	VAL	1493	2.309	9.548	23.070		42.67
ATOM	233	CB	VAL	1493	2.029 0.884	9.321	24.477	1.00	41.05
ATOM	234	CG1	VAL	1493	1.177	10.242	25.013	1.00	40.64
MOTA	235	CG2	VAL	1493	-0.459	11.693	24.722	1.00	42.40
ATOM	236	C	VAL	1493	1.626	9.844	24.427		43.36
ATOM	237	0	VAL	1493	1.129	7.880	24.704		40.09
ATOM	238	N	LEU	1494	1.927	7.212	23.796		39.99
ATOM	240	CA	LEU	1494	1.535	7.374	25.890		37.10
ATOM	241	CB	LEU	1494	2.359	6.036	26.250		35.08
ATOM	242	CG	LEU	1494	2.036	5.542	27.440		35.57
MOTA	243	CD1	LEU	1494	2.123	4.161 3.085	28.007	1.00 3	6.87
ATOM	244	CD2	LEU	1494	2.998	3.860	26.931		6.90
ATOM	245	С	LEU	1494	0.077		29.143		1.99
ATOM	246	0	LEU	1494	-0.311	6.236			3.31
ATOM	247	N	ALA	1495	-0.740	7.318 5.219		_	2.93
ATOM	249	CA	_	1495	-2.147			-	3.35
ATOM	250	CB		1495	-2.923				0.67
ATOM	251	C		1495	-2.661				0.35
					= - 301	J.073	27.025	1.00 2	9.97

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MOTA 252 ALA 1495 -1.944 2.909 26.840 1.00 28.15 0 MOTA GLU -3.898 3.813 27.488 1.00 253 Ν 1496 30.37 27.745 255 GLU 2.536 1.00 MOTA CA 1496 -4.537 31.47 -4.862 256 GLU 2.392 29.223 1.00 MOTA CB 1496 32.48 1.00 -3.627 . 2.239 MOTA 257 CG GLU 1496 30.093 37.81 2.426 31.565 1.00 MOTA 258 CD GLU 1496 -3.938 41.09 GLU 3.548 MOTA 259 OE1 1496 -4.328 31.944 1.00 41.53 ATOM OE2 GLU -3.797 1.453 260 1496 32.341 1.00 44.12 ATOM 261 C GLU 1496 -5.806 2.524 26.916 1.00 32.72 -6.586 MOTA 262 0 GLU 1496 3.478 26.954 1.00 33.91 MOTA 263 N ALA 1497 -5.953 1.494 26.094 1.00 31.06 **ATOM** 265 CA ALA 1497 -7.117 1.353 25.239 1.00 32.33 ATOM 266 CB ALA1497 -6.691 0.879 23.859 1.00 29.56 MOTA 267 C ALA 1497 -8.056 0.343 25.885 1.00 32.26 MOTA 268 0 ALA 1497 -7.648 -0.773 26.197 1.00 33.55 MOTA 269 N ILE 1498 -9.286 0.759 26.160 1.00 32.99 -0.126 1.00 MOTA 271 CA ILE 1498 -10.276 26.766 34.00 MOTA 272 CBILE 1498 -11.329 0.668 27.592 1.00 34.69 MOTA 273 CG2 ILE 1498 -12.341 -0.288 28.240 1.00 34.24 MOTA 1.496 274 CG1 ILE 1498 -10.647 28.686 1.00 33.56 -11.543 MOTA 275 CD1 ILE 1498 2.572 29.258 1.00 31.25 MOTA 276 C ILE 1498 -10.994 -0.830 25.624 1.00 35.71 1.00 ATOM ILE 1498 -11.618 -0.181 24.786 34.88 277 0 **ATOM** 278 N GLY 1499 -10.890 -2.147 25.573 1.00 40.43 MOTA 280 CA : GLY 1499 -11.553 -2.884 24.516 1.00 47.63 -3.233 53.08 MOTA С GLY 1499 -10.670 23.330 1.00 281 -4.226 MOTA 282 0 GLY 1499 -9.934 23.380 1.00 54.97 MOTA 283 LEU 1500 -10.713 -2.394 22.294 1.00 N 54.18 MOTA 285 LEU 1500 -9.957 -2.603 21.055 1.00 CA 55.26 ATOM 286 LEU 1500 -8.444 -2.726 21.305 1.00 CB 55.39 ATOM 287 CG LEU 1500 -7.562 -1.472 21.241 1.00 54.27 ATOM 288 CD1 LEU 1500 -6.110 -1.891 21.367 1.00 52.89 -0.711 MOTA 289 CD2 LEU 1500 -7.768 19.935 1.00 50.91 ~10.453 -3.830 MOTA 290 С LEU 1500 20.288 1.00 55.39 -10.376 -4.963 MOTA 291 0 LEU 1500 20.774 1.00 56.23 MOTA 292 PRO 1505 -13.315 -5.836 25.394 1.00 53.03 N ATOM 293 CD PRO 1505 -13.945 -7.148 25.167 1.00 55.12 MOTA 294 CA PRO 1505 -14.306 -4.848 25.846 1.00 50.62 MOTA 295 CB PRO 1505 -15.635 -5.607 25.715 1.00 50.09 ATOM 296 CG PRO 1505 -15.241 -7.031 25.950 1.00 52.18 MOTA 297 С PRO 1505 -14.039 -4.348 27.273 1.00 46.35 -14.065 MOTA 298 PRO 1505 -3.143 27.524 1.00 45.82 0 MOTA 299 N ASN 1506 -13.711 -5.261 28.181 1.00 42.76 MOTA 301 CA ASN 1506 -13.433 -4.892 29.566 1.00 45.29 MOTA ASN -14.283 -5.728 30.529 1.00 45.92 302 CB 1506 -15.752 -5.395 ATOM 303 ASN 1506 30.441 1.00 CG 46.17 MOTA ASN 30.390 304 OD1 1506 -16.132 -4.232 1.00 48.57 MOTA ND2 ASN -6.418 30.406 305 1506 -16.589 1.00 48.63 MOTA 308 C ASN 1506 -11.954 -5.008 29.939 1.00 45.33 309 MOTA ASN -5.084 1.00 0 1506 -11.597 31.121 44.53 -11.100 MOTA 310 N ARG 1507 -5.010 28.924 1.00 45.63 -5.122 MOTA 312 CA ARG 1507 -9.660 29.117 1.00 45.57 MOTA ARG 1507 -9.131 -6.354 28.375 1.00 53.33 313 CB ATOM 314 ARG 1507 -9.407 -7.685 29.043 1.00 61.39 CG

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ATOM 315 CD ARG 1507	
ATOM 316 MF 370	-8.336 -8.028 30.063 1 00
ATOM 318 C7 PD 1507	-8.525 30.063 1.00 cz z.
ATOM 319 ARG 1507	-7.970 30.585 1.00 74 c.
ATOM 322 ARG 1507	73.842 31.701 1 22 74.64
ATOM 335 NHZ ARG 1507	29.075 32 432
325 C APC 3500	11.068 32 175
ARG 1507	-8.964 -3.897 DO 1.00 83.41
ATOM 327 N WAT 325	-9.370 -3 375 0- 1.00 40.94
1110M 329 CA	~7.956
ATOM 330 CP 11308	-7.190 29.267 1.00 30 32
ATOM 331 CC1 1508	-6.854 28.789 1.00 37.36
ATOM 332 CC2 1508	-8.124 29.905 1.00 3c an
ATOM 333 C VAL 1508	50.739 30.571
(77)	1.796 30.928 1 00
U WAT TO	-2.818 28 100 30.92
N THE	3.387 -3.851 00 1.00 34.38
1110M 337 CA THE 1500	5.406 -2.140 27 1.00 32.85
338 CB THP 7500	$\frac{4.174}{2.523}$ $\frac{27.139}{26}$ $\frac{1.00}{30.47}$
ATOM 339 OC1 7777	4.455 26.491 1.00 21 55
ATOM 341 CG2 THR 1509 -	25.027 1.00 24 5
ATOM 342 C $^{-10}$ 1509 $^{-3}$	3.184 - 25.018 1.00 40 -
ATOM 343 0 -3	-3.458 24.345 1 00
ב משיוי ט	21.299 26.461
N T.VC 7.7	20.219 26.104 1 20.38
CA TVC	-1.442 26 Pac - 27.78
LB I.ve and	.101 -0 312 25 1.00 29.48
348 CG I.VS 1510	.172 -0.558 27 -1.00 30.54
A10M 349 CD 2010 -0	.037
ATOM 350 CF 1510 1.	284 29.118 1.00 33 05
ATOM 351 NZ 1510 1.	145 1 29.840 1.00 40 20
ATOM 355 2 223 1510 0	31.062
ATOM 356 215 1510 .0	77- 32.187 1 20 40.24
ATOM 255 LYS 1510 0	-0.166 25.365
N VAI	-1.142 24 704 - 20.64
CA VAT. 157	1.048 24 056 1.00 28.76
360 CB VAT 1 -0.6	1 347 22 1.00 29.34
ATOM 361 CG1 VAL 15-1.9	51 1.457 22 1.00 29.79
ATOM 362 CG2 VAT 151 -2.6	81 0 22.038 1.00 27.14
ATOM 363 C -2.8	$\frac{22.05}{1.00}$
ATOM 364 0 VAL 1511 0.13	23.243 1.00 22.45
ATOM 365 N VAL 1511 0.2	23.361 1.00 30 00
ATOM 367 CT ALA 1512 0.70	24.338 1 00
ATOM 369 ~ 1512 7 40	2.939 22.196 1 22
ATOM 350 CB ALA 1512	4.192 27 963
Ar.A 15-5	3.935 21 207 23.55
3,0 U ATA 0.50	5.009 21 000 24.69
710M 371 N VAI 15-2 -0.06	1 4 483 22 1.00 25.25
111011 373 CA VAT 1500 0.340	0 6 289 27 1.00 27.18
ATOM 374 CD -0.520	21.360 1.00 20 5
ATOM 375 -1 704	20.573 1.00 22 55
ATOM 376 con 1513 -2.609	7.713 21.422 1.00 32.45
ATOM 37- CG2 VAL 1513 3.7-	8.585 20.574 1 00
VAI 3.55	6.559 22 037 7 22
0.238 O VAT. 1532	8.334 19 939 32.15
1110M 379 N Lvc 15-0.792	9 185 20 - 1.00 34.67
381 CA 7.VC 351 0.207	20.635 1.00 34 65
ATOM 382 CP 713 1514 0.859	1.00 .36 05
ATOM 383 CC 1314 1.349	17.789 1.00 36 45
ATOM 384 CD -15 1514 2.250	0.764 16.489 1.00 36 35
384 CD LYS 1514 2.559	7.563 16.697 1 25 36.37
SSSD/55145. v01	6 854 33 33.49
145. v01	15.390 1.00 45.29

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MOTA	385	CE	LYS	1514	3.080	7.815	14.331	1.00	50.70
MOTA	386	NZ	LYS	1514	4.212	8.685	14.798	1.00	51.41
MOTA	390	С	LYS	1514	-0.121	10.496	17.459	1.00	36.75
ATOM	391	0	LYS	1514	-1.228	10.234	16.978	1.00	35.42
ATOM	392	N	MET	1515	0.294	11.731	17.700	1.00	38.12
MOTA	394	CA	MET	1515	-0.545	12.882	17.432	1.00	41.90
MOTA	395	CB	MET	1515	-1.371	13.238	18.668	1.00	43.08
MOTA	396	CG	MET	1515	-0.536	13.601	19.880	1.00	45.01
ATOM	397	SD	MET	1515	-1.561	13.784	21.324	1.00	46.03
ATOM	398	CE	MET	1515	-1.675	12.072	21.885	1.00	44.02
ATOM	399	С	MET	1515	0.314	14.065	17.021	1.00	44.65
ATOM	400	0	MET	1515	1.543	14.013	17.094	1.00	45.64
MOTA	401	N	LEU	1516	-0.347	15.123	16.568	1.00	47.08
MOTA	403	CA	LEU.	1516	0.329	16.337	16.134	1.00	48.08
ATOM	404	CB	LEU	1516	-0.500	17.033	15.054	1.00	45.50
ATOM	405	CG	LEU	1516	-0.764	16.265	13.764	1.00	43.22
MOTA	406	CD1	LEU	1516	-1.783	17.014	12.946	1.00	40.32
MOTA	407	CD2	LEU	1516	0.540	16.072	12.991	1.00	43.78
MOTA	408	C	LEU	1516	0.516	17.302	17.297	1.00	51.27
ATOM	409	0	LEU	1516	-0.214	17.249	18.291	1.00	50.37
MOTA	410	N	LYS	1517	1.491	18.191	17.157	1.00	55.47
ATOM	412	CA	LYS	1517	1.757	19.207	18.168	1.00	59.10
MOTA	413	CB	LYS	1517	3.203	19.702	18.068	1.00	61.61
MOTA	414	CG	LYS	1517	4.251	18.669	18.462	1.00	64.82
ATOM	415	CD	LYS	1517	5.635	19.109	18.018	1.00	67.42
MOTA	416	CE	LYS	1517	6.696	18.102	18.432	1.00	71.76
ATOM	417	NZ	LYS	1517	8.021	18.411	17.812	1.00	73.57
MOTA	421	С	LYS	1517	0.794	20.365	17.920	1.00	59.91
MOTA	422	0	LYS	1517	0.187	20.456	16.852	1.00	59.88
MOTA	423	N	SER	1518	0.686	21.267	18.886	1.00	61.85
ATOM	425	CA	SER	1518	-0.216	22.409	18.760	1.00	63.70
ATOM	426	CB	SER	1518	-0.158	23.274	20.024	1.00	64.21
MOTA	427	С	SER	1518	0.079	23.263	17.529	1.00	64.37
ATOM	428	0	SER	1518	-0.841	23.757	16.875	1.00	66.16
ATOM	429	N	ASP	1519	1.359	23.410	17.202	1.00	64.15
MOTA	431	CA	ASP	1519	1.767	24.217	16.054	1.00	64.55
ATOM	432	CB	ASP	1519	3.109	24.897	16.343	1.00	65.84
ATOM	433	C	ASP	1519	1.858	23.441	14.742	1.00	63.95
MOTA	434	0	ASP	1519	2.432	23.931	13.769	1.00	64.95
ATOM	435	N	ALA	1520	1.303	22.232	14.719	1.00	62.57
MOTA	437	CA	ALA	1520	1.329	21.398	13.521	1.00	60.34
ATOM	438	CB	ALA	1520	0.704	20.039	13.810	1.00	60.53
ATOM	439	C	ALA	1520	0.616	22.062	12.353	1.00	58.21
ATOM	440	0	ALA	1520	-0.464	22.631	12.506	1.00	58.32
MOTA	441	N	THR	1521	1.241	22.001	11.186	1.00	55.96
ATOM	443	CA	THR	1521	0.673	22.582	9.981	1.00	54.98
MOTA	444	CB	THR	1521	1.783	23.013	9.031	1.00	53.84
MOTA	445	OG1	THR	1521	2.554	21.862	8.659	1.00	55.84
MOTA	447	CG2	THR	1521	2.693	24.026	9.703	1.00	55.01
MOTA	448	C	THR	1521	-0.184	21.545	9.261	1.00	54.25
MOTA	449	0	THR	1521	-0.190	20.371	9.629	1.00	54.74
ATOM	450	N	GLU	1522	-0.877	21.974	8.212	1.00	53.32
MOTA	452	CA	GLU	1522	-1.702	21.066	7.423	1.00	52.64
MOTA	453	CB	GLU	1522	-2.472	21.829	6.339	1.00	53.55

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	ATOM	454	C	GLU	1522							
i	ATOM .	455	0	GLU				20.		.780	1.0	0 53 05
i	ATOM A	4 56	N	LYS	1522			18.8		.504	1.0	55
Z		158	CA		1523			20.3		.544		
I		159		LYS	1523	1.4	29	19.4		. 963	1.00	•
		60	CB	LYS	1523	2.7	30	20.2			1.00	50
				LYS	1523	3.8		19.3	^ ^	620	1.00	48.30
		61		LYS	1523	3.4				164	1.00	49.58
		62		LYS	1523	4.68		18.3	88 4. 	016	1.00	
			NZ	LYS	1523	4.2		17.6		466	1.00	54.08
		67	C :	LYS	1523			16.6		440	1.00	
		68	_	LYS	1523	1.69		18.3		006	1.00	,
		59			1524	1.74		17.20		697	1.00	-0.05
A	FOM 4	71 (1.85		18.82		249	1.00	·
A	COM 47		~_		1524	2.11		17.91		351		42.71
AT	OM 47				1524	2.31	3	18.70			1.00	42.11
	OM 47				1524	3.62	3	19.49			1.00	44.94
	OM 47				L524	3.69		20.51			1.00	48.90
	- ·	_		SP]	.524	4.59		19.08			1.00	51.88
AT				SP]	.524	0.956			-		1.00	50.06
	-··	_	A	SP 1	524	1.164		16.93	· -		1.00	39.85
AT			L		525	-0.261		15.73	8 9.7	48	1.00	39.01
ATO) C	A L		525			17.438	9.2	~ ~	1.00	38.32
ATO		l C			525	-1.461		16.610			1.00	36.16
ATO	DM 482	3 C(_	525 525	-2.720		17.470	9.2		1.00	
ATC	DM 483		Ol LE	_		-4.081		16.760	9.18		1.00	35.13
ATC	M 484				525	-4.184		15.668			1.00	34.70
ATO		~~			525	-5.162		17.789				36.15
ATO		_	LE		525	-1.406		15.560			1.00	32.96
ATO			LE		25	-1.575		14.377	_		00	34.31
ATO			SE		26	-1.136		16.005			.00	33.34
ATO					26	~1.039		15.128	7.03	_	.00	36.40
ATO		CB	SEI	₹ 15	26	-0.669	-	15.931	5.86		.00	37.16
ATO	_	OG	SEI	₹ 15	26	-1.736			4.61		.00	38.84
		C	SEF			-0.021		16.779	4.24			49.61
ATON		0	SER			-0.273		4.016	6.04	1		35.90
ATOM		N	ASF					2.873	5.670			36.68
ATOM		CA	ASP			1.142		4.349	6.59]			35.89
ATOM		CB	ASP			2.177	1	3.342	6.796	-		35.25
ATOM		CG	ASP	152		3.497		3.998	7.201			
ATOM	500	OD1				4.100	1	4.850	6.081			35.58
MOTA	501	OD2		152		3.750	1	4.653	4.895		-	37.19
ATOM	502	C	ASP	152		4.932		5.726	6.395			7.38
ATOM	503	0		152		1.749		2.274	7.799	1.		2.93
ATOM	504	N	ASP	152		2.000		1.090	7.594	1.		1.77
ATOM	506		LEU	152		1.055		2.684		1.0		0.58
ATOM	507	CA	LEU	152	В	0.581	11	730	8.853	1.(1.80
ATOM		CB	LEU	152		0.002		.471	9.857	1.0		3.53
ATOM	508	CG	LEU	1528	3 ~	0.440			11.076	1.0	00 32	2.20
	509	CD1	LEU	1528		0.705		.623	12.275	1.0		2.63
ATOM	510	CD2	LEU	1528		0.705 0.891		.708	12.709	1.0	00 37	3.09
ATOM	511	С	LEU	1528		0.091		.512	13.426	1.0	_	52
ATOM	512	Ó	LEU	1528		0.468		. 792	9.235	1.0		.89
ATOM	513	N	ILE			.494		. 589	9.521	1.0		
ATOM	515	CA	ILE	1529	_	.336	11.	.357	8.393		_	.39
ATOM	516	CB		1529	_	376		591	7.711	1.0	_	. 72
ATOM	517		ILE	1529	_	.336		505	6.895	1.00		.48
ATOM	518	CG2	ILE	1529	-4	.229		662		1.00		.85
	-10	CG1	ILE	1529	-4			344	5.997	1.00		. 54
SSSD/55	140 -							~ = =	7.843	1.00	29.	. 52
2220/33	145. VO1											

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							_	1 00	32.07
		_		-5.143	13.3	-	7.133	1.00	31.50
ATOM 519	CD		1529	-1.698	9.6	808	6.768	1.00	30.75
ATOM 520	_		1529	-2.009	8.4	119	6.780	1.00	33.28
ATOM 521	0 1		1529	-0.749	10.3	100	5.974	1.00	32.48
A	N S		1530	-0.011		250	5.038	1.00	37.20
	CA S		1530	1.114			4.368	1.00	49.93
7120.	CB :	SER	1530			218	3.766	1.00	
		SER	1530	0.604		045	5.756	1.00	29.05
HIO		SER	1530	0.583		909	5.316	1.00	28.66
		SER	1530	0.397		290	6.878	1.00	28.21
77.0.0	N	GLU	1531	1.259	-	207	7.631	1.00	27.30
ATOM 530	CA	GLU	1531	1.880	-	.733	8.839	1.00	28.90
ATOM 532	СВ	GLU	1531	2.65	•	.609	9.672	1.00	27.17
ATOM 533	CG	GLU	1531	3.27	_	.081	10.886	1.00	
ATOM 534	CD	GLU	1531	4.04		.244	11.448	1.00	
ATOM 535	OE1	GLU	1531	4.77	-	.256	11.291	1.00	
ATOM 536	OE2	GLU	1531	3.93	-	.162	8.072	1.00	
ATOM 537		GLU	1531	0.87		.961	8.028	1.00	
ATOM 538	_	GLU	1531	1.16	-	5.621	8.555		29.78
ATOM 539		MET	1532	-0.28	• -	5.734	8.99	1.00	0 28.79
ATOM 540	, as	MET	1532	-1.3		6.553	9.64	1.0	0 28.90
ATOM 542	· ~~	MET		-2.5	· -	5.741	9.99	3 1.0	
ATOM 54	~~	MET		-3.7	• •	6.693	10.76		0 30.19
ATOM 54	<u> </u>	MET		-5.0		7.870	9.49		0 26.70
ATOM 54	~ ~ ~	MET		-5.4	155	4.937	7.79	6 1.0	
ATOM 54	~	MEI		-1.9	935	3.730	7.89		26.62
ATOM 54		ME"		-2.	166	5.624	6.6		00 28.85
ATOM 54		GL		-2.		4.984	5.40	57 1.	
ATOM 54		GL		3 -2.	684	6.027		84 1.	00 25.42
7,2011	~~	GL		3 -2.		6.956	_	19 1.	00 30.05
712 011		~-			099	6.201		21 1.	00 29.47
				ვ -5.	393	5.336		11 1.	00 29.01
	~-				794	6.472			00 33.98
F11011			្ស 153		.011	3.944		68 1	.00 28.01
11101-	,,,,,		ւԾ 153		.694	2.84		573 1	.00 27.39
F110	, , ,		LՄ 153	3 -2	.072	4.29	_	036 1	.00 29.06
			ET 153	34 -0	.416	3.41		621 ¹	.00 29.74
			ET 15		.662	4.15		755 1	.00 33.16
•			ET 15		992	3.27	-	682 1	.00 42.88
1,10	JU2		ET 15	34 ³	3.198	3.12		042 1	.00 50.20
MOTA					3.805	4.16		159	L.00 42.64
MOTA		-			5.137	2.1		493	1.00 26.90
MOTA	505		MET 15		0.641	1.0		.990	1.00 27.05
MOTA	500	_		534	0.755			.803	1.00 25.42
MOTA	50,	_		535	0.512	2.3	-	.737	1.00 25.88
MOTA	500	•		535	0.437	1.2		.181	1.00 27.63
MOTA	5,0	C11		535	0.325	1.7	-	.737	1.00 27.26
MOTA	3,2			535	1.607	2.3	-	.564	1.00 29.49
MOTA	J	CG		535	1.584	2.5		699	1.00 28.22
MOTA	573	SD		535	1.294	4.2		7.396	1.00 26.28
MOTA	574	CE		535	-0.754			7.469	1.00 25.93
MOTA	575	C		1535	-0.645	-0.		7.032	1.00 27.19
MOTA	576	0		1536	-1.890			6.647	1.00 27.20
MOTA	577	N		1536	-3.087			6.310	1.00 25.29
MOTA	579	CA		1536	-4.257	1.	088	0.310	
ATOM	580	CB	LYS						

	•						726				
	ATOM	581	CG	LYS	1526						
	ATOM	582	CD	7 ***	1536	-4.897	1.	770	7 401		
1	ATOM	583	CE	_	1536	-5.884		_	7.491	1.00	23.86
i	ATOM	584	NZ		.536	-6.460	3		7.017	1.00	22.16
	ATOM	588			536	-7.484			8.174		22.25
	MOTA		C	LYS 1	536	-2.785	4.		7.713		23.40
		589	0		536	2.765	-0.		5.423	_	
	MOTA	590	N		537	-3.069	-1.		5.403	_	24.52
	MOTA	592	CA	_		-2.183	-0.0		1.411		26.61
A	TOM	593	CB	1 cm -	537	-1.843	-0.8	_		1.00 2	7.12
A	TOM	594	CG		537	-1.269	0.1	_	.194	1.00 2	8.06
A'	ma	595		MET 15	537	-2.265	1 1		.147		0.36
			SD	MET 15	37	-3.699	1.1		.591		6.31
		596	CE	MET 15	37	-2 079	0.4		.727		0.31
		597	C			-2.912	-0.0	57 -0			2.19
	TOM !	598	0	1000		-0.857	-1.9			_	5.22
AT	OM 5	599	N			-1.060	-3.0			1.00 2	5.98
AT	'OM 6	01	CA			0.188	-1.6			1.00 29	5.34
AT				ILE 15:	38	1.234	-2.0		229		.69
AT			CB	ILE 153	88	2.454	-2.67		535		.39
ATO			CG2	ILE 153	8	3.424	-2.00		^	_	
			CG1	ILE 153			-3.05	1 5.		~ 1	.42
ATO		05 (CD1	LE 153	_	3.223	-1.13				.28
ATC		06 (4.373	-0.37	_			.88
ATC	OM 60	07 (_			0.760	-3.92	_		.00 27	.19
ATO	DM 60		_	LE 153		1.242	-5.03			.00 25	59
ATO	M 61	_		LY 153	9 - (0.193	-3.767			.00 26.	
ATO		_		LY 1539	∂ -(0.661	3.76			.00 26.	
ATO	_	_	G	LY 1539	,		-4.940	6.9		-	
		_	G	LY 1539	•		~5.280	8.1		- •	
ATO			L.	YS 1540	_	.214	-4.637	8.4	-	-	
ATON			_	(S 1540	-	.204	-6.327	8.8	_	00 25.	42
ATOM		S CI		-010	-	· 4 67 .	-6.716	-	_	00 25.	52
ATOM				-5.10			7.283				38
ATOM	1 618			10	-1		6.303	11.08		00 27.3	
ATOM	619			-010				11.55	50 1.0	00 34.2	
ATOM				S 1540			6.943	12.54	6 1.0		
ATOM	_ •		LY		-2		5.927	13.05	7 1.0		<i>9</i>
ATOM			LY	S 1540	٠.	_	4.800	13.83	3 1.0		8 -
	•	0	LY				7.705	10.01			
MOTA	626	N	HIS	-010		627 -	B.600	9.18	_		
ATOM	628	CA	HIS			545	7.538	10.93			2
MOTA	629	CB	HIS		3.		3.440	11 00-			L
ATOM	630	CG			4.	772 - 8	3.228	11.09			
ATOM	631		HIS				.320	10.057		21.88	
ATOM	_	CD2			5.8		.320	10.068	1.00	22.68	
ATOM	632	ND1		1541	6.9		.522	9.444	1.00		
ATOM	634	CE1	HIS	1541	7.0		.268	10.843	1.00	~	
	635	NE2	HIS	1541	7.6		.389	10.697	1.00		
ATOM	637	C	HIS	1541	6.9	66 -11	.167	9.854		•	
ATOM	638	0	HIS		4.2	34 -8	-	12.494	1.00		
ATOM	639	N		1541	4.3	64 -7	_		1.00	/	
ATOM	641		LYS	1542	4.5	-		13.050	1.00	26.77	
	642	CA	LYS	1542	5.12			13.063	1.00	26.38	
3		CB	LYS	1542	5.51		552	14.401	1.00	30.07	
	643	CG	LYS	1542		-	003	L4.692	1.00	21.07	
3	644	CD	LYS	1542	6.06		252 _]	6.077	1.00	31.38	
	645	CE	LYS		6.28	9 -12.	735 1	6.294		42.79	
ATOM (646	NZ	LYS	1542	7.04	1 -13.	_	5.114	1.00	50.84	
	650	C		1542	7.51	1 -14.			1.00	56.75	
-	551		LYS	1542	6.34			5.424	1.00	61.29	
		0	LYS	1542	6.51	-		4.624	1.00	27.65	
SSSD/5514	45 -					9 -8.1	.13 1	5.711	1.00	26.83	
	+3. VU1									-0.03	

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MOTA	652	N	ASN	1543	7.146	-8.445	13.585	1.00	27.20
ATOM	654	CA	ASN	1543	8.354	-7.642	13.735	1.00	25.50
ATOM	655	CB	ASN	1543	9.578	-8.431	13.260	1.00	25.59
MOTA	656	CG	ASN	1543	9.712	-9.767	13.974	1.00	22.64
MOTA	657	OD1	ASN	1543	9.522	-10.821	13.371	1.00	26.76
MOTA	658	ND2	ASN	1543	9.970	-9. 7 27	15.273	1.00	25.56
MOTA	661	С	ASN	1543	8.374	-6.213	13.226	1.00	25.48
MOTA	662	0	ASN	1543	9.417	-5.692	12.842	1.00	24.58
MOTA	663	N	ILE	1544	7.209	-5.575	13.244	1.00	24.60
MOTA	665	CA	ILE	1544	7.065	-4.177	12.868	1.00	22.32
MOTA	666	CB	ILE	1544	6.524	-3.972	11.409	1.00	25.82
ATOM	667	CG2	ILE	1544	7.401	-4.720	10.403	1.00	24.24
ATOM	668	CG1	ILE	1544	5.057	-4.411	11.279	1.00	26.04
MOTA	669	CD1	ILE	1544	4.446	-4.121	9.901	1.00	23.20
MOTA	670	С	ILE	1544	6.075	-3.598	13.881	1.00	22.37
ATOM	671	0	ILE	1544	5.364	-4.345	14.559	1.00	21.68
MOTA	672	N	ILE	1545	6.111	-2.290	14.076	1.00	23.72
ATOM	674	CA	ILE	1545	5.169	-1.650	14.989	1.00	25.92
MOTA	675	CB	ILE	1545	5.602	-0.199	15.364	1.00	27.24
MOTA	676	CG2	ILE	1545	4.452	0.554	16.035	1.00	22.76
ATOM	677	CG1	ILE	1545	6.839	-0.219	16.285	1.00	25.57
MOTA	678	CD1	ILE	1545	6.591	-0.797	17.686	1.00	24.66
ATOM	679	C	ILE	1545	3.877	-1.612	14.179	1.00	26.03
ATOM	680	0	ILE	1545	3.823	-0.988	13.122	1.00	25.70
ATOM	681	N	ASN	1546	2.849	-2.293	14.669	1.00	24.79
ATOM	683	CA	ASN	1546	1.577	-2.354	13.956	1.00	25.51
ATOM	684	CB	ASN	1546	0.922	-3.727	14.137	1.00	25.17
ATOM	685	CG	ASN	1546	1.730	-4.839	13.539	1.00	21.67
MOTA	686	OD1	ASN	1546	1.856	-4.947	12.329	1.00	24.29
MOTA	687	ND2	ASN	1546	2.278	-5.686	14.384	1.00	22.24
MOTA	690	C	ASN	1546	0.578	-1.276	14.349	1.00	26.85
MOTA	691	0	ASN	1546	0.630	-0.724	15.453	1.00	28.67
MOTA	692	N	LEU	1547	-0.301	-0.956	13.407	1.00	27.70
MOTA	694	CA	LEU	1547	-1.357	0.019	13.622	1.00	27.64
MOTA	695	CB	LEU	1547	-1.945	0.481	12.284	1.00	24.87
MOTA	696	CG	LEU	1547	-3.173	1.400	12.337	1.00	23.25
ATOM	697	CD1	LEU	1547	-2.790	2.763	12.929	1.00	23.76
MOTA	698	CD2	LEU	1547	-3.757	1.569	10.923	1.00	23.47
ATOM	699	C	LEU	1547	-2.415	-0.771	14.396	1.00	27.27
ATOM	700	0	LEU	1547	-2.663	-1.952	14.103	1.00	25.27
MOTA	701	N	LEU	1548	-3.000	-0.130	15.400	1.00	27.94
ATOM	703	CA	LEU	1548	-4.017	-0.770	16.223	1.00	26.98
MOTA	704	CB	LEU	1548	-3.623	-0.735	17.708	1.00	24.65
MOTA	705	CG	LEU	1548	-2.327	-1.450	18.108	1.00	25.38
MOTA	706	CD1	LEU	1548	-2.189	-1.428	19.613	1.00	25.73
MOTA	707	CD2	LEU	1548	-2.337	-2.886	17.621	1.00	23.92
MOTA	708	С	LEU	1548	-5.369	-0.113	16.042	1.00	26.65
ATOM	709	0	LEU	1548	-6.392	-0.752	16.238	1.00	27.11
ATOM	710	N	GLY	1549	-5.378	1.163	15.684	1.00	25.04
MOTA	712	CA	GLY	1549	-6.643	1.855	15.516	1.00	25.47
ATOM	713	C	GLY	1549	-6.417	3.336	15.367	1.00	26.23
MOTA	714	0	GLY	1549	-5.267	3.781	15.287	1.00	28.41
ATOM	715	N	ALA	1550	-7.501	4.104	15.349	1.00	25.49
ATOM	717	CA	ALA	1550	-7.408	5.550	15.198	1.00	24.81

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		718	CB	ALA	1550						
		19	C	ALA	1550			913 13	724	1.00	21.79
		20	0	ALA	1550	0.0			691	1.00	25.51
		21	N	CYS	1551				726	1.00	24.09
		23	CA	CYS	1551	-9.49			080	1.00	24.90
			CB	CYS	1551	-9.24			511	1.00	26.80
				CYS	1551	-9.33	_		944	1.00	26.32
				CYS	1551	-9.34		-		1.00	32.31
			_	CYS	1551	-8.36	1 10.3			1.00	28.31
				THR	1552	-10.26	1 9.6			1.00	28.42
AT				THR	1552	-10.19	8 10.6			1.00	28.38
AT				THR	1552	-10.15	9 9.9			1.00	31.26
AT				HR	1552	-11.40	6 9.3			1.00	30.07
ATO		_	_		1552	-9.04	$4 \cdot 8.9$			1.00	29.64
ATO		-	_		1552	-11.35	11.6	52 13.5		1.00 1.00	28.65
ATO			_		1552	-11.29	12.72			1.00	33.31
ATC					1553	-12.420		9 14.2		1.00	31.94 36.09
ATC	M 74				1553 1553	-13.598				00	39.26
ATC			_		L553	-14.864		9 14.1		.00	36.61
ATO					L553	-14.932				.00	37.72
ATO		O		_	.553	-14.762 -15.491			01 1		38.41
ATO:			E2 GI		.553	-13.798					37.88
ATO		•	GI		.553	-13.671					37.67
ATO		_	GL		553	-13.150	13.07 12.75			.00	41.28
IOTA IOTA			AS	P 1	554	-14.282	14.24				41.37
ATON				_	554	-14.487	15.254				44.93
ATOM		CB			554	-15.828	15.009				18.05
ATOM		CG OD			554	-17.007	15.281		_		50.80
ATOM		OD:			554	-17.921	16.019	16.49			6.88
ATOM		C C	2 ASI ASI		554	-17.016	14.776				3.89
ATOM		ō	ASI			-13.367	15.366	17.316			8.98
ATOM	758	N	GLY			13.556	15.056	18.502			8.04 8.73
ATOM	760	CA	GLY			12.205	15.819	16.860			4.30
ATOM	761	С	GLY			11.080	15.960	17.756	1.		2.32
ATOM	762	0	GLY			-9.761 -9.740	15.713	17.052	1.0		0.69
ATOM	763	N	PRO			-8.644	15.465	15.848	1.0		0.71
ATOM	764	CD	PRO			-8.585	15.776	17.782	1.0	00 39	9.49
ATOM	765	CA	PRO	15.	56	-7.298	15.983	19.235		00 40	0.36
ATOM ATOM	766	CB	PRO	15	56	-6.405	15.566 15.771	17.250	1.0		3.37
ATOM	767 760	CG	PRO	155	56	-7.226	16.573	18.470	1.0	-	.47
ATOM	768 769	C	PRO	155	6	7.140	14.154	19.388	1.0		.77
ATOM	770	0	PRO	155	6 .	7.606	13.208	16.746 17.371	1.0	_	. 92
ATOM	772	N	LEU	155	7 -	6.447	14.017	15.627	1.0		. 04
ATOM	773	CA CB	LEU	155	7 -	6.201	12.719	15.027	1.0	-	. 70
ATOM	774	CG	LEU	155		5.528	12.885	13.664	1.0		.81
ATOM	775	CD1	LEU	155		5.004	11.623	12.954	1.00		.49
ATOM	776	CD2	LEU	155		6.146	10.655	12.664	1.00		
ATOM	777	C	LEU LEU	155		4.283	12.014	11.672	1.00		
ATOM	778	0	LEU	155°		5.290	11.925	15.961	1.00		
ATOM	779	N	TYR	1558		4.229	12.410	16.369	1.00		
ATOM	781	CA	TYR	1558		5.718	10.724	16.319	1.00		
CC0-					, -,	1.902	9.863	17.147	1.00		
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MOTA	782	CB	TYR	1558	-5.614	9.500	18.462	1.00	33.55
ATOM	783	CG	TYR	1558	-5.710	10.638	19.461	1.00	35.33
ATOM	784	CD1	TYR	1558	-6.644	10.608	20.499	1.00	35.68
ATOM	785	CE1	TYR	1558	-6.757	11.670	21.394	1.00	38.60
MOTA	786	CD2	TYR	1558	-4.883	11.759	19.349	1.00	38.62
MOTA	787	CE2	TYR	1558	-4.985	12.824	20.235	1.00	40.33
MOTA	788	CZ	TYR	1558	-5.924	12.781	21.254	1.00	41.70
MOTA	789	OH	TYR	1558	-6.040	13.867	22.104	1.00	42.66
MOTA	791	C	TYR	1558	-4.607	8.604	16.345	1.00	31.08
ATOM	792	0	TYR	1558	-5.527	7.937	15.857	1.00	31.28
MOTA	793	N	VAL	1559	-3.328	8.336	16.116	1.00	28.34
MOTA	795	CA	VAL	1559	-2.934	7.132	15.403	1.00	26.39
MOTA	796	CB	VAL	1559	-1.830	7.401	14.364	1.00	29.17
ATOM	797	CG1	VAL	1559	-1.463	6.103	13.648	1.00	26.25
ATOM	798	CG2	LAV	1559	-2.297	8.461	13.360	1.00	29.56
ATOM	799	C	VAL	1559	-2.411	6.226	16.498	1.00	25.14
MOTA	800	0	VAL	1559	-1.396	6.522	17.120	1.00	28.04
ATOM	801	N	ILE	1560	-3.164	5.171	16.783	1.00	25.28
ATOM	803	CA	ILE	1560	-2.832	4.208	17.831	1.00	24.81
ATOM	804	CB	ILE	1560	-4.133	3.669	18.496	1.00	24.63
ATOM	805	CG2	ILE	1560	-3.790	2.812	19.728	1.00	20.93
MOTA	806	CG1	ILE	1560	-5.044	4.854	18.869	1.00	22.94
MOTA	807	CD1	ILE	1560	-6.499	4.502	19.028	1.00	25.34
MOTA	808	C	ILE	1560	-1.994	3.051	17.286	1.00	26.38
MOTA	809	0	ILE	1560	-2.429	2.301	16.398	1.00	26.14
MOTA	810	N	VAL	1561	-0.782	2.911	17.809	1.00	27.31
ATOM	812	CA	VAL	1561	0.112	1.852	17.359	1.00	27.32
MOTA	813	CB	VAL	1561	1.309	2.435	16.527	1.00	25.01
MOTA	814	CG1	VAL	1561	0.785	3.220	15.338	1.00	19.39
MOTA	815	CG2	VAL	1561	2.170	3.340	17.397	1.00	26.08
MOTA	816	C	VAL	1561	0.615	1.029	18.548	1.00	25.89
MOTA	817	0	VAL	1561	0.364	1.373	19.713	1.00	25.64
ATOM	818	N	GLU	1562	1.288	-0.076	18.250	1.00	24.49
MOTA	820	CA	GLU	1562	1.806	-0.949	19.284	1.00	25.00
ATOM	821	CB	GLU	1562	2.357	-2.231	18.677	1.00	23.69
ATOM	822	CG	GLU	1562	1.272	-3.170	18.219	1.00	24.29
MOTA	823	CD	GLU	1562	1.814	-4.393	17.514	1.00	27.65
MOTA	824	OE1	GLU	1562	1.218	-5.480	17.649	1.00	29.50
MOTA	825	OE2	GLU	1562	2.832	-4.270	16.807	1.00	32.34
MOTA	826	С	GLU	1562	2.840	-0.279	20.170	1.00	27.27
MOTA	827	0	GLU	1562	3.596	0.576	19.729	1.00	26.18
MOTA	828	N	TYR	1563	2.822	-0.663	21.441	1.00	30.39
MOTA	830	CA	TYR	1563	3.715	-0.121	22.454	1.00	32.48
MOTA	831	CB	TYR	1563	2.932	0.132	23.750	1.00	33.91
MOTA	832	CG	TYR	1563	3.788	0.535	24.928	1.00	34.93
MOTA	833	CD1	TYR	1563	4.606	1.664	24.871	1.00	34.50
MOTA	834	CE1	TYR	1563	5.374	2.051	25.967	1.00	37.77
MOTA	835	CD2	TYR	1563	3.758	-0.201	26.108	1.00	33.54
ATOM	836	CE2	TYR	1563	4.519	0.171	27.205	1.00	34.94
ATOM	837	CZ	TYR	1563	5.321	1.296	27.128	1.00	37.22
MOTA	838	OH	TYR	1563	6.087	1.648	28.206	1.00	45.36
MOTA	840	C	TYR	1563	4.896	-1.039	22.730	1.00	31.53
MOTA	841	0	TYR	1563	4.737	-2.252	22.895	1.00	30.43
ATOM	842	N	ALA	1564	6.082	-0.444	22.761	1.00	32.28

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7	ATOM	844	CA	ALA	1564		_					
7	MOTA	845	СВ	ALA	1564		-	167	23.0	26]	1.00	32.59
		346	С	ALA				957	21.8		.00	
A	MOTA	347	0	ALA	1564			608	24.3		.00	
A	MOT	348	N	SER	1564			427	24.3		.00	31.81
		350	CA		1565		9 -1.	296	25.4		.00	34.11
A		51		SER	1565	9.05	9 -0.		26.7			34.09
				SER	1565	7.40	0 -1.		27.82		.00	35.05
			_	SER	1565	7.689	9 -3.		27.57		.00	30.13
				SER	1565	9.526	ō -0.				.00	38.17
				SER	1565	9.947			27.04		.00	35.03
		_		LYS	1566	10.321			27.90		.00	37.12
	10M 8			LYS	1566	11.756			26.33		00	34.55
				YS	1566	12.291			26.56		00	33.48
				YS	1566	11.674			26.50		00	31.90
				YS	1566	12.162	~5.2		27.58		00	28.63
AT	_			YS	1566	11.763			27.50		00	34.97
				YS	1566	12.288	-6.0		28.76		00	36.82
AT			, r		1566	12.567	-7.4		28.748		00	41.32
AT(-	L		1566	13.785	-0.6		25.691		00	34.98
AT(G:		L567	11.892	-0.74		25.607		00	38.03
AT(A GI		L567	12.582	0.33		25.049		00	36.00
ATO		_	GI	ĹΥ.	.567	13.245	1.32		24.222		00	34.14
ATC		•	GI		567	12.975	0.86		22.933		0	32.01
ATC			AS		568	14.091	-0.22		22.439			31.95
ATO			A AS		568	14.774	1.71		22.360	1.0	_	33.51
ATO	,		AS		568	15.203	1.37		21.121	1.0		34.20
ATO.		CG	As		568	16.420	2.62		20.332	1.0		34.07
ATO			1 As		568	17.453	3.32		20.910	1.0		35.09
ATO		ND	2 AS:		568	16.317	2.70		1.156	1.0		34.36
ATO	_	C	AS		568	15.927	4.62		1.066	1.00		88.38
ATO		0	ASI		68	16.490	0.40		1.325	1.00		3.38
ATON		N	LE		69	16.276	0.315		2.414	1.00		4.93
ATOM		CA	LEU		69	17.333	-0.317		0.263	1.00		1.11
ATOM	_	CB	LEU	_	69	17.437	-1.316		0.298	1.00		0.44
ATOM		CG	LEU		69	18.438	-2.008		8.928	1.00		9.46
ATOM	0.50	CD1	LEU			18.285	-3.148		3.741	1.00		9.01
ATOM		CD2	LEU				-4.219		9.840	1.00		8.81
ATOM		C	LEU			18.263	-3.740	17	7.338	1.00		5.62
ATOM		0	LEU		_	18.706	-0.805	20	762	1.00		.16
ATOM	894	N	ARG	15		19.400	-1.501		.496	1.00		7.32
ATOM	896	CA	ARG	157		19.097	0.396	20	.344	1.00		.74
ATOM	897	CB	, ARG	157		20.386	0.951	20	.758	1.00		.72
MOTA	898	CG	ARG	157		20.597	2.349	20	.160	1.00		.82
ATOM	899	CD	ARG	157	_	21.873	3.009	20	.662	1.00		.90
ATOM	900	NE	ARG	157		21.966	4.481			1.00		.32
ATOM	902	CZ	ARG	157	_	0.749	5.222	20		1.00		.32
ATOM	903	NH1	ARG		-	0.376	5.600			1.00		. 90
ATOM	906	NH2	ARG	157		1.118	5.316			1.00		
ATOM	909	C	ARG	157		9.246	6.284			1.00		.15
ATOM	910	0	ARG	157	_	0.434	1.022			1.00	53.	
ATOM	911	N	GLU	1570	_	1.324	0.444			1.00	35.	
ATOM	913	CA		157	_	9.444	1.695			1.00	35.	
ATOM	914	CB	GLU	1571		9.331	1.835	24.			35.	
ATOM	915	CG	GLU	1571		8.055	2.607	24.		.00	36.	
			GLU	1571	. 18	3.061	4.056	24.			39.	
CCCD/c=							•		-00 I	.00	46.	75

51.36 1.00 24.311 4.721 55.22 16.694 1.00 1571 24.417 GLU CD 3.996 916 53.59 MOTA 15.676 1.00 1571 24.267 GLU OE1 5.972 917 34.82 MOTA 16.635 1.00 1571 25.022 GLU OE2 0.469 918 35.05 19.314 MOTA 1.00 1571 26.013 GLU 0.242 C 919 33.35 MOTA 20.018 1.00 1571 24.469 GLU 0 -0.441 920 31.83 MOTA 18.520 1.00 1572 24.986 TYR -1.796 N MOTA 921 18.366 30.77 1.00 1572 TYR 24.102 CA -2.544 MOTA 923 17.365 28.50 1.00 1572 24.408 TYR -4.008 CB 17.170 924 MOTA 30.48 1.00 1572 TYR 25.313 CG -4.420 925 30.97 MOTA 16.193 1.00 1572 25.574 TYR -5.760 CD1 926 MOTA 15.977 26.14 1.00 23.772 1572 TYR CE1 -4.985 927 26.21 MOTA 17.933 1.00 24.027 1572 TYR CD2 -6.329 928 MOTA 17.725 30.30 1.00 1572 TYR 24.935 -6.708 CE2 929 MOTA 16.742 33.52 1.00 1572 TYR 25.214 CZ-8.041 930 34.83 16.518 MOTA 1.00 1572 25.044 TYR -2.556 OH 931 34.93 19.692 MOTA 1.00 25.992 1572 TYR -3.308 C 933 34.34 MOTA 19.959 1.00 24.020 1572 TYR -2.370 0 934 35.38 MOTA 20.517 1.00 1573 23.961 LEU -3.053 N 935 1.00 MOTA 21.803 32.71 1573 22.531 LEU -3.027 CA MOTA 937 29.16 22.357 1.00 1573 21.464 LEU CB -3.891 21.669 MOTA 938 26.98 1.00 1573 20.087 LEU CG -3.503 939 22.161 MOTA 28.85 1.00 1573 21.710 LEU CD1 -5.351 940 37.54 MOTA 21.932 1.00 1573 24.933 LEU -2.420 CD2 36.67 941 22.799 MOTA 1.00 1573 25.659 LEU С -3.123 942 37.90 23.511 1.00 MOTA 1573 24.969 LEU -1.092 943 0 39.77 1.00 22.814 MOTA 1574 25.838 GLN -0.368 N 40.09 944 23.729 MOTA 1.00 1574 25.572 GLN CA 1.138 946 42.28 23.624 MOTA 1.00 1574 24.217 GLN CB 1.549 MOTA 947 44.28 24.208 1.00 1574 23.896 GLN CG 3.018 24.030 47.55 948 MOTA 1.00 1574 24.615 GLN CD 3.755 949 23.362 46.09 MOTA 1.00 1574 22.790 GLNOE1 3.448 950 40.75 24.613 MOTA 1.00 1574 27.310 GLN -0.697 NE2 951 41.29 MOTA 23.490 1.00 28.059 1574 GLN-0.939 С 954 1.00 40.10 MOTA 24.440 1574 27.696 GLN0 -0.783 955 22.220 1.00 38.81 MOTA 1575 ALA29.069 -1.088 N 956 21.842 35.69 MOTA 1.00 1575 ALA29.273 CA -0.819 40.63 958 20.349 MOTA 1.00 1575 29.503 ALA -2.514 CB 959 22.192 43.39 MOTA 1.00 1575 30.690 ALA -2.843 С 960 38.39 22.098 MOTA 1.00 1575 28.561 ALA-3.357 0 961 37.69 22.602 MOTA 1.00 1576 28.896 ARG -4.729 N 962 38.16 22.945 MOTA 1.00 1576 28.137 ARG CA -5.689 964 37.89 22.034 MOTA 1.00 1576 28.589 ARG -5.547 CB 965 MOTA 20.594 37.36 1.00 1576 27.711 ARG CG -6.281 966 19.622 34.99 MOTA 1.00 1576 28.265 ARG -6.255 CD 967 36.94 18.267 MOTA 1.00 1576 28.484 ARG -5.150 ΝE 968 MOTA 17.565 36.18 1.00 1576 28.209 ARG CZ-3.960 970 MOTA 18.083 1.00 40.93 1576 28.909 ARG NH1 -5.237 971 38.93 MOTA 16.310 1.00 1576 ARG 28.704 NH2 -5.073 974 24.413 39.75 MOTA 1.00 1576 ARG 28.699 -6.249 C 977 39.21 24.801 MOTA 1.00 1576 28.570 ARG -4.036 O 978 38.97 25.233 MOTA 1.00 28.413 1577 ARG -4.196 979 N 36.06 1.00 MOTA 26.671 1577 28.000 ARG -2.870 CA 981 36.41 27,307 1.00 MOTA 1577 26.610 ARG CB -2.408 982 26.992 MOTA 1577 ARG CG 983 MOTA

							7	32				
	ATOM	984	CD.	ARG	155-							
	ATOM	985	NE	ARG	1577	- ,	.695	- 1	094	26 225		
	ATOM	987	CZ		1577	27	.776	- C	.806	26.337	1.00	36.17
	ATOM	988	NH1	ARG	1577		.284		.309	24.907	1.00	38.45
	ATOM	991		ARG	1577		. 764			24.387	1.00	39.00
	ATOM	994	NH2	ARG	1577	28	. 311	<u> </u>	.262	25.175	1.00	38.88
	ATOM		С	ARG	1577	27	.247		.469	23.071	1.00	37.76
	ATOM	995	0	ARG	1577	26	. Z4 /		.571	29.772	1.00	
		996	N		1578	20.	680		.217	30.800	1.00	40.59
	ATOM	997	CD	D= -	1578	28.	358	-5.		29.796		38.52
	ATOM	998	CA	-		29.	077			28.692	1.00	43.19
		999	CB	DD-	L578	28.	952	-5.			1.00	44.84
2	MOTA	1000	CG	nn.	578	30.	065		-	31.088	1.00	45.06
Į		1001	C	DD -	.578	30.4	431			30.689		44.86
A		1002			578	29.5	513			29.308	1.00	44.56
		1002	0	PRO 1	578	29.8	300	-4.		31.734		44.93
	_			PRO 1	579	29.6	540	-3.4		1.043		13.13
7.		1004	CD	PRO 1	579	20.0	747	~4.4	1 14 3	•	_ '	
			CA		579	29.3	15	~5.4	l92 3		_	17.61
	TOM 1	006	~-		579	30.1	73	-3.2		_	_	8.39
	TOM 1	007	~~		579	30.1	38	-3.7			1.00 4	8.74
	rom 1	008 (29.0	27	-4.7			L.00 4	9.73
	rom 1	^		-	79	31.59		-2.8			.00 4	9.21
AT	OM 1	010 N	- ~		79	32.48		-3.7	_		.00 4	9.67
AT				LU 15		19.16		-5.4		3.361 1		2.07
AT				LU 15	92	20.60				.444 1		1.83
AT		_		LU 15:	92	20.96		-5.14		.491 1		1.82
AT	~		٠.	LU 159	92	21.44		4.42		.784 1		.61
ATO		15 o	G1	LU 159		22.65		6.41		225		
			GI			20 00		6.33	6 32			.99
AT(A GI		_ `	20.82		7.57	5 32			.67
ATC		19 CI				21.534		8.84	4 32	_		.41
ATC		50 G.	GL			20.595	5 -1	0.01	-		00 61	.23
ATO		21 0	GL		-	22.141	L - 8	3.95	-	_	00 61	.20
ATO			GL		_	1.494	- 8	3.63		_	00 59.	. 26
ATO	M 102					3.388	- 9	405	-	945 1.		84
ATO	M 102				12	4.101		5.558		888 1.	00 57.	94
ATO		_			2	5.501		.141		625 1.0	00 54.	91
ATOM		_	GLI	V 1594	20	6.439	0	· +4T		865 1.0	00 55.	
ATOM	_		GLN	J 1594	2.	7.682		.252		579 1.0		
ATOM					28	3.241		.997		180 1.C		
			GLN	1594) 11E	-10	.858	30.4	88 1.0		
ATOM			GLN	1594		3.117	-9	.662	32.3	93 1.0	- • •	
ATOM	-055		GLN		23	.331	-10.	438	28.6		^	
ATOM	1034	N	LEU	1595	42	.637	-11.	389	29.0	1.0		
ATOM		CA	LEU		23	-438	-10.	091	27.3			3
ATOM	1037			1595	22	. 782	-10.	836	26.3			0
ATOM	1038	CG	LEU	1595	22	.459	- 9	907	26.30		45.1	
ATOM	1039		LEU	1595	21	.463	-8.	016	25.13	35 1.00	41.3	
ATOM		CD1	LEU	1595	21	.617	7	012	25.52		39.4	
ATOM	1040	CD2	LEU	1595	20	060	-7.	583	24.64	4 1.00		
ATOM	1041	C ,	LEU	1595	22	747	-9.	389	25.48	0 1.00		L
	1042	0	LEU	1595	23.	747	-11.9	900	25.85	8 1.00		•
ATOM	1043	N	SER	1596	44.	953	-11.6	75	25.84	-	43.30	
MOTA	1045	CA	SER		23.	230	-13.0	81	25.55		43.62	
ATOM	1046	CB		1596	24.	085	-14.1	50	25 000		42.92	
ATOM	1047	OG	SER	1596	23.4	410	-15.5	02	25.07		41.86	
ATOM	1049		SER	1596	22.3		-15.5		25.298		40.86	
ATOM	1050	C	SER	1596	24.3		-12 C		24.595	1.00	37.88	
	1030	0	SER	1596	23.6		-13.9; -13.0;		23.587	1.00	41.59	
SSSD/55	145 . ~	-13.0	77	22.966	1.00	41.94	
	173. VU]											

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MOTA	1051	N	SER	1597	25.275	-14.637	23.018	1.00	39.60	
MOTA	1053	CA	SER	1597	25.557	-14.518	21.603	1.00	39.74	
MOTA	1054	CB	SER	1597	26.729	-15.409	21.223	1.00	41.38	
MOTA	1055	OG	SER	1597	27.824	-15.147	22.077	1.00	50.59	
ATOM	1057	C	SER	1597	24.315	-14.921	20.818	1.00	38.16	
ATOM	1058	0	SER	1597	24.036	-14.353	19.769	1.00	38.03	
ATOM	1059	N	LYS	1598	23.560	-15.891	21.327	1.00	36.40	
MOTA	1061	CA	LYS	1598	22.362	-16.312	20.634	1.00	35.97	
MOTA	1062	CB	LYS	1598	21.791	-17.594	21.228	1.00	36.69	
ATOM	1063	CG	LYS	1598	20.989	-18.402	20.198	1.00	40.42	
MOTA	1064	CD	LYS	1598	20.164	-19.499	20.838	1.00	40.37	
ATOM	1065	CE	LYS	1598	19.792	-20.572	19.829	1.00	46.34	
MOTA	1066	NZ	LYS	1598	20.993	-21.338	19.362	1.00	45.29	
MOTA	1070	С	LYS	1598	21.324	-15.194	20.696	1.00	37.49	
ATOM	1071	0	LYS	1598	20.567	-14.983	19.738	1.00	38.10	
MOTA	1072	N	ASP	1599	21.316	-14.458	21.807	1.00	35.21	
MOTA	1074	CA	ASP	1599	20.380	-13.352	21.983	1.00	34.02	
MOTA	1075	CB	ASP	1599	20.556	-12.686	23.346	1.00	37.78	
MOTA	1076	CG	ASP	1599	19.970	-13.493	24.483	1.00	40.05	
MOTA	1077	OD1	ASP	1599	20.270	-13.143	25.642	1.00	42.73	
MOTA	1078	OD2	ASP	1599	19.204	-14.450	24.235	1.00	42.39	
MOTA	1079	С	ASP	1599	20.633	-12.306	20.922	1.00	32.84	
MOTA	1080	0	ASP	1599	19.694	-11.779	20.311	1.00	30.59	
MOTA	1081	N	LEU	1600	21.912	-11.999	20.724	1.00	31:11	
MOTA	1083	CA	LEU	1600	22.323	-10.998	19.744	1.00	32.17	
ATOM	1084	CB	LEU	1600	23.823	-10.722	19.875	1.00	32.30	
MOTA	1085	CG	LEU	1600	24.275	-10.162	21.235	1.00	31.08	
MOTA	1086	CD1	LEU	1600	25.794	-9.931	21.242	1.00	30.59	
ATOM	1087	CD2	LEU	1600	23.549	-8.863	21.514	1.00	28.89	
ATOM	1088	С	LEU	1600	21.949	-11.390	18.311	1.00	30.77	
MOTA	1089	0	LEU	1600	21.352	-10.601	17.574	1.00	29.87	
MOTA	1090	N	VAL	1601	22.269	-12.623	17.933	1.00	30.19	
MOTA	1092	CA	VAL	1601	21.954	-13.115	16.602	1.00	29.25	
MOTA	1093	CB	VAL	1601	22.593	-14.497	16.349	1.00	31.27	
MOTA	1094	CG1	VAL	1601	22.355	-14.936	14.914	1.00	31.60	
MOTA	1095	CG2	VAL	1601	24.093	-14.434	16.622	1.00	31.91	
MOTA	1096	С	VAL	1601	20.438	-13.181	16.405	1.00	29.06	
MOTA	1097	0	VAL	1601	19.946	-12.914	15.310	1.00	27.71	
MOTA	1098	N	SER	1602	19.702	-13.511	17.468	1.00	29.10	
MOTA	1100	CA	SER	1602	18.243	-13.585	17.400	1.00	29.29	
MOTA	1101	CB	SER	1602	17.680	-14.189	18.679	1.00	30.81	
MOTA	1102	OG	SER	1602	16.266	-14.074	18.692	1.00	35.78	
MOTA	1104	С	SER	1602	17.649	-12.199	17.156	1.00	28.98	
MOTA	1105	0	SER	1602	16.662	-12.039	16.426	1.00	26.82	
MOTA	1106	N	CYS	1603	18.274	-11.202	17.765	1.00	29.06	
MOTA	1108	CA	CYS	1603	17.870	-9.823	17.599	1.00	29.22	
MOTA	1109	CB	CYS	1603	18.784	-8.943	18.438	1.00	29.66	
MOTA	1110	SG	CYS	1603	18.575	-7.212	18.103	0.50	23.69	PRT1
MOTA	1111	С	CYS	1603	17.988	-9.422	16.112	1.00	29.23	
MOTA	1112	0	CYS	1603	17.087	-8.796	15.552	1.00	27.52	
ATOM	1113	N	ALA	1604	19.113	-9.778	15.491	1.00	27.87	
MOTA	1115	CA	ALA	1604	19.376	-9.484	14.077	1.00	26.37	
MOTA	1116	CB	ALA	1604	20.783	-9.941	13.690	1.00	23.88	
ATOM	1117	C	ALA	1604	18.349	-10.203	13.223	1.00	25.82	

							1	34				
	ATOM	1118	0	ALA	1.004							
	ATOM	1119		TYR	1604	<i>-,</i>	788	-9	.631	12.289		
	ATOM	1121	CA		1605	,	119	-11			1.00	25.84
	ATOM	1122	CB	TYR	1605	17.	152	-12		13.544	1.00	25.56
	ATOM	1123		TYR	1605	17.		-13.		12.827	1.00	27.81
	ATOM	1124	CG	TYR	1605	15.	974			13.456	1.00	26.66
	ATOM		CD1	TYR	1605	16.		-14.	_	12.886	1.00	30.75
	ATOM	1125	CE1	TYR	1605	15.0	100	-15.		L1.640	1.00	30.20
	ATOM	1126	CD2	TYR	1605	14.7	700	-15.		11.126	1.00	30.03
		1127	CE2	TYR	1605	12 -		-14.	707]	3.596	1.00	
	ATOM	1128	CZ	TYR	1605	13.7		~15.	500 <u>1</u>	3.097	1.00	30.73
		1129	OH		1605	13.9		-16.	l17 1	1.867	1.00	30.71
	ATOM	1131	С	CC		12.9	23	-16.9	_	1.417		30.93
	MOTA	1132	0	FF11	1605	15.7	48 .	-11.6		2.775	1.00	32.31
	MOTA	1133	N		1605	15.1	47 -	-11.5			1.00	26.15
P	ATOM :	1135	~-	~	1606	15.24	14 -	11.2		1.702	1.00	26.64
A		1136			1606	13.92		10.5		3.926	1.00	25.48
					.606	13.58		10.2		.023	1.00	26.86
	_		~-		606	13.35		11 -		.482	1.00	26.83
		770		GLN 1	606	13.15		11.5		.332	1.00	25.84
	TO L			GLN 1	606	12.20		11.16		.791	_	30.86
		_		SLN 1	606	14.05		10.4				31.87
		143 (C (IN 1	606	13.83		11.63				31.67
) (506			-9.31	0 13		. .	
			1 A		507	12.83		9.05	8 12			27.52
	OM 11	L47 C			07	14.904		8.52	3 13			6.05
	'OM 11	.48 C			07	14.963	-	7.30				6.68
	OM 11	49 C				16.225	_	6.48				5.66
AT	OM 11					16.363		5.274		_		8.50
AT	OM 11					16.151		6.03]			.00 2	6.04
AT(OM 11:		• •			14.934		7.641		^ ^	.00 2	4.45
ATO		_		_		14.184	~ 7	7.033			00 2	4.89
ATC	M 115		AI		98 ;	15.738		3.619		_	00 25	5.86
ATO					8 3	L5.773		0.039			00 25	.24
ATO					8 1	6.813	-10	.039			00 22	.95
ATO	• -		AL	A 160		4.383	-10	.117	8.9	20 1.	00 20	.24
ATO	_		AL.	A 160		3.963	- 9	.541	8.6	79 1.		.71
ATO		_	AR	3 160	9 7	3.676	- 9	.319	7.5	32 1.0		.48
ATO	_		AR	160		2.327	-10	.216	9.5	85 1.(.10
ATON			ARC		_	2.32/	-10	. 708	9.3	01 1.0		
			ARG	1609		1.840	-11.	640	10.3	97 1.0		. 55
ATOM			ARG			2.407	-13.	005	10.29	90 1.0	-	
ATOM			ARG			L.537	-13.	931	11.05		٠ ·	
ATOM		' CZ	ARG			.849	-14.	874	10.19		•	
ATOM	0		ARG		_	974	-15.	771	10.63	_	-	
ATOM		NH2	_		_	.678	-15.	834	11.92	_		
MOTA	1174	C		1609	_	.416	-16.	620	9 70			32
ATOM	1175	Õ	ARG	1609		.329	-9.	560	9.78			27
ATOM	1176	N	ARG	1609	10	.469	-9.6	521	9.12		25.	55
ATOM	1178		GLY	1610	11.	418	_0.5	721	8.23			
ATOM	1179	CA	GLY	1610	10.	555	-8.5	0.5	9.996		23.9	
ATOM		C	GLY	1610	10	800	-7.4	06	9.870	1.00		9
ATOM	1180	0	${ t GLY}$	1610		855	-6.7		8.512		25.9	2
	1181	N	MET	1611			-6.4	24	7.772		22.9	4
ATOM	1183	CA	MET	1611	12.	076	-6.5	89	8.163	1.00	23.4	
ATOM	1184	CB	MET	1611	12.		-5.9	89	6.888	1.00	23.1	
ATOM	1185	CG	MET		13.	956	-5.7	10	6.849		22.5	
ATOM	1186	SD	MET	1611	14.	398	-4.54	12	7.729	1.00	22.18	
			11111	1611	13.4	178	-3.00)6	7.426	1.00	22.63	
SSSD/55	145. v01							-	, .¥∠b	1.00	25.23	1

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MOTA	1187	CE	MET	1611	13.812	-2.688	5.675	1.00	21.38
MOTA	1188	C	MET	1611	12.050	-6.848	5.681	1.00	23.96
MOTA	1189	0	MET	1611	11.673	-6.326	4.633	1.00	25.26
MOTA	1190	N	GLU	1612	12.130	-8.163	5.822	1.00	24.34
MOTA	1192	CA	GLU	1612	11.755	-9.043	4.733	1.00	25.56
ATOM	1193	CB	GLU	1612	12.018	-10.494	5.121	1.00	24.96
MOTA	1194	CG	GLU	1612	11.703	-11.488	4.009	1.00	26.79
MOTA	1195	CD	GLU	1612	11.812	-12.931	4.450	1.00	26.96
ATOM	1196	OE1	GLU	1612	11.557	-13.212	5.636	1.00	30.98
ATOM	1197	OE2	GLU	1612	12.154	-13.791	3.611	1.00	32.31
MOTA	1198	С	GLU	1612	10.267	-8.829	4.415	1.00	25.70
ATOM	1199	0	GLU	1612	9.860	-8.753	3.252	1.00	24.30
ATOM	1200	N	TYR	1613	9.463	-8.723	5.465	1.00	23.55
MOTA	1202	CA	TYR	1613	8.037	-8.501	5.294	1.00	22.94
ATOM	1203	CB	TYR	1613	7.314	-8.586	6.650	1.00	24.00
MOTA	1204	CG	TYR	1613	5.841	-8.281	6.549	1.00	22.93
ATOM	1205	CD1	TYR	1613	4.945	-9.245	6.097	1.00	21.60
MOTA	1206	CE1	TYR	1613	3.582	-8.962	5.963	1.00	21.14
MOTA	1207	CD2	TYR	1613	5.347	-7.018	6.869	1.00	25.81
ATOM	1208	CE2	TYR	1613	3.979	-6.718	6.733	1.00	24.45
ATOM	1209	CZ	TYR	1613	3.112	-7.697	6.281	1.00	23.28
ATOM	1210	OH	TYR	1613	1.775	-7.411	6.126	1.00	22.95
ATOM	1212	С	TYR	1613	7.803	-7.138	4.637	1.00	22.57
ATOM	1213	0	TYR	1613	7.022	-7.024	3.699	1.00	24.72
ATOM	1214	N	LEU	1614	8.460	-6.101	5.156	1.00	22.16
ATOM	1216	CA	LEU	1614	8.334	-4.755	4.615	1.00	22.60
MOTA	1217	СВ	LEU	1614	9.175	-3.772	5.440	1.00	22.56
ATOM	1218	CG	LEU	1614	8.577	-3.415	6.802	1.00	24.92
MOTA	1219	CD1	LEU	1614	9.535	-2.541	7.580	1.00	21.46
ATOM	1220	CD2	LEU	1614	7.218	-2.711	6.611	1.00	21.87
ATOM	1221	С	LEU	1614	8.699	-4.683	3.124	1.00	23.76
ATOM	1222	0	LEU	1614	7.975	-4.077	2.326	1.00	23.84
ATOM	1223	N	ALA	1615	9.809	-5.314	2.744	1.00	23.48
ATOM	1225	CA	ALA	1615	10.232	-5.340	1.352	1.00	22.70
ATOM	1226	CB	ALA	1615	11.591	-6.019	1.215	1.00	21.52
ATOM	1227	C	ALA	1615	9.188	-6.063	0.505	1.00	22.87
ATOM	1228	0	ALA	1615	8.854	-5.591	-0.581	1.00	24.23
ATOM	1229	N	SER	1616	8.652	-7.176	1.015	1.00	22.76
MOTA	1231	CA	SER	1616	7.638	-7.954	0.295	1.00	22.88
ATOM	1232	CB	SER	1616	7.315	-9.251	1.039	1.00	21.39
ATOM	1233	OG	SER	1616	6.400	-9.036	2.102	1.00	26.24
ATOM	1235	C	SER	1616	6.360	-7.131	0.044	1.00	24.88
ATOM	1236	0	SER	1616	5.635	-7.358	-0.927	1.00	24.73
ATOM	1237	N	LYS	1617	6.104	-6.173	0.927	1.00	23.82
ATOM	1239	CA	LYS	1617	4.970	-5.287	0.810	1.00	22.47
ATOM	1240	СВ	LYS	1617	4.455	-4.914	2.199	1.00	23.62
MOTA	1241	CG	LYS	1617	3.792	-6.072	2.927	1.00	27.16
ATOM	1242	CD	LYS	1617	2.551	-6.487	2.169	1.00	30.84
ATOM	1243	CE	LYS	1617	1.810	-7.602	2.852	1.00	33.57
ATOM	1244	NZ	LYS	1617	2.484	-8.894	2.653	1.00	44.30
ATOM	1248	C	LYS	1617	5.346	-4.034	0.035	1.00	23.56
ATOM	1249	0	LYS	1617	4.639		0.091	1.00	25.16
ATOM	1250	N	LYS	1618	6.495	-4.066	-0.638	1.00	24.69
ATOM	1252	CA	LYS	1618	6.953	-2.943	-1.468	1.00	24.04
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	ATOM	1253	CB	LYS	3.65	•					
	ATOM	1254			1618	5.86	3 -2	2.581	2		
	ATOM	1255		LYS	1618	5.77			-2.492	1.00	26.96
	ATOM	1256		LYS	1618	5.56	-		-3.709	1.00	29.14
	ATOM		CE	LYS	1618	5.66	_	.942	3.345	1.00	33.91
	ATOM	1257	NZ	LYS	1618		_	.858 .	4.558	1.00	
		1261	C	LYS	1618	4.43	_	.821 -	5.380	1.00	32.98
	ATOM	1262	0	LYS	1618	7.40			0.713		36.73
	ATOM	1263	N			7.55	7-0.		1.302	1.00	24.01
	ATOM	1265	CA		1619	7.689	-1.		0.573	1.00	23.73
	ATOM	1266	СВ	~	1619	8.108	-0.			1.00	25.91
		1267	SG		1619	7.444		_	1.418	1.00	25.65
	70000	1268			1619	7.941		7 7 7	2.792	1.00	24.93
	7 mas -		C	CYS :	1619	9.631	0.	313	1.064	_	28.14
		1269	0	CYS 1	1619	10.304	-0.	628 ₁			23.07
		L270	N		620	10.304	-1.	530 ₁		_	
		272	CA		620	10.170	0.5		262		20.98
	ATOM 1	273	CB			11.604	0.8			1.00	22.95
A	TOM 1	274	CG2		620	12.202	1.6			1.00	23.81
A	TOM 1	~	CG1	_	620	13.670	1.9			1.00 2	24.36
A		~	~~ -		620	12.108	0.7		.506]		.7.24
	m		~		520	12.171			.987 1	00 2	3.13
				ILE 16	520	11.633	1.5		286 1		5.37
			0 ;	ILE 16	20	10.981	1.7		_	-	4.30
			I V		21	10.981	2.76	532.			4.70
		81 (~ ~	_		12.348	1.29	9 73.	_		5.21
		82 C		IIS 16		12.427	2.04				5.62
	'OM 12	83 C				13.181	1.23			.00 25	5.53
ΑT	OM 12	- .				13.004	1.77	_		.00 22	2.76
AT	OM 12			IS 16:	21	12.356	1.26		528 1.		.42
AT				IS 162	21 :	13.474			501 1.	00 24	.74
ATO				IS 162		13.119	3.01		927 1.	-	.62
ATO			E2 H:	IS 162	_	2.439	3.23		79 1.		.02
			H				2.18	79.6			.70
ATC		1 0	H	S 162		.3.073	3.40]	4.9	• •	_	.23
ATC		2 N	AR		_	2.528	4.405		-	00 26	. 36
ATO		4 CA			-	4.271	3.406				.89
ATO						5.082	4.608			- •	35
ATO:	M 1296					4.268	5.766			0 25.	05
ATO	M 129	_			2 1:	3.709	5 444			0 20.	89
ATO			AR	G 1622		3.089	5.444			0 19.	
ATON			AR		12	.684	6.656	1.48	8 0.5	- •	
ATOM	_	_	ARC	3 1622		. 606	6.300	0.13	1 0.5		
			ARC	1622			5.577	-0.16			
ATOM			ARG	1622		-801	5.137	0.79			
ATOM	0,	C	ARG			.366	5.239	-1.42			
ATOM		0	ARG		15	.877	5.058	5.379	0.50		
ATOM		N			16	.787	5.863				7
ATOM	1311	CA	ASP		15	. 555	4.527	5.268			7
ATOM			ASP	1623	16.			6.552		24.6	7
ATOM		CB	ASP	1623	15		4.899	7.748		28.8	-
ATOM	1313	CG	ASP	1623			6.173	8.410	1.00		
	1314	OD1	ASP	1623			5.735	9.469			
ATOM	1315	OD2	ASP	1623	16.	_	7.520	10.321	1.00	36.6	/
ATOM	1316	С	ASP		17.	937 ₆	3.385	9.463		43.56	5
ATOM	1317	0		1623	16.	408 g	.766		1.00	36.29	
ATOM	1318		ASP	1623	16.		.937	8.766	1.00	28.22	
ATOM	1320	N	LEU	1624	16.	`		9.956	1.00	26.87	
ATOM		CA	LEU	1624	16.9		.592	8.278	1.00	26.34	
ATOM	1321	CB	LEU	1624	16.9		.428	9.132	1.00	26.59	
- • T OIAI	1322	CG	LEU	1624	17 ~	-	.168	8.265	1.00		
CCC- '-					17.0	82 -1	.175	8.978	1.00	24.59	
SSSD/55	145. v01							-		24.72	

ATOM	1323	CD1	LEU	1624	15.844	-1.408	9.856	1.00	24.35
MOTA	1324	CD2	LEU	1624	17.258	-2.261	7.931	1.00	24.63
MOTA	1325	С	LEU	1624	18.210	1.595	10.004	1.00	26.87
MOTA	1326	0	LEU	1624	19.322	1.777	9.497	1.00	28.19
MOTA	1327	N	ALA	1625	18.009	1.570	11.317	1.00	27.77
MOTA	1329	CA	ALA	1625	19.069	1.741	12.309	1.00	24.54
ATOM	1330	CB	ALA	1625	19.355	3.210	12.494	1.00	19.81
MOTA	1331	C	ALA	1625	18.498	1.173	13.592	1.00	26.44
MOTA	1332	0	ALA	1625	17.289	0.961	13.679	1.00	27.58
ATOM	1333	N	ALA	1626	19.342	0.940	14.594	1.00	25.38
MOTA	1335	CA	ALA	1626	18.872	0.397	15.865	1.00	24.65
ATOM	1336	CB	ALA	1626	20.054	0.023	16.774	1.00	23.35
ATOM	1337	С	ALA	1626	17.929	1.373	16.578	1.00	25.54
MOTA	1338	0	ALA	1626	17.057	0.951	17.325	1.00	27.70
MOTA	1339	N	ARG	1627	18.104	2.671	16.344	1.00	25.06
MOTA	1341	CA	ARG	1627	17.242	3.675	16.959	1.00	25.48
MOTA	1342	CB	ARG	1627	17.706	5.089	16.597	1.00	28.15
MOTA	1343	CG	ARG	1627	17.759	5.370	15.084	1.00	33.13
ATOM	1344	CD	ARG	1627	18.157	6.811	14.774	1.00	33.29
MOTA	1345	NE	ARG	1627	18.442	7.011	13.351	1.00	35.74
MOTA	1347	CZ	ARG	1627	19.652	6.889	12.813	1.00	37.40
ATOM	1348	NH1	ARG	1627	20.695	6.585	13.575	1.00	39.73
MOTA	1351	NH2	ARG	1627	19.817	7.012	11.507	1.00	36.90
MOTA	1354	C	ARG	1627	15.812	3.491	16.479	1.00	24.81
MOTA	1355	0	ARG	1627	14.871	3.853	17.173	1.00	24.05
ATOM	1356	N	ASN	1628	15.667	2.910	15.293	1.00	24.80
MOTA	1358	CA	ASN	1628	14.368	2.686	14.685	1.00	25.97
MOTA	1359	CB	ASN	1628	14.383	3.132	13.225	1.00	30.08
MOTA	1360	CG	ASN	1628	14.417	4.640	13.096	1.00	33.62
ATOM	1361	OD1	ASN	1628	13.775	5.347	13.864	1.00	35.11
MOTA	1362	ND2	ASN	1628	15.212	5.141	12.169	1.00	36.31
MOTA	1365	C	ASN	1628	13.802	1.288	14.824	1.00	26.03
MOTA	1366	0	ASN	1628	12.951	0.869	14.031	1.00	26.87
ATOM	1367	N	VAL	1629	14.330	0.550	15.797	1.00	26.04
MOTA	1369	CA	VAL	1629	13.854	-0.783	16.128	1.00	25.09
MOTA	1370	CB	VAL	1629	14.924	-1.876	15.959	1.00	27.00
MOTA	1371	CG1	VAL	1629	14.390	-3.197	16.546	1.00	20.99
MOTA	1372	CG2	VAL	1629	15.295	-2.051	14.462	1.00	23.26
MOTA	1373	C	VAL	1629	13.504	-0.671	17.600	1.00	27.59
MOTA	1374	0	VAL	1629	14.340	-0.285	18.418	1.00	25.81
MOTA	1375	N	LEU	1630	12.245	-0.929	17.923	1.00	28.17
MOTA	1377	CA	LEU	1630	11.768	-0.845	19.296	1.00	30.20
MOTA	1378	CB	LEU	1630	10.445	-0.077	19.332	1.00	30.26
MOTA	1379	CG	LEU	1630	10.484	1.285	18.626	1.00	29.81
ATOM	1380	CD1	LEU	1630	9.119	1.983	18.745	1.00	28.46
MOTA	1381	CD2	LEU	1630	11.576	2.141	19.233	1.00	28.37
MOTA	1382	C	LEU	1630	11.639	-2.242	19.904	1.00	29.32
MOTA	1383	0	LEU	1630	11.414	-3.219	19.189	1.00	30.84
MOTA	1384	N	VAL	1631	11.800	-2.342	21.221	1.00	28.90
ATOM	1386	CA	VAL	1631	11.732	-3.629	21.905	1.00	26.84
MOTA	1387	CB	VAL	1631	13.067	-3.919	22.670	1.00	28.88
MOTA	1388	CG1	VAL	1631	13.077	-5.341	23.236	1.00	21.54
MOTA	1389	CG2	VAL	1631	14.259	-3.699	21.744	1.00	24.30
MOTA	1390	С	VAL	1631	10.561	-3.645	22.881	1.00	29.02

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i	ATOM	1391	0	VAL	1625	,						
7	ATOM	1392	N	THR	1631			-2.7	'37 2·	3.706	1 00	
I	MOTA	1394	CA		1632		733	-4.6		2.764	1.00	29.31
· Z	MOTA	1395	CB	THR	1632		562	-4.8			1.00	30.84
A	TOM	1396		THR	1632	7.4		-5.6		.616	1.00	32.24
		1398	OG1	THR	1632	7.8		-7.0		.912	1.00	31.45
			CG2	THR	1632	7.2				.910	1.00	30.86
	mos.	1399	С	THR	1632	8.9		-5.1		.470	1.00	28.04
		1400	0	THR	1632	10.0		~5.49		.943	1.00	34.17
The second secon		1401	N	GLU	1633			-6.0]	19 25	.105	1.00	35.02
	TOM]	L403	CA	GLU	1633	7.9		-5.52	4 25	. 866	1.00	
		404	CB .	GLU	1633	8.1		-6.13	8 27	177	1.00	36.16
	rom 1	405		~		6.86		-6.06		^ -		36.34
	OM 1		~-	~	1633	6.95	57.	-6.64			1.00	37.07
AT	OM 1			~	1633	8.03		-6.00		_	1.00	44.57
AT				~	1633	8.12		4.75		_	1.00	49.38
AT			_		1633	8.78		6.75			1.00	51.03
AT			_		1633	8.60		7 500	-		1.00	51.63
ATO	~		_	LU j	1633	9.34		7.585		042]		36.42
ATO		11 1	Į į	SP 1	.634	8.18		8.085		374 1		38.56
			:A A		634			8.240		64 1		37.70
ATC			B A		634	8.550		9.637	25.7			
ATC		15 C	G A		634	7.408		0.378	25.0			38.53
ATO		16 O		_	634	6.04]		0.106	25.6			4.08
ATO	M 14	17 O				5.865	-10	367	26.8			1.60
ATO:	M 14:		A	_	634	5.137	' - 9	631	24.9	- -		2.37
ATO	M 14:		AS		534	9.826	-9	.776	24.9			7.23
ATO	M 142				534	10.127	-10	.865		_		6.56
ATON			AS		35	10.569		.683	24.4		.00 з	6.74
ATOM					35	11.819		.662	24.7		00 3	6.56
ATOM					35	12.888		.587	23.94			7.10
ATOM					35	13.226	- 0	. 38 /	24.54			5.92
ATOM				N 16	35	13.275		.226	25.97			5.54
ATOM			2 AS:	16	35	13.423		058	26.34			.84
	-	_	ASI		_	11.632	-10.		26.80	6 1.0		.58
ATOM			ASi			12 446		980	22.45	1 1.0		.78
ATOM			VAI			12.446	-9.	677	21.83	4 1.0		
ATOM	1433	CA	VAL			10.533	-8.	498	21.886	1.0	_	.00
ATOM	1434	CB	VAI		-	10.279	-8.	711	20.469			.35
ATOM	1435	CG1				8.778	-8.	946	20.181			. 76
MOTA	1436					8.538	-9.(081	18.675			.60
ATOM	1437		VAL			8.315	-10.2	209	20.897			
ATOM	1438	0		163		0.768	-7.4		19.781		•	51
ATOM	1439	N	VAL	163	_	0.506	-6.3		. –	4.0	•	
ATOM	1441		MET	163	7 1	1.575	-7.6		20.254	1.00		87
ATOM	1442	CA	MET	163	7 1.	2.119			18.738	1.00	28.	15
ATOM		CB	MET	1637	7 1:	3.366	-6.5		17.980	1.00	26.	
ATOM	1443	CG	MET	1637	7 14	4.479	-6.9		17.204	1.00	27.	
	1444	SD	MET	1637			-7.5		L8.051	1.00		
ATOM	1445	CE	MET	1637		5.124	-6.4	10]	9.288	1.00		
MOTA	1446	C	MET	1637		5.120	-7.45	59 2	0.689	1.00	_	
ATOM	1447	0	MET	1637		040	-6.08		6.993	1.00		
ATOM	1448	N	LYS			.480	-6.92		6.303		24.7	
ATOM	1450	CA		1638		.755	-4.79			1.00	24.5	0
3 5000	1451	CB	LYS	1638		.746	-4.25		6.931	1.00	25.7	
3.000	1452		LYS	1638	8	.486	-3.88		6.029	1.00	23.6	7
3.000		CG	LYS	1638			J.08		6.799	1.00	21.7	
3	1453	CD	LYS	1638			-5.09		7.298	1.00	24.6	
	1454	CE	LYS	1638			-4.68		3.005	1.00	23.8	
CCCD /= -				-	. د	400	-5.89	7 18	3.256	1.00	23.06	•
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MOTA	1455	NZ	LYS	1638	4.871	-6.398	16.976	1.00	24.60
MOTA	1459	, C	LYS	1638	10.260	-3.042	15.293	1.00	24.37
MOTA	1460	0	LYS	1638	10.658	-2.055	15.901	1.00	26.58
MOTA	1461	N	ILE	1639	10.271	-3.119	13.971	1.00	25.69
MOTA	1463	CA	ILE	1639	10.721	-2.005	13.148	1.00	25.94
MOTA	1464	CB	ILE	1639	10.935	-2.447	11.668	1.00	26.49
MOTA	1465	CG2	ILE	1639	11.218	-1.236	10.762	1.00	21.19
MOTA	1466	CG1	ILE	1639	12.103	-3.433	11.604	1.00	27.58
ATOM	1467	CD1	ILE	1639	12.120	-4.232	10.355	1.00	32.96
MOTA	1468	C	ILE	1639	9.675	-0.892	13.242	100	27.32
MOTA	1469	0	ILE	1639	8.466	-1.133	13.103	1.00	25.45
MOTA	1470	N	ALA	1640	10.156	0.320	13.498	1.00	27.43
MOTA	1472	CA	ALA	1640	9.321	1.499	13.632	1.00	26.96
MOTA	1473	CB	ALA	1640	9.557	2.133	15.006	1.00	25.21
ATOM	1474	C	ALA	1640	9.641	2.510	12.538	1.00	26.80
ATOM	1475	0	ALA	1640	10.691	2.446	11.896	1.00	27.55
ATOM	1476	N	ASP	1641	8.716	3.440	12.328	1.00	27.06
MOTA	1478	CA	ASP	1641	8.862	4.526	11.349	1.00	30.54
ATOM	1479	CB	ASP	1641	9.993	5.484	11.753	1.00	33.12
ATOM	1480	CG	ASP	1641	9.668	6.310	12.999	1.00	36.17
MOTA	1481	OD1	ASP	1641	10.477	7.203	13.334	1.00	42.24
MOTA	1482	OD2	ASP	1641	8.633	6.076	13.648	1.00	33.22
ATOM	1483	C	ASP	1641	9.049	4.107	9.898	1.00	29.94
ATOM	1484	0	ASP	1641	9.598	4.861	9.102	1.00	30.13
ATOM	1485	N	PHE	1642	8.569	2.920	9.553	1.00	30.22
MOTA	1487	CA	PHE	1642	8.680	2.426	8.191	1.00	30.91
ATOM	1488	CB	PHE	1642	8.462	0.909	8.159	1.00	26.24
MOTA	1489	CG	PHE	1642	7.156	0.470	8.750	1.00	27.82
ATOM	1490	CD1	PHE	1642	5.986	0.495	7.988	1.00	27.08
MOTA	1491	CD2	PHE	1642	7.089	0.026	10.066	1.00	26.70
MOTA	1492	CE1	PHE	1642	4.761	0.088	8.532	1.00	25.18
MOTA	1493	CE2	PHE	1642	5.872	-0.383	10.624	1.00	27.59
ATOM	1494	CZ	PHE	1642	4.705	-0.354	9.855	1.00	28.05
MOTA	1495	C	PHE	1642	7.729	3.139	7.219	1.00	33.35
ATOM	1496	0	PHE	1642	7.983	3.165	6.018	1.00	36.19
ATOM	1497	N	GLY	1643	6.661	3.746	7.736	1.00	32.76
ATOM	1499	CA	GLY	1643	5.710	4.419	6.863	1.00	31.44
ATOM	1500	C	GLY	1643	5.805	5.927	6.910	1.00	32.94
MOTA	1501	0	GLY	1643	4.945	6.636	6.399	1.00	33.10
ATOM	1502	N	LEU	1644	6.872	6.407	7.525	1.00	35.45
ATOM	1504	CA	LEU	1644	7.124	7.828	7.684	1.00	39.04
ATOM	1505	CB	LEU	1644	8.387	8.011	8.514	1.00	37.80
ATOM	1506	CG	LEU	1644	8.414	9.120	9.549	1.00	42.51
ATOM	1507	CD1	LEU		7.301	8.887	10.563	1.00	44.08
MOTA	1508	CD2	LEU	1644	9.779	9.127	10.243	1.00	44.47
ATOM	1509	С	LEU	1644	7.259	8.580	6.357	1.00	42.20
MOTA	1510	0	LEU	1644	7.895	8.107	5.414	1.00	44.14
ATOM	1511	N	ALA	1645	6.607	9.732	6.267	1.00	43.89
ATOM	1513	CA	ALA	1645	6.677	10.569	5.082	1.00	45.62
ATOM	1514	CB	ALA	1645	5.463	11.493	5.028	1.00	45.06
ATOM	1515	C	ALA	1645	7.966	11.388	5.186	1.00	45.82
MOTA	1516	0	ALA	1645	8.240	11.994	6.228	1.00	45.85
MOTA	1517	N	ARG	1646	8.766	11.389	4.129	1.00	45.16
MOTA	1519	CA	ARG	1646	10.015	12.140	4.138	1.00	47.06

			140			
ATOM 1520	CB ARG					
ATOM 1521	2	1646 11	.126 11	.318		
ATOM 1522	2.40	1646 10		_	4.794	1.00 48.00
ATOM 1523	1110	1646 10			2.742	1.00 46.83
ATOM 1525	A 20	1647 10			.823	1.00 45.76
T Const	CA ASP	1647 11		.814 2	.578	1.00 48.96
	CB ASP			.291 1	.288	1.00 50.93
3 mars	CG ASP 1	.647 11.		769 1	.073	
T man			_	228 -0	.360	_
7.000	$\Omega \Omega \Omega = 0$			850 ~0	. 956	
ATOM 1530	~		340 16.	980 -0	. 896	
7 mas -	^ -			104 1.		
ATOM 1532	N		491 14.		_	
	C13 -		²⁷⁴ 13.:	• • •	_	1.00 48.32
ATOM 1535	CB **-		96 12.8		_	1.00 50.84
ATOM 1536	CCO	14.9	984 11.5	571 -0.		1.00 52.58
ATOM 1537 (CC1 10	48 14.2	^{'04} 10.3			1.00 50.85
ATOM 1538 (10	⁴⁸ 14.6	38 11 A			.00 49.34
ATOM 1539 C			33 10.8			.00 48.22
ATOM 1540 C	′ то	⁴⁸ 15.5	23 13.9			.00 42.86
ATOM 1541 N	TO.	⁴⁸ 16.64	18 14.2			.00 55.57
ATOM 751-	TO	¹⁹ 14.94			23 1	.00 57.24
ATOM 15.	A HIS 164	15.65			36 1	.00 56.80
ATOM 15:-	~ 104	9 15.01			20 1.	.00 58.03
ATOM 1545		9 15.22			59 1.	00 58.71
ATOM 3.5.5	D2 HIS 164	9 16.30		8 -3.9		00 60.28
ATOM 1511	D1 HIS 164			6 -4.30		00 60.74
7 TO 1 O E	El HIS 164			6 -4.87		
ATOM 1 TO	E2 HIS 1649	/0		4 -5.74	2 1.	
	HIS 1649	-2.95	05.	3 -5.41	7 1.	
-223	HIS 1649	-3.723		3 ~0.59	1 1.0	
14	HIS 1650			-1.00	4 1.0	
ATOM 1556 CA	HIS 1650		0	0.65		-0.50
ATOM 1557 CB	HIS 1650	-9.500		1.634		-5.50
ATOM 1558 CG	HIS 1650	43.638		1.863		. • •
ATOM 1559 CD2		-0.404	19.433	0.738	_	43.20
ATOM 1560 ND1		13.492	20.752	0.536	_	
ATOM 1562 CE1		12.710	18.904	~0.339		
ATOM 1563 NEO	1000	12.402	19.907	-1.157		
ATOM 1565 C	HIS 1650	12.863	21.015	-0.647		
ATOM 1566 O	-450	15.925	17.575	2.972	1.00	
ATOM 1567 N		15.796	18.271	3.969	1.00	
ATOM 1569 CA		16.584	16.419	2.987	1.00	20
ATOM 1570 CB		17.197	15.920		1.00	
ATOM 1571 CG2		17.574	14.434	4.204	1.00	60.03
ATOM 1572 CG1	ILE 1651	18.280	13.920	4.069	1.00	62.54
ATOM 1573 CD1	ILE 1651	16.329	13.584	5.323	1.00	63.48
ATOM 1574 C	ILE 1651	16.635	12.124	3.800	1.00	65.18
ATOM 1555	ILE 1651	18.457	16.698	3.603	1.00	67.18
ATOM 1555	ILE 1651	19.326	16 000	4.557	1.00	59.16
ATOM 7 7	ASP 1652	18.532	16.907	3.716	1.00	59.25
ATOM 1570 CA	ASP 1652	19.702	17.176	5.793	1.00	58.91
ATOM 1	ASP 1652	19.312	17.915	6.260	1.00	58.25
ATOM 7.5.	ASP 1652	20.506	18.788	7.444	1.00	61.14
ATOM TOOL ODI	ASP 1652	21 614	19.569	8.028	1.00	01.14
-002 OD2	ASP 1652	21.614	19.574	_	1.00	65.33
ATOM 1583 C	ASP 1652	20.337	20.191	_	1.00	67.11
		20.786	16.922		1.00	69.04
SSSD/55145. v01					00	56.75

					7-2-2	-			
						16.307	7.741	1.00	56.06
	1 5 0 4	0	ASP	1652	20.699	16.307	5.826	1.00	55.40
MOTA	1584	N	TYR	1653	21.794	15.849	6.088	1.00	54.50
MOTA	1585	CA	TYR	1653	22.900	15.783	4.872	1.00	52.80
MOTA	1587	CB	TYR	1653	23.825	14.854	3.796	1.00	52.10
MOTA	1588	CG	TYR	1653	23.334	14.654	2.685	1.00	51.50
MOTA	1589	CD1	TYR	1653	24.123	14.566	1.724	1.00	53.52
MOTA	1590	CE1	TYR	1653	23.701	13.658	3.917	1.00	52.88
MOTA	1591	CD2	TYR	1653	22.099	14.214	2.966	1.00	54.63
MOTA	1592	CE2	TYR	1653	21.664	13.302	1.870	1.00	54.35
MOTA	1593	CZ	TYR	1653	22.469	13.025	0.933	1.00	53.23
MOTA	1594	OH	TYR	1653	22.049	12.107	7.339		55.40
MOTA	1595	C	TYR	1653	23.717	16.158	7.900	1.00	54.47
MOTA		0	TYR	1653	24.381	15.284	7.773		56.72
MOTA	_		TYR	1654	23.673	17.409	8.947		58.87
MOTA			TYR		24.421	17.826	8.733		57.91
MOTA			TYR		24.978	19.235	7.685		0 60.49
ATOM			TYR		26.068	19.269	6.325		0 61.37
ATOM					25.760	19.301	5.35		0 63.72
MOTA					26.769	19.289			0 61.74
MOTA					27.412	19.227			
OTA					28.425	19.216			0 65.12
OTA					28.102			_	0 64.17
OTA					29.117	19.248			00 60.17
ATO		_	TY		23.628	17.732	_		00 61.09
OTA		. —	TY		24.173	17.93			00 60.54
ATC			ГД 		22.348	17.39			00 62.12
OTA					21.49	17.27			00 64.32
OTA				rs 1655	20.01	9 17.38			00 67.17
OTA				YS 165	19.05	4 17.34	_		00 73.05
TA				YS 165	17.64	4 17.60		60 1.	00 77.36
ATC				YS 165	5 16.62	6 17.24			.00 81.10
				YS 165	5 15.23	0 17.49			.00 62.19
				YS 165	5 21.75				.00 61.36
			· -	YS 165	5 21.90			380 1	.00 62.26
			-	YS 165	6 21.83	16.0		236 1	.00 62.28
				YS 165	6 22.0	69 14.9			.00 62.05
				LYS 165	6 23.0	27 15.3 74 15.4		957 1	.00 62.62
				LYS 16	56 24.4			-	00 66.45
A'				LYS 16		25 6			1.00 67.28
		05-		LYS 16	56 26.8		. • -	109	L.00 68.45
				LYS 16	56 27.6			824	1.00 61.86
			C		56 20.	774 14.3			1.00 62.95
		.637	0	LYS 16	56 19.	714 15.		.420	1.00 60.10
		1638	N		57 20.				1.00 57.73
		1639	CA		557 19.		_	.121	1.00 56.04
		1641	CB		557 19.		-	.896	1.00 55.21
		1642	OG1		557 21.			.731	1.00 53.07
		1643			657 20.			.472	1.00 57.74
		1645	CG2 C	_	657 19.			.870	1.00 57.76
	MOTA	1646			657 20.		-	249	1.00 58.80
	MOTA	1647	0		658 18			3.249	1.00 60.33
	MOTA	1648	N		658 18	.548 13	• —	9.627	1.00 61.37
	MOTA	1650	CA		1658 17	.318 12		0.290	1.00 60.43
	MOTA	1651	CB			.811 12	.779 2	0.406	_ • • •
	MOTA	1652	С	IIIK .					

				142				
ATOM 1	653 O	THR	1684					
ATOM 16	554 N			.350 13	3.599 2	1.155		
3	56 CA		1659 20	.311]]		_	1.00 60.	
			1659 21.				1.00 59.9	97
3.000						.827	1.00 58.2	
		ASN 1			_	.645	1.00 59.9	
3	59 OD1	ASN 1	659 22			.723	1.00 60.1	
		* *		-	.265 22	00-	1.00 61.2	
ATOM 16	63 C		~ .		.867 21	_		
ATOM 16	64 O	_	•	781 11	.717 20	_		9
ATOM 166	65 N		_	868 11	418 20			
ATOM 166	57 CA		660 22.	54 ⁻ 3 12.			.00 57.34	
ATOM 166		OT	560 23.				.00 56.48	
ATOM 166	_	~	560 24.5	39 12		_	.00 54.87	7
ATOM 167			560 25.7				.00 53.04	Į
3.000			61 23.8	_		394 1	.00 54.11	
	_	ARG 16	61 24.5	•		918 1.	.00 51.37	
3.000		ARG 16	61 24.2				00 48.96	
3 77 74 .		ARG 16	2		428 15.			
ATOM 1675	5 CD	ARG 16			796 17.:			
ATOM 1676		ARG 16		92 7.3	325 17.2			
ATOM 1678	·			L3 6.6			00 50.78	
ATOM 1679			()2 5.2				
ATOM 1682		ARG 166	~ + . 20	16 4.5				
ATOM 1685		ARG 166	25.42	6 4.7				
ATOM 1686		ARG 166	1 24.07				00 47.88	
ATOM 1687	4"	RG 166	1 23.03	· -			00 46.53	
3.000	N T	EU 166	2 24.83			25 1.0	00 45.01	
7 mose	CA L	EU 166:	2 24.54			32 1.0		
7	CB L	EU 1662	-1.54			76 1.0		
ATOM 1691	CG L	EU 1662			31 11.39	99 1.0	· · · ·	
ATOM 1692		EU 1662		3 13.33	11.96	55 1.0		
ATOM 1693	an a				8 11.53			
ATOM 1694	C LE			14.53	6 11.51			
ATOM 1695	_		~3.740	10.36				
ATOM 1696			24.647	9.43				
ATOM 1697			22.632	10.42				
ATOM 1698	CD PR	_005	21.717				37.09	
· - •	CA PR	0 1663	21.894				38.18	
3.000	CB PR	0 1663	20.535	9.424		7 1.00	35.59	
3.000	CG PRO		20.335	10.098		1.00		
ATOM 1701	C PRO		20.343	10.856		1.00		
ATOM 1702	O PRO		22.556	9.045	8.876		39.13	
ATOM 1703	N VAI		22.362	7.933	8.378		33.05	
ATOM 1705	CA VAL		23.333	9.960	8.299		31.16	
7) TOM 1			24.020	9.669		00	32.07	
7.00			24.831	10.886		1.00	32.49	
ATOM A TO			23.898	11.906	6.477	1.00	32.68	
ATOM TELE	CG2 VAL	1664	25.670		5.864	1.00	32.25	
3	C VAL	1664	24.957	11.523	7.571	1.00	33.22	
	O VAL	1664	25.337	8.469	7.171	1.00	29.57	
ATOM 1711 N	1 LYS	1665	25.328	7.864	6.175	1.00		
ATOM 1713 C	CA LYS		25.303	8.116	8.409		27.39	
λ TOM	B LYS	1665	26.189	6.991	8.673	1.00	.28.82	
ATOM and		1665	26.815	7.100	10.065	1.00	27.87	
ATOM 2725		1665	27.967	8.089		1.00	26.99	
ATOM 3.55	D LYS	1665	28.283		10.079	1.00	29.23	
ATOM 3.75		1665	29.543	8.619	11.466	1.00	30.64	
		1665	29.826	9.478	11.426	1.00	30.94	
ATOM 1722 C	LYS	1665	25 546	10.128	12.737		31.63	
CCCD /=-			25.546	5.637	8.465		26.76	
SSSD/55145. v01						•	~0./6	

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			. (15	8.589	1.00	26.78
	LYS 1665	20.21-	4.615 5.630	8.137	1.00	25.79
ATOM 1723 O	TRP 1666	24.20	4.381	7.865	1.00	26.56
ATOM TITE	TRP 1666	23.561	4.273	8.724	1.00	25.63
ATOM 1725 CB	TRP 1666	22.299	3.872	10.174	1.00	26.95
ATOM 172	TRP 1666	22.564	4.717	11.232	1.00	24.83
ATOM 1,20	TRP 1666	23.052	3.920	12.398	1.00	24.49
ATOM 1700 CE2	TRP 1666	23.134	6.062	11.306	1.00	24.54
ATOM 1731 CE3	TRP 1666	23.433	2.636	10.730	1.00	20.10
ATOM TO	1666	22.376	2.660	12.063	1.00	21.86
ATOM THE	TRP 1666	22.716	4.433	13.627	1.00	25.71
ATOM 1735	1666	23.575	6.569	12.523	1.00	26.00
ATOM 1755	1666	23.870	5.754	13.665	1.00	26.04
ATOM 1730	1666	23.939	4.263	6.386	1.00	
ATOM 173	TRP 1666	23.188	3.214	5.931	1.00	20
ATOM 1730	TRP 1666	22.754	5.330	5.631	1.00	
ATOM 1735	MET 1667	23.404	5.361	4.215	1.00	01
ATOM 1710	MET 1667	23.046	6.802	3.744	1.00	
ATOM 1712	MET 1667		7.621	4.434	1.00	
ATOM 1745	MET 1667		9.276	3.706	1.0	
ATOM 1711	MET 1667		8.904	2.23		
ATOM 1		21.019	4.693	3.23		_
ATOM 1745	MET 166		4.894	3.29	4 1.0	
ATOM TOWN	MET 166		3.963	3 2.28	6 1.0	
71511	ALA 166	- 4 217	3.33	, 1.23	7 1.0	• =
ATOM 1	ALA 166		2.49	5 0.34	0 1.0	
ATOM 1752	B ALA 166	-4 005	4.49	5 0.43		- ·
A10	ALA 166	-4 101	5.55	1 0.3		
	ALA 166	006	4.31	4 -0.1	53 1.	00 26.35
	N PRO 166		3.14		-	00 27.78
ATOM 1756	CD PRO 16		5.39		-	00 25.51
	CA PRO 16		4.73	31 -1.5		.00 25.36
ATOM 1758	CD -		3.74			.00 26.47
ATOM 1759	-	606	5.9	00 -2.0		.00 28.42
ATOM 1760		669 25.686 669 25.617	7.0			.00 26.88
ATOM 1761	0	570 24.95	1 5.0		. –	.00 29.03
ATOM 1762	14	670 24.05°	7 5. 4			00 31.79
ATOM 1764	CA CI	670 23.59	7 4.2		065 1	00 32.47
ATOM 1765	CB	670 22.58	g 3.3			1.00 32.43
ATOM 1766	CG GE5	670 23.21	.2 2		822	1.00 25.01
ATOM 1767	CD 1	670 22.42	1.	-		1.00 28.75
ATOM 1768	OB1	670 24.45	8 2.			1.00 28.37
ATOM 1769	OEZ CZII	1670 22.86	54, 6.		.001	1.00 25.72
ATOM 1770	GT 11	1670 22.3	58 7.		.053	1.00 30.08
ATOM 1771	J 1	1671 22.4	51 6.		.465	1.00 31.24
ATOM 1772	M	1671 21.3	47 6.		.287	1.00 26.42
ATOM 1774	7.7	1671 20.7	51 6		.013	1.00 31.36
ATOM 1775		1671 21.8	199 8		1.249	1.00 33.11
ATOM 1776		1671 21.2	298 ⁹		3.387	1.00 32.73
ATOM 177	71711	1672 23.0	068 8	•	0.100	1.00 33.96
ATOM 177		1672 23.	715 ⁹		0.940	1.00 33.89
ATOM 178	TEII	1672 24.	931 ⁸		1.502	1.00 37.62
ATOM 178	~~ T.F(1)	1672 25.	783		2.581	1.00 39.57
ATOM 178	TEII	1672 25.	010 10	0.800	2.50-	
ATOM 178	3 CD1 LEU					

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ATOM 1784 CD2 LEU 1672	
ATOM 1785 C 1672	27.054 9.491 2.087 1.00
ATOM 1786 0 1672	24.157 10.202 - 1.00 32.30
ATOM 1787 N 1672	23 769
ATOM 1789 CA PAGE 1673	24.959 9.660 -1.102 1.00 37.87
ATOM 1790 CD PHE 1673	15 466 30 21.954 1.00 35 pg
ATOM 1701 22 FRE 1673 2	6 739 35.0/1 1.00 35.02
ATOM 1792 CD: PHE 1673 2	7 850 2 -3.639 1.00 34 66
ATOM 1793 CD2 PHE 1673 2	8 502 -2.634 1.00 33 04
ATOM 1794 CD2 PHE 1673 2	8.242 10 -2.494 1.00 32 65
ATOM 1795 CE2 PHE 1673 2	9.540 -1.827 1.00 36 99
ATOM 1706 PHE 1673 2	2.279 10.75 1.00 37.95
ATOM 1797 C PHE 1673 29	1,927 2.55 20.881 1.00 39 90
ATOM 1700 0 FILE 1673 24	483 10 10 10 10 17 00
ATOM 1700 1 1673 24	430 37 -4.210 1.00 36 34
ATOM 1802 C ASP 1674 23	705 0 5- 4.754 1.00 37 19
ATOM 1802 CT ASP 1674 22	780 27- 4.568 1.00 38 22
ATOM 1803 CT ASP 1674 23	008 2 -5.693 1.00 38 51
ATOM 707 ASP 1674 24	439 -6.633 1.00 40.34
ATOM TARE ODI ASP 1674 25	092 -7.122 1.00 43 97
ATOM 1005 ASP 1674 24	906 -7.254 1.00 42.70
ATOM 1807 0 ASP 1674 21.	200 -7.369 1.00 47.04
ATOM 1808 W ASP 1674 20.	457 -5.360 1.00 40 21
ATOM 1810 CT ARG 1675 20	975 0.872 -6.271 1.00 39.07
ATOM 1811 CT ARG 1675 19	589 -4.072 1.00 39.03
ATOM 1812 CB ARG 1675 18	3.900 -3.631 1.00 42 25
ATOM 7010 ARG 1675 10	11.2/1 -3.964 1.00 48 19
ATOM 1814 ARG 1675 19 4	62 13 -3.267 1.00 59 20
ATOM 1916 75 ARG 1675 20 0	79 -4.019 1.00 67.01
ATOM 1817 ARG 1675 19.6	89 16 -3.352 1.00 75 11
ATOM 1820 NV 1675 18.6	-3.525 1.00 78 74
ATOM 1823 C ARG 1675 20.3	11 17 4.341 1.00 79 91
ATOM 1824 0 ARG 1675 18.7	20 -2.890 1.00 87 24
ATOM 1825 N ARG 1675 17.56	4.221 1.00 39 00
ATOM 1827 05 1076 19 34	5 7 4.488 1.00 39 77
ATOM 1829 CD 1LE 1676 18.63	6 6 -4.434 1.00 35 50
ATOM 1829 CG 1LE 1676 19.43	4 -4.958 1.00 33 51
ATOM 1830 CG2 ILE 1676 18.58	3.759 -6.039 1.00 34 50
ATOM 1831 CD: LE 1676 19.84	3 -6.649 1.00 33 90
ATOM 1932 TLE 1676 20 86	0.732 ~7.120 1.00 37 co
ATOM 1832 0 1676 18.390	1.00 42 67
ATOM 1834 N - 1676 19.326	-3.809 1.00 30 04
ATOM 1836 CD 11R 16/7 17.124	1.00 28 62
ATOM 1927 - 16 724	1.00 30 60
ATOM 1939 22 11K 1677 15.781	1.107 -2.359 1.00 25 07
ATOM 1022 11R 1677 16 402	1.00 26 40
ATOM 1840 CD1 TYR 1677 16.663	7 -0.555 1.00 27 67
ATOM 1015 11R 1677 17 200	7.533 -0.999 1.00 27 45
ATOM 1842 CD2 11R 1677 16.935	8.483 -0.191 1.00 26 55
ATOM 1843 CF 11R 1677 17.536	5.883 0.721 1.00 24 50
ATOM 1844 000 11R 1677 17.698	0.828 1.538 1.00
ATOM 1846 C TYR 1677 18.270	1.080 1.00 28 80
ATOM 1847 6 11K 1677 16.055	1.914 1.00 34 97
ATOM 1047 O TYR 1677 15 144	3.235 -2.911 1.00 22 70
ATOM 1848 N THR 1678 16.477	3.335 -3.728 1.00 26.22
SSSD/55145. v01	2.076 -2.420 1.00 21.83
	~4.03

ATOM	1850	CA	THR	1678	15.968	0.791	-2.865	1.00	22.14
MOTA	1851	CB	THR	1678	16.907	0.191	-3.928	1.00	23.91
MOTA	1852	OG1	THR	1678	18.229	0.105	-3.373	1.00	27.47
MOTA	1854	CG2	THR	1678	16.949	1.053	-5.188	1.00	24.94
ATOM	1855	C	THR	1678	15.999	-0.176	-1.692	1.00	22.79
ATOM	1856	0	THR	1678	16.427	0.170	-0.592	1.00	23.39
ATOM	1857	N	HIS	1679	15.563	-1.402	-1.929	1.00	21.98
ATOM	1859	CA	HIS	1679	15.613	-2.417	-0.888	1.00	22.97
ATOM	1860	CB	HIS	1679	14.872	-3.671	-1.351	1.00	22.04
MOTA	1861	CG	HIS	1679	13.421	-3.444	-1.621	1.00	25.41
ATOM	1862	CD2	HIS	1679	12.674	-3.611	-2.740	1.00	26.60
ATOM	1863	ND1	HIS	1679	12.556	-2.954	-0.663	1.00	26.13
MOTA	1865	CE1	HIS	1679	11.348	-2.830	-1.178	1.00	28.66
ATOM	1866	NE2	HIS	1679	11.394	-3.221	-2.441	1.00	29.66
ATOM	1868	C	HIS	1679	17.097	-2.719	-0.650	1.00	23.14
ATOM	1869	0	HIS	1679	17.511	-3.074	0.459	1.00	21.69
ATOM	1870	N	GLN	1680	17.895	-2.506	-1.697	1.00	22.38
ATOM	1872	CA	GLN	1680	19.335	-2.726	-1.658	1.00	22.33
ATOM	1873	CB	GLN	1680	19.948	-2.594	-3.058	1.00	22.52
ATOM	1874	CG	GLN	1680	19.895	-3.872	-3.879	1.00	29.15
ATOM	1875	CD	GLN	1680	18.865	-3.847	-4.991	1.00	33.60
ATOM	1876	OEl	GLN	1680	17.819	-3.212	-4.871	1.00	38.43
ATOM	1877	NE2	GLN	1680	19.159	-4.542	-6.085	1.00	33.44
MOTA	1880	C	GLN	1680	20.007	-1.740	-0.732	1.00	22.61
ATOM	1881	0	GLN	1680	20.943	-2.093	-0.027	1.00	22.00
ATOM	1882	N	SER	1681	19.562	-0.490	-0.745	1.00	22.06
ATOM	1884	CA	SER	1681	20.184	0.479	0.137	1.00	23.41
ATOM	1885	CB	SER	1681	19.886	1.923	-0.306	1.00	20.06
MOTA	1886	OG	SER	1681	18.503	2.166	-0.479	1.00	22.90
ATOM	1888	C	SER	1681	19.778	0.206	1.583	1.00	23.08
MOTA	1889	0	SER	1681	20.528	0.531	2.506	1.00	24.13
MOTA	1890	N	ASP	1682	18.608	-0.412	1.770	1.00	23.19
MOTA	1892	CA	ASP	1682	18.107	-0.775	3.104	1.00	22.37
MOTA	1893	CB	ASP	1682	16.660	-1.275	3.018	1.00	24.55
MOTA	1894	CG	ASP	1682	15.616	-0.172	3.222	1.00	24.22
MOTA	1895	OD1	ASP	1682	14.428	-0.479	3.005	1.00	25.02
MOTA	1896	OD2	ASP	1682	15.949	0.968	3.625	1.00	24.82
MOTA	1897	С	ASP	1682	18.980	-1.888	3.690	1.00	20.47
ATOM	1898	0	ASP	1682	19.172	-1.984	4.906	1.00	21.83
ATOM	1899	N	VAL	1683	19.480	-2.746	2.806	1.00	20.14
ATOM	1901	CA	VAL	1683	20.340	-3.856	3.179	1.00	20.49
ATOM	1902	CB	VAL	1683	20.493	-4.842	2.003	1.00	22.38
ATOM	1903	CG1	VAL	1683	21.757	-5.691	2.159	1.00	19.57
ATOM	1904	CG2	VAL	1683	19.264	-5.740	1.942	1.00	22.35
ATOM	1905	С	VAL	1683	21.677	-3.315	3.683	1.00	20.22
ATOM	1906	0	VAL	1683	22.202	-3.789	4.684	1.00	21.41
ATOM	1907	N	TRP	1684	22.210	-2.311	3.003	1.00	21.33
ATOM	1909	CA	TRP	1684	23.440	-1.666	3.449	1.00	22.21
ATOM	1910	СВ	TRP	1684	23.768	-0.473	2.540	1.00	18.78
ATOM	1911	CG	TRP	1684	24.924	0.391	3.037	1.00	22.80
ATOM	1912	CD2	TRP	1684	26.237	0.477	2.472	1.00	24.60
ATOM	1913	CE2	TRP	1684	26.989	1.364	3.286	1.00	24.34
ATOM	1914	CE3	TRP	1684	26.853	-0.099	1.352	1.00	24.32
ATOM	1915	CD1	TRP	1684	24.933	1.208	4.138	1.00	22.28
									20

								0						
	ATOM	1916	NE1	TRP	1604									
	ATOM	1918	CZ2	TRP	1684			1	.791	4	297	7 0		
	ATOM	1919	CZ3		1684	-0.,	324		.669		022	1.00		
	ATOM	1920	CH2		1684		193		.213		090	1.00		
	MOTA	1921	C		1684	28.9	906		.088			1.00		
	ATOM	1922	0		1684	23.1	.98	- 1	.183		918	1.00		00
	ATOM	1923			1684	23.9	82		475		399	1.00		26
	3	1925	N		1685	22.1	08	-0	447	5.8		1.00	24.5	
			CA		1685	21.7	44	٥.	050	5.1		1.00	22.8	
		1926	CB	SER]	L685	20.3	98		057	6.4		1.00	24.0	
		1927	OG	SER 1	.685	20.42	24		783	6.3	85	1.00	21.9	
		1929	C	SER 1	685	21.65			787	5.3	88	1.00	24.7	
		L930	0		685	22.05	9	-1.		7.4	64	1.00	24.2	
	TOM 1	.931	N		686	22.07		~0.		8.63		1.00		
		.933		_	686	21.09	9	~2.3	221	7.03		1.00	23.94	
	TOM 1	934	OT.	_		20.99	3	-3.3	393	7.89			23.20	
A'	TOM 1				686	20.21	6	-4.5		7.21		1.00	23.87	
A'.	70				586	20.06	2	-5.7			_	1.00	19.56	
A'			~~~		86	19.24	0	-5.7		8.07		1.00	22.19	
			~~~		86	20.77	3	-6.8	90	9.20		1.00	21.55	
			~~~		86	19.125		-6.8		7.79	-	.00	21.94	
				HE 16	86	20.663		-0.8	0.1	10.03		.00	21.66	
				HE 16	86	19.842		-8.0		8.62		.00	22.47	
AT		41 0	-	HE 16		22.389		-7.9		9.743		.00	23.14	
	_	42 0) P	HE 16		22.579		-3.89		8.300		.00	22.62	
AT			G]	Y 16				-4.42		9.407		.00	23.09	
ATO			A GI			23.354		-3.72		7.401				
AT(46 C				24.718		-4.11		7.721			23.50	
ATO		47 O				25.230		-3.24		8.867			23.83	
ATC		18 N	VA			25.901		-3.74	_	9.778			21.95	
ATC						24.928		-1.94	_	8.817			23.76	
ATO	M 195					25.331		-1.00	_	9.877		00	20.60	
ATO	M 195	-				25.020		0.48					22.34	
ATO					8	25.547		1.438		9.488		00 2	20.94	
ATO					8 ;	25.675		0.832		.543	1.	00 2	1.65	
ATO		_	VA1		3 ;	24.598	_	1.400		3.160	1.		2.71	
ATON			VAI	1688	3 2	25.199		1 470		.182	1.0	00 2	2.71	
ATOM		,	LEU	1689) ;	23.310		1.479		.255	1.0		2.78	
ATOM			LEU			2.534	_	1.706		.082	1.0		2.81	
			LEU			1.064	-	2.111		.253	1.0	0 2	5.21	
ATOM			LEU	1689		0.004		2.357	11	.866	1.0		5.78	
ATOM	-201		LEU		_	0.006		2.491	12	.976	1.0		9.18	
ATOM		CD2	LEU	1689	_	8.643	- 2	2.109	12.	408	1.0			
ATOM		C	LEU	1689	1	9.959		8.895		553	1.0		3.57	
ATOM	1964	0	LEU	1689	2.	3.158	- 3	.375		871	1.0		.77	
ATOM	1965	N	LEU		2:	3.249	- 3	.483		099	1.00		.88	
ATOM	1967	CA	LEU	1690	23	3.588	-4	.323		031			.50	
ATOM	1968	СВ	LEU	1690	24	.221		.544	12.		1.00		.84	
ATOM	1969	CG		1690	24	.669		.444	11.		1.00		.43	
ATOM	1970	CD1	LEU	1690	23	.672	- 7	.309			1.00		.35	
ATOM	1971		LEU	1690	24	.415	-7	.962	10.		1.00	26	. 57	
ATOM		CD2	LEU	1690	23	.042		380	9.4	446	1.00	26.		
ATOM	1972	C	LEU	1690	25	.430		360	11.5		1.00	24.		
	1973	0	LEU	1690	25	.646		168	13.3		1.00	25.		
ATOM	1974	N	TRP	1691	22		~5.	706	14.4		.00	24.		
ATOM	1976	CA	TRP	1691	20	.211	-4.	227	12.8		00	26.		
MOTA	1977	CB	TRP	1691	21.	405	-3.	728	13.5		.00			
ATOM	1978	CG	TRP	1691	28.	072	-2.	659	12.6		.00	25.		
				T031	29.	394	-2.	195	13.1			24.		
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ATOM	1979	CD2	TRP	1691	29.623	-1.104	14.056	1.00	26.95
MOTA	1980	CE2	TRP	1691	31.022	-1.015	14.259	1.00	27.64
MOTA	1981	CE3	TRP	1691	28.783	-0.191	14.708	1.00	26.28
MOTA	1982	CD1	TRP	1691	30.634	-2.715	12.856	1.00	28.38
MOTA	1983	NE1	TRP	1691	31.609	-2.009	13.518	1.00	29.56
MOTA	1985	CZ2	TRP	1691	31.599	-0.045	15.086	1.00	27.78
MOTA	1986	CZ3	TRP	1691	29.356	0.769	15.533	1.00	27.63
MOTA	1987	CH2	TRP	1691	30.753	0.835	15.713	1.00	30.68
ATOM	1988	С	TRP	1691	27.025	-3.147	14.876	1.00	26.38
ATOM	1989	0	TRP	1691	27.686	-3.414	15.883	1.00	24.82
MOTA	1990	N	GLU	1692	25.926	-2.393	14.916	1.00	27.62
MOTA	1992	CA	GLU	1692	25.442	-1.790	16.162	1.00	27.02
ATOM	1993	CB	GLU	1692	24.193	-0.963	15.919	1.00	29.27
ATOM	1994	CG	GLU	1692	24.345	0.236	15.028	1.00	24.77
ATOM	1995	CD	GLU	1692	23.046	0.992	14.962	1.00	25.98
ATOM	1996	OE1	GLU	1692	22.238	0.694	14.058	1.00	22.29
ATOM	1997	OE2	GLU	1692	22.803	1.837	15.850	1.00	25.12
ATOM	1998	С	GLU	1692	25.092	-2.856	17.191	1.00	27.88
ATOM	1999	0	GLU	1692	25.333	-2.673	18.379	1.00	30.18
ATOM	2000	N	ILE	1693	24.500	-3.956	16.734	1.00	26.65
ATOM	2002	CA	ILE	1693	24.118	-5.054	17.618	1.00	26.14
ATOM	2003	CB	ILE	1693	23.279	-6.144	16.858	1.00	25.37
MOTA	2004	CG2	ILE	1693	23.144	-7.445	17.704	1.00	21.48
ATOM	2005	CG1	ILE	1693	21.897	-5.563	16.496	1.00	24.80
ATOM	2006	CD1	ILE	1693	21.017	-6.479	15.642	1.00	22.40
ATOM	2007	C	ILE	1693	25.345	-5.698	18.239	1.00	27.17
ATOM	2008	Ö	ILE	1693	25.424	-5.864	19.452	1.00	27.30
ATOM	2009	N	PHE	1694	26.329	-6.017	17.414	1.00	29.98
ATOM	2011	CA	PHE	1694	27.518	-6.674	17.925	1.00	30.61
ATOM	2012	СВ	PHE	1694	28.140	-7.556	16.843	1.00	28.30
MOTA	2013	CG	PHE	1694	27.197	-8.611	16.353	1.00	30.91
ATOM	2014	CD1	PHE	1694	26.627	-8.526	15.088	1.00	34.46
MOTA	2015	CD2	PHE	1694	26.743	-9.601	17.224	1.00	32.71
ATOM	2016	CE1	PHE	1694	25.622	-9.409	14.701	1.00	34.24
ATOM	2017	CE2	PHE	1694	25.737	-10.490	16.844	1.00	32.44
ATOM	2018	CZ	PHE	1694	25.170	-10.387	15.592	1.00	32.70
ATOM	2019	C	PHE	1694	28.512	-5.796	18.689	1.00	31.74
MOTA	2020	0	PHE	1694	29.469	-6.299	19.276	1.00	35.15
ATOM	2021	N	THR	1695	28.275	-4.489	18.698	1.00	31.12
ATOM	2023	CA	THR	1695	29.101	-3.575	19.473	1.00	29.96
ATOM	2024	CB	THR	1695	29.532	-2.351	18.657	1.00	28.09
ATOM	2025	OG1	THR	1695	28.373	-1.685	18.150	1.00	30.65
MOTA	2027	CG2	THR	1695	30.450	-2.767	17.510	1.00	23.37
ATOM	2028	C	THR	1695	28.240	-3.128	20.664	1.00	30.01
ATOM	2029	0	THR	1695	28.617	-2.233	21.427	1.00	31.14
MOTA	2020	N	LEU	1696	27.078	-3.766	20.797	1.00	27.96
ATOM	2032	CA	LEU	1696	26.113	-3.490	21.862	1.00	30.25
ATOM	2032	CB	LEU	1696	26.633	-3.450	23.216	1.00	33.54
ATOM	2033	CG	LEU	1696	26.899	-5.482	23.216	1.00	32.61
							24.711	1.00	33.54
ATOM	2035	CD1	LEU	1696	27.473	-5.777 -6.233	23.126		
ATOM	2036	CD2	LEU	1696	25.602	-6.233		1.00	36.37
ATOM	2037	C	LEU	1696	25.717	-2.031	21.958	1.00	28.19
MOTA	2038	0	LEU	1696	25.792	-1.431	23.018	1.00	29.18
ATOM	2039	N	GLY	1697	25.251	-1.472	20.853	1.00	28.24

					97 24.	851 -0	.082	20.858		_
		042 (_		20.499		-0.25
		043	_	LY 16				20.495	_	
)44 N	_	LY 16				19.790		5
AT				LY 16						25
AT		47 C	G	LY 16				19.396		
ATO		48 O	G	LY 169				18.388		
ATO		49 N	S	ER 169				17.601		
AT(A S	ER 169			_	18.411		
ATC			B SI	ER 169				7.510	1.00	
ATC			G SI	ER 169	9 28.5			8.288	1.00	91.01
ATC		55 C	SI	ER 169				7.440	1.00	40.03
ATC		_	SE					6.282	1.00	32.20
ATO			PF		-			6.408	1.00	31.67
ATO		8 CI) PR	20 170	0 27.1			5.082	1.00	32.62
ATO			A PR		- · · -			4.773	1.00	34.19
ATO		0 CB	PR	0 170			_	3.856	1.00	31.76
ATO			PR	0 170	0 27.1			2.759	1.00	32.04
ATO			PR			-		3.502	1.00	33.17
ATO			PR	0 1700				3.609	1.00	28.70
ATO			TY	R 1701				3.871	1.00	28.57
ATON			TY	R 1701				3.164	1.00	28.61
ATON			TY	R 1701		_		2.870	1.00	29.92
ATOM			TY	7 1701				510	1.00	30.15
ATOM	_		l TYF	7 1701	30.79			.339	1.00	36.17
ATOM			L TYF	1701		_		.664	1.00	39.26
ATOM			YYF.	1701				.571	1.00	41.51
ATOM			TYR	1701				.893	1.00	37.48
ATOM			TYR	1701				.805	1.00	42.94
ATOM			TYR	1701	32.11			.146	1.00	45.72
ATOM	-	_	TYR	1701	32.27			.043	1.00	53.99
ATOM ATOM	2077		TYR	1701	31.93			. 941	1.00	31.09
ATOM	2078		PRO	1702	32.649			.649 .189	1.00	31.93
ATOM	2079		PRO	1702	33.212				1.00	34.66
ATOM	2080	CA	PRO	1702	32.631				1.00	36.83
ATOM	2081	CB	PRO	1702	33.116				1.00	33.54
ATOM	2082	CG	PRO	1702	32.903				1.00	32.18
ATOM	2083	C	PRO	1702	33.628					40.82
ATOM	2084 2085	0	PRO	1702	34.750					34.78
ATOM		N ~	GLY	1703	33.220	10.528				33.97
ATOM	2087	CA	GLY	1703	34.085	11.66				36.45
ATOM	2088	C	GLY	1703	34.245	12.006		_		34.40
MOTA	2089	0	GLY	1703	34.977					34.34
ATOM	2090	N	VAL	1704	33.552	11.275				34.20
	2092	CA	VAL	1704	33.641	11.512				35.02
ATOM	2093	CB	VAL	1704	33.614	10.176				32.77
ATOM	2094	CG1	VAL	1704	33.628	10.435				1.32
ATOM	2095	CG2	VAL	1704	34.796	9.297		_		1.46
ATOM	2096	C	VAL	1704	32.510	12.410	_			7.62
ATOM	2097	0	VAL	1704	31.337	12.410				3.35
ATOM	2098	N	PRO	1705	32.849	13.589	11.6	_		3.94
ATOM	2099	CD	PRO	1705	34.181	14.221	10.9			2.43
ATOM	2100	CA	PRO	1705	31.826	14.505	10.9			2.77
ATOM	2101	CB	PRO	1705	32.545	15.853	10.4			3.61
CCCD /= -						45.655	10.5	υ 9 1.	00 3	3.21
SSSD/551	115 401									



ATOM	2102	CG	PRO	1705	33.935	15.482	10.141	1.00	35.53
MOTA	2103	С	PRO	1705	31.395	14.138	9.052	1.00	33.91
MOTA	2104	0	PRO	1705	32.113	13.409	8.354	1.00	32.65
ATOM	2105	N	VAL	1706	30.255	14.684	8.619	1.00	33.82
MOTA	2107	CA	VAL	1706	29.689	14.447	7.280	1.00	33.97
MOTA	2108	CB	VAL	1706	28.617	15.513	6.943	1.00	37.41
MOTA	2109	CG1	VAL	1706	28.045	15.282	5.556	1.00	41.12
ATOM	2110	CG2	VAL	1706	27.507	15.484	7.971	1.00	38.89
ATOM	2111	C	VAL	1706	30.712	14.428	6.135	1.00	32.32
MOTA	2112	0	VAL	1706	30.819	13.450	5.398	1.00	32.58
MOTA	2113	N	GLU	1707	31.477	15.504	6.004	1.00	31.15
ATOM	2115	CA	GLU	1707	32.478	15.630	4.956	1.00	29.82
ATOM	2116	СВ	GLU	1707	33.172	16.989	5.048	1.00	30.05
ATOM	2117	С	GLU.	1707	33.531	14.541	4.959	1.00	28.52
ATOM	2118	0	GLU	1707	33.995	14.134	3.896	1.00	30.85
ATOM	2119	N	GLU	1708	33.958	14.110	6.143	1.00	28.70
ATOM	2121	CA	GLU	1708	34.978	13.073	6.235	1.00	29.50
MOTA	2122	CB	GLU	1708	35.590	13.010	7.641	1.00	31.28
ATOM	2123	CG	GLU	1708	36.281	14.289	8.103	1.00	41.63
MOTA	2124	CD	GLU	1708	37.454	14.718	7.237	1.00	49.91
ATOM	2125	OE1	GLU	1708	38.020	13.876	6.498	1.00	53.57
ATOM	2126	OE2	GLU	1708	37.821	15.916	7.308	1.00	58.45
ATOM	2127	С	GLU	1708	34.365	11.730	5.878	1.00	30.00
ATOM	2128	0	GLU	1708	35.016	10.874	5.257	1.00	28.43
ATOM	2129	N	LEU	1709	33.103	11.559	6.257	1.00	30.08
ATOM	2131	CA	LEU	1709	32.392	10.324	5.964	1.00	29.19
ATOM	2132	CB	LEU	1709	30.995	10.347	6.592	1.00	28.97
ATOM	2133	CG	LEU	1709	30.109	9.186	6.137	1.00	30.66
ATOM	2134	CD1	LEU	1709	30.664	7.866	6.659	1.00	29.24
ATOM	2135	CD2	LEU	1709	28.684	9.403	6.593	1.00	29.29
ATOM	2136	C	LEU	1709	32.294	10.130	4.449	1.00	28.26
MOTA	2137	0	LEU	1709	32.450	9.011	3.948	1.00	28.86
MOTA	2138	N	PHE	1710	32.016	11.220	3.735	1.00	26.86
MOTA	2140	CA	PHE	1710	31.903	11.192	2.285	1.00	28.86
MOTA	2141	CB	PHE	1710	31.632	12.593	1.743	1.00	31.88
MOTA	2142	CG	PHE	1710	30.249	13.095	2.014	1.00	37.62
MOTA	2143	CD1	PHE	1710	29.265	12.247	2.509	1.00	42.63
ATOM	2144	CD2	PHE	1710	29.931	14.424	1.792	1.00	43.53
ATOM	2145	CE1	PHE	1710	27.977	12.718	2.783	1.00	45.99
ATOM	2146	CE2	PHE	1710	28.648	14.905	2.061	1.00	46.25
ATOM	2147	CZ	PHE	1710	27.670	14.045	2.559	1.00	44.45
ATOM	2148	C	PHE	1710	33.193	10.660	1.681	1.00	30.42
ATOM	2149	0	PHE	1710	33.174	9.807	0.792	1.00	29.01
MOTA	2150	N	LYS	1711	34.309	11.152	2.212	1.00	30.64
ATOM	2152	CA	LYS	1711	35.650	10.762	1.786	1.00	32.89
ATOM	2153	CB	LYS	1711	36.670	11.655	2.502	1.00	37.91
ATOM	2154	CG	LYS	1711	38.108	11.479	2.088	1.00	42.99
ATOM	2155	CD	LYS	1711	38.976	12.528	2.752	1.00	47.45
ATOM	2156	CE	LYS	1711	40.380	12.505	2.182	1.00	52.35
ATOM	2157	NZ	LYS	1711	41.104	11.272	2.587	1.00	58.47
MOTA	2161	C	LYS	1711	35.913	9.273	2.071	1.00	32.23
ATOM	2162	Ö	LYS	1711	36.445	8.559	1.216	1.00	30.79
ATOM	2163	N	LEU	1712	35.533	8.807	3.264	1.00	31.37
MOTA	2165	CA	LEU	1712	35.704	7.399	3.630	1.00	29.46
		-		· · · · 					





ATO	OM 0						-50					
		166	CB	LEU	1712	35.2	20 .	7.117				
AT(167	CG		1712	36.0					1.00	28.57
ATO		168	CD1		1712	35.3		7.662	6.2		1.00	30.18
ATC			CD2		1712	37.4		7.349	7.5	_	.00	26.92
ATO			C		1712	34.9		.083	6.2		.00	30.88
ATO		L71	0		1712	35.43		.539	2.6	51 1	.00	28.99
ATO					L713			.551	2.1		.00	30.73
ATO		.74			713	33.67		.915	2.3	88 1	.00	30.13
ATO		75 - (-	713	32.85		.158	1.4	56 1	.00	32.10
ATO		76 (~		713	31.41		.685	1.4		.00	35.23
ATOM	M 21	77 (713	30.61		.292	2.69		.00	37.47
ATON					713	29.26		. 982	2.72		.00	40.85
ATOM			_			30.44		788	2.72		00	39.61
ATOM	1 21		_		713	33.44		147	0.04		00	
ATOM	1 218		_	_	713	33.54		090	-0.57		00	32.70
ATOM	1 218			_	714	33.85		309	-0.44		00	31.86
ATOM		_		_	714	34.44(387	-1.77			32.42
ATOM		_			714	34.826		824	-2.11			32.56
ATOM		_	_		714	33.640	9.	736	-2.29	_		33.02
ATOM		-	_		14	32.736	9.	235	-3.39	_ `		35.56
ATOM	218				14	31.635	10.		-3.682			37.94
ATOM	219				14	30.727			-4.779	_		42.57
ATOM	219	_	LY			35.664	6.4		-1.885			47.40
ATOM	219	_	LY			35.927	5.8		-2.937			35.36
ATOM	219		GL.	-		36.376	6.3		-0.775			36.68
ATOM	219				15	37.577	5.5		-0.749			34.51
ATOM	2198					38.566	6.1					35.31
ATOM	2199	- •		- · •	L5	38.967	7.5		0.250			37.07
ATOM					15	39.735	8.3		0.163			13.62
ATOM	2200				.5	39.906	7.8		0.893			9.75
ATOM	2201				.5	40.163	9.4		2.029	1.0	_	9.71
ATOM	2202	_	GL		.5	37.321	4.04		0.572	1.00		5.13
ATOM	2203	_	GLU	171	5	38.259	3.26		0.487	1.00		4.08
ATOM	2204	N	GLY	171	6	36.049	3.67		0.438	1.00) 3	4.82
ATOM	2206	CA	GLY	171	6	35.695			0.366	1.00		1.53
ATOM	2207	C	GLY	171		35.966	2.28		0.133	1.00		7.58
ATOM	2208	_	\mathtt{GLY}	171		36.069	1.76		1.262	1.00		3.60
	2209	N	HIS	171		36.062	0.56	,	1.464	1.00		7.81
ATOM	2211	CA	HIS	1717		36.319	2.66		2.236	1.00	25	9.10
ATOM	2212	CB	HIS	1717		36.501	2.26		.617	1.00	29	9.30
	2213	CG	HIS	1717		36.788	3.51	_	.486	1.00	30	.54
	2214	CD2	HIS	1717		37.961	3.21		.930	1.00		.88
~	2215	ND1	HIS	1717	-	55.798	3.02		.586	1.00		.21
	2217	CE1	HIS	1717		6.342	3.108		.881	1.00		. 22
	2218	NE2	HIS	1717	_		2.865		.061	1.00		.51
	2220	C	HIS	1717	_	7.651	2.809		. 907	1.00		. 94
ATOM 2	2221	0	HIS	1717	2	5.180	1.416		.183	1.00		.42
ATOM 2	2222	N	ARG	1718		4.017	1.666		. 885	1.00	30.	
ATOM 2	2224	CA	ARG	1718		5.526	0.450	5.	028	1.00	27.	
	225	CB	ARG			4.559	-0.423	5.	688	1.00	27.	
	226	CG	ARG	1718		4.562	-1.813		.	1.00		
	227	CD		1718		1.078	-1.860			1.00	29.	
	228	NE	ARG	1718		2.609	-1.412			1.00	28.	
	230	CZ	ARG	1718		2.091	-1.467			1.00	27.	
3		NH1	ARG	1718		1.173	-0.476				24.	
		~411T	ARG	1718	32	.768	0.668			1.00 1.00	24.	
SSSD/5514	5. v01							-•		00	23.	98

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WO 98/07835

	132	
		0.019 1.00 21.60
2234 NH2 ARG 1718	31.595 -0.603	7 148 1.00 30.11
ATOM 2234 NH2 APG 1718	35.005 -0.521	7 428 1.00 30.60
ATOM 2237	36.201 -0.623	9 074 1.00 30.69
ATOM 2238	34.056 -0.430	2.501 1.00 31.77
ATOM 2239 N MEI 1719	34 350 -0.490	24 56
ATOM 2241 CA MEI 1710	33.072 -0.302	10.333
ATOM 2242 CB MET 17	32,408 1.060	10.174
ATOM 2243 CG MET 1/19	31 015 1.307	11.314 -
ATOM 2244 SD FIELD	29.797 0.338	10.544
A10.1 2245 CE MET 1719	34.998 -1.810	9.003
2246 C MET 1/19	34.802 -2.802	9.169 2.0
ATOM 2247 O MET 1/19	34.00-	10.920 21.
2249 N ASP 1/20	33	11.303 -
ATOM 2235	50,	(2.330 =
ATOM 2250 CB ASP 1720	37.32	11.747 1.00 44.09
ATOM 2251 CG ASP 1720	30,00	10.596 1.00 50.97
ATOM 2252 CO ASP 1720		12.443 1.00 48.07
ATOM 2253 ODI 1720	3,5,0	70 079 1.00 31.40
ATOM 2254 ODZ 200 1720	35.524 -3.977	70 561 1.00 32.00
ATOM 2255 C ACD 1720	34.466	10 101 1.00 32.70
ATOM 2256 0 1721	35.943	12.25 1.00 32.28
ATOM 225/ N +VC 1721	25 133 -6.26.	12 575 1.00 33.63
ATOM 2259 CA LIS 1721	35.726 -7.64°	1 00 35.68
ATOM 2260 CB 113 172	34 854 -8.77	3 1 00 36.22
ATOM 2261 CG 113 172	$\frac{35.392}{10.12}$	1 00 42.65
ATOM 2262 CD 113 212	36 054 -10.74	9 13.900 1 00 46.15
ATOM 2263 CE 1113 11-	. 36 354 -12.18	9 13.730 - 1 00 35.55
ATOM 2264 NZ 113 1.0	35 039 -6.05	1 00 37.78
7TOM 2268 C 113 11-	ac ned -5.94	26 14.900 -
ATOM 2269 O LYS 1/2	-5.07 -6.0	17 14.001
2270 N PRO 1/2	-6 11	05 14.179 1.00 32.77
2271 CD PRO 174	22 32.50 -5.8	27 16.305 1.00 37
DATE CA PRO 17	22 55.00	46 16.465 1.00 34.53
OOTO CB PRO 17	24 32.2	75 15.122 1.00 32
CG PRO 17	22 31.00	17.023 1.00 331
ATOM 2275 C PRO 17	22 54.24 -8.1	36 16.47/ 1.00 33
ATOM 2275 O PRO 17	7.7	320 18.222 1.00 45.01
SER IN	23	18.940 1.00
ATOM 2277	123	EO8 20.160 1.00 46.88
ATOM ZEE 1	123 -0	027 21.208 1.00 53.47
ATOM DOG SER 1	723 33.32	721 19.359 1.00 46.67
ATOM 2201 CEP 1	143	172 19.417 1.00 46.21
ATOM 2283 CER 1	723 32.22	- 10 EQU 1.00 47.00
ATOM 2284 U DAN 1	724 34.237 -10.	10 000 1.00 54.70
ATOM 2285 N TON 1	724 33.092 -10.	21 355 1.00 57.86
ATOM 2287 CA	724 32.559 -10	.319 22.370 1.00 61.99
ATOM 2286 CD	33.679 -10	.091 22.5
ATOM 2289 CG ASN	34.531 -10	.959 22.565 2.00 63.56
ATOM 2290 OD1 ASN	33 712 -8	.899 22.953 21
ATOM 2291 ND2 ASN	32 015 -10	.779 18.855 1 00 51.56
ATOM 2294 C ASN	1/24 52.59 -10	1423 19.108 1.00
7TOM 2295 O ASN	1/24 50.454 -11	087 17.683 1.00
CYS	1/25 52.50	1 136 16.508 1.00 14 03
ATOM 2230 CA CYS	1/25	9.771 15.811 1.00
ATOM ZZZZZ CB CYS	1/25	9 816 14.194 1.00 41.83
ATOM 2233 CC CYS	1/25	9.816 14.194 1.00 42.30 2.135 15.640 1.00 42.30
ATOM 2300 D-	1725 32.341 -1	
ATOM 2301 C C15		

							_	152					
	ATOM	2302	0	CYS	2 22 -								
	ATOM	2303	N		1725		566	-12	.045	1 5	400	_	
	ATOM	2305	CA	THR	1726	31.	627	-13	.134	10	. 493	1.00	- + • • •
	MOTA	2306		THR	1726	32.	259	-14	.153		141	1.00	37.46
	ATOM	2307	CB	THR	1726		339	-15	.153		320	1.00	35.29
	ATOM		OG1	THR	1726	30.		-15	.367		132	1.00	
	ATOM	2309	CG2	THR	1726	31.		-14	.952		523	1.00	
		2310	C	THR	1726	22.		-16	.019	15.	454	1.00	,
	ATOM	2311	0	THR	1726	32.6	68	-13.	622	12.	963	1.00	30.22
	ATOM	2312	N	ASN		32.]	.58	-12.	593	12.	518		33.53
	ATOM	2314	CA	ASN	1727	33.6	19	-14.		12.		1.00	32.93
	7 mas -	2315	CB		1727	34.0	30	-13.	867			1.00	32.72
į	3 0000	2316	CG	ASN	1727	35.1	66	-14.	724	10.9		1.00	35.91
		2317		ASN	1727	36.4	63			10.4		1.00	40.64
			OD1	ASN	1727	37.0	47	-14.	233	11.1	.68	1.00	46.52
		2318	ND2	ASN	1727	36.9	* /) 1	-13.4		11:1	58	1.00	49.98
7		2321	C	3 ~	1727	20.9		-15.		11.8	14	1.00	
	TOM 2	322	_	_ :	1727	32.82		-14.0	006	10.0			49.04
	TOM 2	323		_		32.68		-13.2	36	9.1		1.00	34.27
	TOM 2	325	~~		1728	31.96	9	-14.9		10.3		1.00	32.96
A	TOM 2		an.		1728	30.77	8	-15.2	35			1.00	32.49
A'	TO		~~		1728	30.06	4 .	-16.5	04	9.5		1.00	31.99
			-		L728	28.83		-16.8	C C	9.97		1.00	34.15
					.728	28.18		10.8	66	9.15		1.00	35.63
				LU 1	728	28.20		18.1		9.60	8 1	1.00	39.72
	_	_		LU 1	728	27.65		18.4	53 1	0.82		.00	42.25
		31 C	' G		728	20.054		18.89	96	8.74			
		32 o	G		_	29.814		14.04	9	9.54			39.87
		33 N				29.309	-	13.60		8.51	. ~		30.76
AT		35 C	_		729	29.559	- :	13.54		0.75		.00	29.58
ATO	OM 23		_		729	28.670	-:	12.40		0.911			30.01
AT(OM 23:				729	28.225	- 3	12.27				.00	30.21
ATO				<i></i>	/29	27.208		3.35		364		.00 3	0.13
ATC	M 233			- .		7.119	_ 7	.3.48		.748			3.61
ATO				-,	29 2	5.844	. 7	3.48.		.262			3.71
ATO		_	$_{ m LE}$	U 17	29 2	9.316	-1	3.02		.139			0.31
ATO			LE			8.619	-1	1.133	10	.390			0.26
			TY		_	0.619	-1	0.229	9	. 938	1.		
ATO	_		TY		_	0.648	-1	1.063	10.	.435	1.		8.89
ATO			TYI		_	1.343	- 9	9.893		912			8.91
ATOM		6 CG	TYF			2.804	- 9	9.861		359	1.0		3.91
ATON		7 CD1				3.537	- 8	3.639			1.0		0.09
ATOM	1 2348			5		3.037	- 7	3.358		857	1.0	00 30	1.15
ATOM	2349			5	0 33	.688		.227		103	1.0	0 29	.97
ATOM	2350				0 34	.716			. 9.		1.0	0 28	. 99
ATOM			TYR	173	0 35	.386	0	.757		119	1.0		.24
ATOM			TYR	173	_	.861	- /	.620	8.6	632	1.0		.25
	-052	OH	TYR	173			~6	.362	8.8	389	1.0		.41
ATOM	-054	C	TYR	1730	_	.485	~ 5	.227	8.4		1.0		- 41
ATOM	2355	0	TYR			.260	- 9	. 943	8.3				
ATOM	2356	N	MET	1730		.078	-8.	920	7.7		1.00		
ATOM	2358	CA		1731		390	-11.	138			1.00	~ / ,	46
ATOM	2359		MET	1731	31.		-11.	275	7.8		1.00		68
ATOM	2360	CB	MET	1731	31.		-4. -10	770	6.3		1.00	28.	68
ATOM		CG	MET	1731	31		-12.	//8	5.9		1.00		
ATOM	2361	SD	MET	1731			-13.	U87	4.5		1.00		10
	2362	CE	MET	1731		441 .	-14.	804	4.06		1.00		
ATOM	2363	C	MET	1731	32.		14.	550	2.67	`			
ATOM	2364	0	MET		29.	917 -	10.8	358	5.91	_	1.00	58.	
ATOM	2365	N		1731	29.	782 ~	10.2	227			1.00	27.4	12
	-		MET	1732	28.8		11.1	97	4.87		00	30.8	10
SSSD/55	145 001								6.68	8 1	.00	28.5	
55	· 13. VU		•									_	

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MOTA	2367	CA	MET	1732	27.522	-10.777	6.389	1.00	26.47
MOTA	2368	CB	MET	1732	26.562	-11.308	7.458	1.00	25.79
MOTA	2369	CG	MET	1732	25.116	-10.838	7.274	1.00	26.01
MOTA	2370	SD	MET	1732	24.004	-11.550	8.469	1.00	26.22
ATOM	2371	CE	MET	1732	23.787	-13.195	7.783	1.00	23.74
MOTA	2372	C	MET	1732	27.445	-9.243	6.319	1.00	25.15
ATOM	2373	0	MET	1732	26.886	-8.691	5.379	1.00	25.41
MOTA	2374	N	MET	1733	28.024	-8.564	7.308	1.00	26.48
ATOM	2376	CA	MET	1733	28.057	-7.104	7.331	1.00	27.09
MOTA	2377	CB	MET	1733	28.903	-6.594	8.488	1.00	25.91
MOTA	2378	CG	MET	1733	28.235	-6.556	9.824	1.00	31.64
MOTA	2379	SD	MET	1733	29.442	-6.111	11.094	1.00	29.59
MOTA	2380	CE	MET	1733	28.886	-7.126	12.420	1.00	28.14
ATOM	2381	С	MET	1733	28.720	-6.613	6.056	1.00	28.43
MOTA	2382	0	MET	1733	28.185	-5.753	5.372	1.00	31.37
ATOM	2383	N	ARG	1734	29.891	-7.169	5.747	1.00	28.57
ATOM	2385	CA	ARG	1734	30.642	-6.783	4.551	1.00	27.00
ATOM	2386	СВ	ARG	1734	32.007	-7.488	4.510	1.00	25.98
ATOM	2387	CG	ARG	1734	32.927	-7.154	5.707	1.00	28.13
ATOM	2388	CD	ARG	1734	33.229	-5.672	5.765	1.00	29.97
ATOM	2389	NE	ARG	1734	33.922	-5.256	4.553	1.00	40.49
ATOM	2391	cz	ARG	1734	35.238	-5.361	4.363	1.00	43.95
ATOM	2392	NH1	ARG	1734	36.023	-5.853	5.318	1.00	41.81
ATOM	2395	NH2	ARG	1734	35.760	-5.048	3.184	1.00	46.20
ATOM	2398	С	ARG	1734	29.859	-7.037	3.268	1.00	24.57
ATOM	2399	0	ARG	1734	29.992	-6.290	2.314	1.00	24.94
ATOM	2400	N	ASP	1735	29.071	-8.107	3.235	1.00	24.79
ATOM	2402	CA	ASP	1735	28.254	-8.420	2.061	1.00	23.88
ATOM	2403	CB	ASP	1735	27.669	-9.830	2.150	1.00	25.95
MOTA	2404	CG	ASP	1735	28.724	-10.913	2.024	1.00	27.60
ATOM	2405	OD1	ASP	1735	29.842	-10.632	1.529	1.00	27.75
ATOM	2406	OD2	ASP	1735	28.432	-12.051	2.430	1.00	28.90
ATOM	2407	C	ASP	1735	27.139	-7.396	1.941	1.00	22.61
ATOM	2408	0	ASP	1735	26.777	-6.996	0.833	1.00	22.66
ATOM	2409	N	CYS	1736	26.611	-6.965	3.085	1.00	20.61
MOTA	2411	CA	CYS	1736	25.561	-5.952	3.109	1.00	23.63
MOTA	2412	CB	CYS	1736	25.007	-5.767	4.534	1.00	21.98
MOTA	2413	SG	CYS	1736	23.934	-7.126	5.111	1.00	22.95
MOTA	2414	С	CYS	1736	26.129	-4.633	2.599	1.00	23.62
ATOM	2415	0	CYS	1736	25.403	-3.797	2.047	1.00	22.15
ATOM	2416	N	TRP	1737	27.438	-4.461	2.775	1.00	24.37
ATOM	2418	CA	TRP	1737	28.123	-3.247	2.342	1.00	23.77
MOTA	2419	CB	TRP	1737	29.162	-2.810	3.371	1.00	19.38
MOTA	2420	CG	TRP	1737	28.601	-2.520	4.718	1.00	21.62
MOTA	2421	CD2	TRP	1737	29.268	-2.688	5.971	1.00	24.81
ATOM	2422	CE2	TRP	1737	28.371	-2.278	6.980	1.00	25.95
MOTA	2423	CE3	TRP	1737	30.534	-3.165	6.340	1.00	29.02
MOTA	2424	CD1	TRP	1737	27.359	-2.024	5.007	1.00	23.21
MOTA	2425	NEl	TRP	1737	27.213	-1.876	6.362	1.00	21.80
ATOM	2427	CZ2	TRP	1737	28.710	-2.305	8.347	1.00	26.68
ATOM	2428	CZ3	TRP	1737	30.873	-3.198	7.699	1.00	31.06
ATOM	2429	CH2	TRP	1737	29.959	-2.774	8.685	1.00	30.18
ATOM	2430	С	TRP	1737	28.788	-3.372	0.978	1.00	24.88
ATOM	2431	0	TRP	1737	29.737	-2.646	0.689	1.00	25.11

	ATOM	2432	N	HIS	1720						
	ATOM	2434	CA	HIS	1738			4.278	0.13	12 1 00	
	*	2435	СВ	HIS	1738	28.8		4.406	-1.19		,
	3	2436	CG	HIS	1738	28.2	80 -	5.573	-1.98	_	
	7.000	2437	CD2		1738	29.1		5.073	-3.08	•	21
		2438		HIS	1738	29.7	_	5.437			
		2440	ND1		1738	29.6		7.352	-4.14	_	25.67
	-	2441			1738	30.5		.478	-3.09		27.55
		443			1738	30.5		.329	-4.11		27.51
	ma			HIS	1738	28.7			-4.77		30.93
		444		HIS :	1738	27.65		.087	-1.953		25.59
			N j	ALA :	1739	29.78		.451	-1.905		22.01
	ma		CA ;		1739	29.75		.651	-2.612	1.00	23.84
			CB 7		1739	22./5		.418	-3.388	1.00	24.93
				_	.739	31.13		.177	-4.024	1.00	
		450 (_	.739	28.67	1 -1.	. 508	-4.462	1.00	26.39
		451 l	_			27.96	3 -0.	535	-4.727	1.00	25.35
Α٦	FOM 24				740	28.54	3 -2.	680	-5.073		28.20
AT			**	~	740	27.528	3 -2.	904	-6.101	1.00	22.68
AT					740	27.999				1.00	26.46
					740	27.063		_	-7.117	1.00	29.70
	_				740	29.433			-8.334	1.00	26.01
AT			**	AL 17	740	26.213	-		-7.537	1.00	31.22
AT	_ 		**	AL 17	740	26.138			-5.443	1.00	25.07
			PF		41	25.155			4.903	1.00	23.55
ATO			D PR		41	25.133			5.514	1.00	25.30
AT(A PR		41		-1.1	190 -	6.153	1.00	22.43
ATO		52 CI	3 PR			23.844	-2.8		4.921		24.09
ATO		3 CG	PR			22.962	-1.6	75 -	5.402		
ATC		4 C	PR			23.928	-0.5		5.491		23.12
ATO		5 0	PRO			23.272	-4.1		5.313		22.04
ATO	M 246	6 N	SEI			22.727	-4.9		4.466	_	22.18
ATO	M 246					23.437	-4.5		5.580		21.23
ATO	M 246					22.928	~5.8		7.088		3.87
ATO	M 247		SEF			23.071	-5.90		_		4.36
ATOM			SER			24.436	-6.02				7.39
ATON		. •	SER		2 2	23.636	-7.05				9.25
ATOM		. •	SER		2 2	23.145	-8.17			1.00 ₂	3.96
ATOM			GLN			24.810	-6.83			1.00 2	4.30
ATOM	,		GLN	174		5.558	-7.03		.915		4.39
ATOM	,		GLN	174	3 2	7.046	-7.93		.345		3.15
ATOM	/0		GLN	1743	3 2	7.359	-7.75		.638]	1.00 23	3.83
ATOM		CD	GLN	1743	_	6.816	-7.78		.126]	.00 22	8.84
	-	OE1	GLN	1743	_	7.318	-9.03	•	.808 1		.20
MOTA		NE2	GLN	1743		. 318	-10.139	5 -7.			.50
ATOM	2484	C	GLN	1743		5.775	-8.87	L -8.			.45
ATOM	2485	0	GLN	1743		5.309	-8.171	-3.			.45
ATOM	2486	N	ARG	1744		5.816	-9.135	-3.			.12
ATOM	2488	CA	ARG		_	1.557	-7.280	-3.			. 96
ATOM	2489	CB		1744	24	.242	-7.424				.67
ATOM	2490	CG	ARG	1744	23	.699	-6.110			.00 22	
ATOM	2491		ARG	1744	24	.672	-4.959			00 19	
ATOM	2492	CD	ARG	1744	24	.049	-3.640	-1.		00 21.	26
ATOM		NE	ARG	1744		.923	-2.552	-0.8		00 20.	
ATOM	2494	CZ	ARG	1744		.540		-1.3		00 25.	
	2495	NHl	ARG	1744		.257	-1.313	-1.5		00 24.	
ATOM	2498	NH2	ARG	1744	25		-0.955	-1.4	81 1.	00 22.	
ATOM	2501	C	ARG	1744	20,		-0.448	-2.0	36 1.		
CCC- :		•			43.	184	-8.505	-1.6		00 22.	
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ATOM	2502	0	ARG	1744	22.437	-8.800	-2.588	1.00	23.08
MOTA	2503	N	PRO	1745	23.162	-9.170	-0.467	1.00	20.76
MOTA	2504	CD	PRO	1745	24.087	-9.078	0.681	1.00	21.71
MOTA	2505	CA	PRO	1745	22.160	-10.207	-0.243	1.00	22.34
MOTA	2506	CB	PRO	1745	22.632	-10.859	1.057	1.00	20.58
MOTA	2507	CG	PRO	1745	23.298	-9.727	1.783	1.00	20.36
ATOM	2508	С	PRO	1745	20.814	-9.512	-0.048	1.00	23.62
MOTA	2509	0	PRO	1745	20.759	-8.318	0.255	1.00	25.29
MOTA	2510	N	THR	1746	19.731	-10.235	-0.275	1.00	23.39
MOTA	2512	CA	THR	1746	18.404	-9.675	-0.080	1.00	22.77
MOTA	2513	CB	THR	1746	17.386	-10.368	-1.004	1.00	23.24
ATOM	2514	OG1	THR	1746	17.409	-11.783	-0.763	1.00	23.11
MOTA	2516	CG2	THR	1746	17.724	-10.103	-2.475	1.00	24.96
MOTA	2517	С	THR	1746	18.009	-9.954	1.365	1.00	24.98
MOTA	2518	0	THR	1746	18.664	-10.758	2.043	1.00	24.30
MOTA	2519	N	PHE	1747	16.944	-9.318	1.853	1.00	24.95
MOTA	2521	CA	PHE	1747	16.501	-9.596	3.221	1.00	25.16
MOTA	2522	CB	PHE	1747	15.395	-8.628	3.661	1.00	23.64
MOTA	2523	CG	PHE	1747	15.916	-7.283	4.089	1.00	24.34
MOTA	2524	CD1	PHE	1747	16.715	-7.167	5.226	1.00	21.21
ATOM	2525	CD2	PHE	1747	15.649	-6.137	3.334	1.00	21.42
ATOM	2526	CE1	PHE	1747	17.252	-5.932	5.597	1.00	20.99
ATOM	2527	CE2	PHE	1747	16.178	-4.907	3.699	1.00	20.36
MOTA	2528	CZ	PHE	1747	16.985	-4.807	4.840	1.00	19.30
MOTA	2529	C	PHE	1747	16.034	-11.049	3.311	1.00	23.57
MOTA	2530	0	PHE	1747	16.182	-11.702	4.344	1.00	25.32
MOTA	2531	N	LYS	1748	15.520	-11.573	2.202	1.00	23.19
MOTA	2533	CA	LYS	1748	15.066	-12.958	2.167	1.00	23.67
MOTA	2534	CB	LYS	1748	14.462	-13.285	0.799	1.00	26.67
MOTA	2535	CG	LYS	1748	14.018	-14.739	0.622	1.00	30.49
ATOM	2536	CD	LYS	1748	13.642	-14.996	-0.837	1.00	38.98
MOTA	2537	CE	LYS	1748	13.182	-16.432	-1.087	1.00	44.52
ATOM	2538	NZ	LYS	1748	11.997	-16.790	-0.245	1.00	52.75
MOTA	2542	С	LYS	1748	16.264	-13.865	2.445	1.00	25.65
ATOM	2543	0	LYS	1748	16.184	-14.778	3.270	1.00	27.19
MOTA	2544	N	GLN	1749	17.378	-13.603	1.762	1.00	24.56
MOTA	2546	CA	GLN	1749	18.588	-14.397	1.950	1.00	26.33
MOTA	2547	CB	GLN	1749	19.702	-13.953	0.993	1.00	27.97
MOTA	2548	CG	GLN	1749	19.416	-14.066	-0.484	1.00	37.31
ATOM	2549	CD	GLN	1749	20.518	-13.415	-1.315	1.00	40.24
MOTA	2550	OE1	GLN	1749	20.296	-12.408	-1.970	1.00	38.83
MOTA	2551	NE2	GLN	1749	21.726	-13.983	-1.259	1.00	47.83
MOTA	2554	C	GLN	1749	19.099	-14.223	3.377	1.00	23.92
ATOM	2555	0	GLN	1749	19.459	-15.196	4.040	1.00	25.27
MOTA	2556	N	LEU	1750	19.155	-12.976	3.829	1.00	23.12
MOTA	2558	CA	LEU	1750	19.641	-12.662	5.175	1.00	24.34
MOTA	2559	CB	LEU	1750	19.607	-11.149	5.427	1.00	23.08
MOTA	2560	CG	LEU	1750	20.633	-10.311	4.665	1.00	23.84
ATOM	2561	CD1	LEU	1750	20.274	-8.806	4.724	1.00	22.10
MOTA	2562	CD2	LEU	1750	22.013	-10.586	5.246	1.00	24.91
MOTA	2563	С	LEU	1750	18.840	-13.400	6.236	1.00	27.40
MOTA	2564	0	LEU	1750	19.408	-13.915	7.211	1.00	27.11
MOTA	2565	N	VAL	1751	17.527	-13.482	6.031	1.00	26.83
MOTA	2567	CA	VAL	1751	16.665	-14.174	6.970	1.00	25.31

7.0	no													
				VAL	1751	15.1	76	-13.	994	6 5	00 =			
	_			/AL	1751			-14.9		6.5		00	25.8	
				/AL	1751			-12.5		7.3		00	28.4	
			C 1	/AL	1751			-15.6		6.9		00	21.5	
			7 0	7AL	1751	17.1				7.02		00	25.8	7
		573	M G	LU	1752	17.2		-16.2		8.10		00	23.4	1
AT		75 (CA G	LU	1752	17.6		-16.2		5.85			29.98	8
AT	OM 25	76 (CB G	LU	1752	17.65		-17.6		5.79		00	33.12	2
AT	OM 25	77 (1752			-18.1		4.34		00	35.99	9
ATO	OM 25	78 (1752	16.28		-18.0		3.67		00	43.58	
ATO	OM 25	79 c			1752	16.30		-18.5		2.23	0 1.0	00	48.64	
ATO	OM 25				1752	15.45		-18.1		1.43	1 1.0	00	48.99	
ATC	DM 25		_		1752	17.15		-19.4		1.90	2 1.0		55.41	
ATO	OM 25					18.99		-17.8		6.46	7 1.0		33.15	
ATC		_			1752	19.17		-18.84		7.23	6 1.0		30.71	
ATC					1753	19.95		-17.01		6.18			31.12	
ATO			_		L753	21.27		-17.13		6.77			30.51	
ATO				_	1753	22.24		-16.10	8	6.15			29.15	
ATO					.753	22.48		-16.34	4	4.672			33.53	
ATO					.753	22.36	1	-17.49		4.215				
ATO					753	22.819		-15.37	1	3.955			34.92	
ATO			AS		753	21.215	5 .	-16.96		8.287			38.26	
ATO		_	AS		753	21.739		-17.80		9.025		_	28.54	
ATON			LE		754	20.537		15.92		8.753			28.95	
ATON					754	20.421		15.67		0.193			27.25	
ATOM					754	19.754		14.32		0.455			28.08	
ATOM					754	20.733		13.199		0.160			23.31	
ATOM					754	20.007		11.863		0.094			24.47	
ATOM					754	21.846		13.207		1.216			19.58	
ATOM		_	LEt		754	19.688		16.789		0.921	1.00		21.17	
ATOM			LEU		754	20.037		17.135		2.048	1.00	-	31.61	
			ASF	17	755	18.690		17.367		0.259	1.00	-	2.64	
ATOM			ASP	17	55	17.931		18.460			1.00		2.61	
ATOM			ASP	17	55	16.823		18.883		0.833	1.00		4.20	
ATOM	2605		ASP	17	55	15.808		19.780		872	1.00		7.70	
ATOM	2606			17	55	15.445		19.521		.526	1.00		4.27	
ATOM	2607		ASP	17	55	15.370		20.745		.692	1.00		7.16	
ATOM	2608	С	ASP	17	55	18.894		19.616		.876	1.00		1.35	
ATOM	2609	0	ASP	17	55	18.858	- 2	20.273		.073	1.00		4.63	
ATOM	2610	N	ARG	17	56	19.782		9.826		.119	1.00	36	5.24	
ATOM	2612	CA	ARG	17	56	20.784		0.870		.108	1.00		2.60	
ATOM	2613	CB	ARG	17		21.548		0.939		.190	1.00		3.69	
ATOM	2614	CG	ARG	175		22.639	- 2	2.003		.867	1.00	35	5.42	
ATOM	2615	CD	ARG	175		23.212	- 2	2.003		.800	1.00	40	.87	
ATOM	2616	NE	ARG	175		23.739	-2	2.094		. 395	1.00	42	.73	
ATOM	2618	CZ	ARG	175	_	24.882		0.813		. 926	1.00		.45	
ATOM	2619	NH1	ARG	175				0.274	7.	340	1.00		.90	
ATOM	2622	NH2	ARG	175		25.634		0.905		243	1.00		.63	
ATOM	2625	C	ARG	175		25.276		9.105	6.	844	1.00		.86	
ATOM	2626	O	ARG	175		21.748		0.598		345	1.00		. 78	
ATOM	2627	N	ILE			21.929		l.436		228	1.00		.24	
MOTA	2629	CA	ILE	175		22.325		9.402			1.00		.35	
ATOM	2630	CB	ILE	175		23.281		0.018	12.		1.00		.54	
ATOM	2631	CG2	ILE	175		23.905		.631	12.		1.00	34		
ATOM	2632	CG1		175		4.955		.303	13.		1.00	32.		
		CGI	ILE	175	/ 2	4.547		.626	10.		1.00	33.		
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ATOM	2633	CD1	ILE	1757	24.908	-16.247	10.185	1.00	31.44
ATOM	2634	C	ILE	1757	22.698	-19.036	13.803	1.00	36.49
ATOM	2635	0	ILE	1757	23.337	-19.548	14.716	1.00	36.40
ATOM	2636	N	VAL	1758	21.487	-18.515	13.988	1.00	36.91
MOTA	2638	CA	VAL	1758	20.881	-18.498	15.322	1.00	38.68
ATOM	2639	СВ	VAL	1758	19.425	-17.962	15.312	1.00	37.77
ATOM	2640	CG1	VAL	1758	18.806	-18.059	16.708	1.00	38.39
ATOM	2641	CG2	VAL	1758	19.392	-16.524	14.854	1.00	36.69
MOTA	2642	C	VAL	1758	20.891	-19.908	15.895	1.00	41.38
MOTA	2643	0	VAL	1758	21.405	-20.138	16.997	1.00	42.41
MOTA	2644	N	ALA	1759	20.379	-20.851	15.111	1.00	40.59
MOTA	2646	CA	ALA	1759	20.325	-22.247	15.508	1.00	40.84
MOTA	2647	CB	ALA	1759	19.741	-23.074	14.384	1.00	40.20
MOTA	2648	С	ALA	1759	21.703	-22.787	15.897	1.00	42.52
ATOM	2649	0	ALA	1759	21.822	-23.594	16.809	1.00	44.78
MOTA	2650	N	LEU	1760	22.740	-22.339	15.208	1.00	43.16
MOTA	2652	CA	LEU	1760	24.095	-22.800	15.493	1.00	46.98
MOTA	2653	CB	LEU	1760	24.921	-22.761	14.203	1.00	47.66
MOTA	2654	CG	LEU	1760	24.286	-23.545	13.060	1.00	52.77
MOTA	2655	CD1	LEU	1760	24.973	-23.222	11.745	1.00	56.58
MOTA	2656	CD2	LEU	1760	24.343	-25.038	13.369	1.00	53.06
MOTA	2657	С	LEU	1760	24.811	-21.986	16.573	1.00	47.43
MOTA	2658	0	LEU	1760	25.917	-22.335	16.989	1.00	46.58
ATOM	2659	N	THR	1761	24.183	-20.914	17.034	1.00	48.65
MOTA	2661	CA	THR	1761	24.814	-20.055	18.021	1.00	49.69
MOTA	2662	CB	THR	1761	24.382	-18.570	17.831	1.00	50.15
MOTA	2663	OG1	THR	1761	24.783	-18.127	16.529	1.00	49.87
MOTA	2665	CG2	THR	1761	25.063	-17.671	18.843	1.00	48.64
ATOM	2666	C	THR	1761	24.673	-20.497	19.475	1.00	50.33
ATOM	2667	0	THR	1761	23.584	-20.825	19.947	1.00	48.81
MOTA	2668	N	SER	1762	25.811	-20.511	20.166	1.00	50.25
ATOM	2670	CA	SER	1762	25.891	-20.890	21.566	1.00	50.98
ATOM	2671	CB	SER	1762	27.362	-20.887	22.002	1.00	54.71
ATOM	2672	OG	SER	1762	27.537	-21.423	23.308	1.00	57.99
ATOM	2674	C	SER	1762	25.083	-19.914	22.425	1.00	49.39
ATOM	2675	O N	SER	1762	25.297	-18.694	22.370	1.00	48.00
MOTA	3474	N CA	SER	461	79.623	25.766	14.533	1.00	48.84
ATOM ATOM	3476 3477	CB	SER SER	461 461	79.566	24.645	13.593 13.809	1.00	46.93
ATOM	3478	С	SER	461	78.276 79.676	23.838 25.114	12.138	1.00	46.66 43.02
ATOM	3478	0	SER	461	79.678	24.301	11.210	1.00	40.19
ATOM	3480	N	GLU	462	79.892	26.427	11.210	1.00	41.48
ATOM	3482	CA	GLU	462	79.791	27.034	10.628	1.00	39.59
ATOM	3483	CB	GLU	462	80.021	28.560	10.028	1.00	40.66
ATOM	3484	C	GLU	462	81.054	26.480	9.796	1.00	36.60
ATOM	3485	0	GLU	462	80.852	26.121	8.641	1.00	35.10
ATOM	3486	Ŋ	TYR	463			10.380	1.00	
ATOM	3488	CA	TYR	463	82.252 83.430	26.416 25.916	9.673	1.00	36.07 35.60
ATOM	3489	CB	TYR	463	84.597	26.906	9.755	1.00	38.15
ATOM	3490	CG	TYR	463	84.372	28.104	8.861	1.00	44.08
MOTA	3491	CD1	TYR	463	84.137	29.368	9.406	1.00	44.99
ATOM	3492	CE1	TYR	463	83.833	30.451	8.593	1.00	46.88
ATOM	3493	CD2	TYR	463	84.305	27.959	7.464	1.00	43.95
ATOM	3494	CE2	TYR	463	84.003	29.044	6.642	1.00	41.86
111011	J . J .	-ue	- **	103	04.003	22.044	0.042	2.00	44.00



							120					
		3495	CZ	TYR	463							
		3496	ОН	TYR		83.7		0.282		215	1.00	43.00
I	MOTA	3498	C	TYR	463	83.4		1.364		431	1.00	
I	MOTA	3499	0	TYR	463	83.9		4.520	10.0		1.00	44.37
I	MOTA	3500	N	GLU	463	84.4	10 2	3.828		L 4 7		33.90
		3502	CA		464	83.74	2 2	4.098	11.2		1.00	33.90
		3503	CB	GLU	464	84.16	7 2	2.753	11.6		1.00	32.81
		504	CG	GLU	464	85.66		2.727	11.9		1.00	34.64
				GLU	464	86.07		3.633			1.00	37.48
				GLU	464	87.55		3.987	13.0		1.00	45.48
				GLU	464	87.92		.996	13.0		1.00	55.80
				GLU	464	88.34			13.6		1.00	61.78
				GLU	464	83.42		.271	12.3		.00	58.34
				3LU	464	83.08		.296	12.8		.00	33.05
			7]	LEU	465	83.14		.119	13.70		.00	34.54
	10M 3	512 (CA I		465	03.14		.001	12.94		.00	32.59
			B I		465	82.462		.463	14.11	-	.00	33.74
		514 (465	81.484		.341	13.74		.00	31.20
AT	'OM 35	15 c			465	80.510	19	.433	12.57	_	.00	
AT	OM 35					79.355		492	12.85		.00	32.77
AT	OM 35	17 C			165	80.021	20.	846	12.35		.00	26.22
AT	OM 35	18 0	_		165	83.511		889	15.05			31.59
ATO		_			65	84.641	19.	574	14.64	_		35.64
ATO					66	83.150			16.34			33.77
ATO					66	81.865			16.96	_		36.71
ATC	- •.		-		66	84.074	19.		17.346	_		36.97
ATO				_	66	83.247	19.		10 604		00	36.17
ATO				_	66	82.274	20.		18.626			36.83
ATO		_	PR		66	84.419	17.		18.394		00 4	10.80
ATO			PR	0 46	56	83.626	17.		16.950		00 3	37.39
ATO		_	GL	U 46	57	85.611			16.297			4.71
	_		GL	U 46	7	86.030	17.3		l7.315			8.40
ATO			GL			87.493	15.9		16.976	1.0		2.59
ATO			GL	U 46	7	87.922	15.9		6.540	1.0		9.21
ATON			GL			89.276	14.6		5.891	1.0		8.93
ATOM			L GL			90.013	14.7		5.213	1.0		4.76
ATOM		OE2	GLt				15.7		5.426	1.0		3.57
ATOM		l C	GLU			89.592	13.8		4.458	1.0		9.03
ATOM		0	GLU			85.825	15.0	37 1	8.146	1.0).74
ATOM		N	ASP			85.938	15.43	30 19	9.309	1.0		52
ATOM		CA	ASP			85.472	13.80)2 17	7.831	1.00		
ATOM	3539		ASP			85.273	12.77	'6 <u>1</u> 8	3.851	1.00		.57
ATOM	3540		ASP	200		83.793	12.64		224	1.00	-	. 86
ATOM		OD1		468		83.566	11.69		397			.27
ATOM	3542	OD2	ASP	468		82.429	11.67		.919	1.00		.36
ATOM	3543		ASP	468		84.514	10.99		.807	1.00		.50
ATOM	3544	C	ASP	468		85.803	11.47		.00/	1.00		.55
ATOM	3545	0	ASP	468		85.068	10.70		.278	1.00		. 75
ATOM		N	PRO	469	8	37.100	11.20		.650	1.00	41.	. 80
ATOM	3546	CD	PRO	469	8	38.001	12 000		.481	1.00	41.	71
ATOM	3547	CA	PRO	469	8	37.801	12.062		.276	1.00	41.	
	3548	CB	PRO	469	,	9.091	10.01			1.00	40.	
ATOM	3549	CG	PRO	469	Ω	9.366	10.042		.831	1.00	40.	
ATOM	3550	C	PRO	469	0	7 022	11.505		938	1.00	39.	
ATOM	3551	0	PRO	469	8	7.033	8.720			1.00	41.	
ATOM	3552	N	ARG	470		7.032	7.822			1.00	41.	
ATOM	3554	CA	ARG			6.361	8.639			1.00		
			-40	470	8	5.600	7.446	19.		1.00	40.	
SSSD/55	145. v01									00	41.0	J 3
	,											

ATOM	3555	СВ	ARG	470	84.827	7.677	21.075	1.00	44.18
ATOM	3556	CG	ARG	470	85.628	8.240	22.218	1.00	47.89
ATOM	3557	CD	ARG	470	84.719	8.518	23.400	1.00	50.56
ATOM	3558	NE	ARG	470	83.576	9.345	23.023	1.00	51.20
ATOM	3560	CZ	ARG	470	82.695	9.845	23.881	1.00	52.24
ATOM	3561	NH1	ARG	470	82.818	9.608	25.183	1.00	51.31
MOTA	3564	NH2	ARG	470	81.672	10.564	23.432	1.00	52.73
ATOM	3567	С	ARG	470	84.596	7.004	18.723	1.00	39.03
MOTA	3568	0	ARG	470	84.401	5.813	18.518	1.00	40.72
ATOM	3569	N	TRP	471	83.972	7.965	18.050	1.00	37.77
ATOM	3571	CA	TRP	471	82.948	7.656	17.059	1.00	36.73
MOTA	3572	CB	TRP	471	81.672	8.401	17.432	1.00	35.05
ATOM	3573	CG	TRP	471	81.044	7.862	18.673	1.00	34.85
ATOM	3574	CD2	TRP	471	80.235	6.687	18.766	1.00	34.96
ATOM	3575	CE2	TRP	471	79.831	6.564	20.116	1.00	35.12
ATOM	3576	CE3	TRP	471	79.810	5.721	17.838	1.00	33.25
ATOM	3577	CD1	TRP	471	81.106	8.390	19.933	1.00	29.97
ATOM	3578	NE1	TRP	471	80.377	7.616	20.805	1.00	32.18
ATOM	3580	CZ2	TRP	471	79.017	5.512	20.560	1.00	33.98
ATOM	3581	CZ3	TRP	471	79.002	4.673	18.282	1.00	33.71
ATOM	3582	CH2	TRP	471	78.618	4.580	19.632	1.00	33.28
ATOM	3583	C	TRP	471	83.275	7.930	15.599	1.00	37.27
ATOM	3584	O .	TRP	471	82.580	7.445	14.695	1.00	36.61
ATOM	3585	N	GLU	472	84.341	8.680	15.361	1.00	37.93
MOTA	3587	CA	GLU	472	84.706	9.054	14.004	1.00	37.08
ATOM	3588	CB	GLU	472	85.865	10.049	14.045	1.00	36.30
ATOM	3589	CG	GLU	472	86.026	10.851	12.773	1.00	33.51
MOTA	3590	CD	GLU	472	84.931	11.895	12.580	1.00	33.80
ATOM	3591	OE1	GLU	472	84.385	12.408	13.581	1.00	35.19
ATOM	3592	OE2	GLU	472	84.641	12.226	11.412	1.00	32.51
ATOM	3593	C	GLU	472	85.021	7.923	13.032	1.00	37.88
MOTA	3594	0	GLU	472	85.774	7.000	13.351	1.00	38.20
ATOM	3595	N	LEU	473	84.422	7.992	11.846	1.00	37.55
MOTA	3597	CA	LEU	473	84.678	7.004	10.813	1.00	36.93
ATOM	3598	CB	LEU	473	83.404	6.244	10.443	1.00	37.08
MOTA	3599	CG	LEU	473	83.680	5.086	9.470	1.00	39.14
MOTA	3600	CD1	LEU	473	84.196	3.877	10.250	1.00	38.39
ATOM	3601	CD2	LEU	473	82.433	4.716	8.672	1.00	39.46
MOTA	3602	С	LEU	473	85.207	7.732	9.577	1.00	38.52
MOTA	3603	0	LEU	473	84.660	8.764	9.182	1.00	38.67
MOTA	3604	N	PRO	474	86.334	7.259	9.005	1.00	39.02
MOTA	3605	CD	PRO	474	87.259	6.259	9.571	1.00	38.39
ATOM	3606	CA	PRO	474	86.918	7.877	7.809	1.00	38.24
ATOM	3607	CB	PRO	474	88.188	7.049	7.590	1.00	38.40
MOTA	3608	CG	PRO	474	88.580	6.680	8.979	1.00	35.50
MOTA	3609	С	PRO	474	85.942	7.727	6.642	1.00	37.56
MOTA	3610	0	PRO	474	85.415	6.641	6.400	1.00	37.88
MOTA	3611	N	ARG	475	85.720	8.809	5.907	1.00	37.73
MOTA	3613	CA	ARG	475	84.779	8.790	4.795	1.00	40.01
ATOM	3614	CB	ARG	475	84.655	10.183	4.182	1.00	38.31
ATOM	3615	CG	ARG	475	84.217	11.236	5.198	1.00	35.15
ATOM	3616	CD	ARG	475	84.069	12.631	4.586	1.00	33.92
ATOM	3617	NE	ARG	475	83.718	13.603	5.616	1.00	30.45
ATOM	3619	CZ	ARG	475	82.475	13.880	5.993	1.00	26.48
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					100			
ATOM	3620 N	H1 ARG	475	01 444				
ATOM		H2 ARG	475	81.444				00 24.80
ATOM	3626 C		475	82.271			56 1.0	0 25.16
	3627 0	ARG	475	85.054				0 42.18
	3628 N		476	84.125			28 1.0	
	3630 CA		476	86.322			35 1.0	
ATOM :	3631 CE		476	86.676				
ATOM :	3632 CG		476	88.192	6.34			
ATOM 3	633 OD		476	88.944	5.97		35 1.0	
ATOM 3	634 OD		476	89.303	4.78			
ATOM 3	635 C	ASP	476	89.176	6.86		27 1.00	57.39
ATOM 3	636 O	ASP	476	86.149 86.051				
ATOM 3	637 N	ARG	477	85.814	4.10		1 1.00	
ATOM 3	639 CA		477	85.285	4.86		0 1.00	
ATOM 3	640 CB	ARG	477		3.61			
ATOM 3	641 CG	ARG	477	85.834	3.364		2 1.00	49.79
ATOM 3	642 CD	ARG	477	87.237 87.960	2.806			
ATOM 3	543 NE	ARG	477	87.310	2.981			56.76
	45 CZ	ARG	477	87.728	2.293		9 1.00	59.35
ATOM 3	46 NH1	ARG	477	88.793	2.371			62.23
	49 NH2		477	87.067	3.103			63.66
	52 C	ARG	477	83.755	1.741			64.35
	53 O		477	83.160	3.547			48.04
	54 N		478	83.129	2.693			48.09
	56 CA	-	478	81.685	4.412			45.38
ATOM 36			478	81.168	4.469	-		41.60
ATOM 36		LEU .	478	79.651	5.578	4.790	_	38.39
ATOM 36			178	79.113	5.699	4.894		36.38
ATOM 36		LEU 4	178	79.293	4.595	5.802	1.00	33.98
ATOM 36	_	LEU 4	178	81.279	7.068 4.774	5.441	1.00	40.06
ATOM 366		LEU 4	78	81.696	5.780	2.433	1.00	41.92
ATOM 366		VAL 4	79	80.466	3.904	1.870	1.00	43.99
ATOM 366		VAL 4	79	79.992	4.082	1.844	1.00	42.29
ATOM 366		VAL 4	79	80.227	2.816	0.471	1.00	41.07
ATOM 366 ATOM 366		VAL 4	79	79.719	3.057	-0.397	1.00	41.13
		VAL 4	79	81.700	2.448	-1.810	1.00	40.19
ATOM 366 ATOM 367	_	VAL 4	79	78.500	4.345	-0.420	1.00	41.36
3.000	-		79	77.719	3.451	0.540 0.885	1.00	40.44
	-		80	78.112	5.582	0.253	1.00	39.86
			30	76.706	5.973	0.293	1.00	41.37
			30	76.568	7.492	0.166	1.00	41.63
			30	77.236	8.332	1.261	1.00	39.91
ATOM 3676 ATOM 367		LEU 48		76.890	9.800	1.039	1.00	39.23
		LEU 48	0	76.791	7.877	2.647		37.73
	_	LEU 48	0	75.899	5.273	-0.788		35.18
		LEU 48	0	76.395	5.048	-1.890		42.21
	_	GLY 48		74.650	4.947	-0.476		45.27
ATOM 3682 ATOM 3683	_	GLY 48		73.812	4.257	-1.433		41.51
		GLY 48		72.446		-1.433		10.19
		GLY 48	1	72.262		-1.540		11.58
	_	LYS 48	2 '	71.474				11.35
		LYS 48:	2 .	70.105				2.65
		LYS 482	2 6	59.240				4.17
ATOM 3689	C]	LYS 482		59.475				5.66
					- -	0.004	1.00 4	4.86

5.148 -0.994 1.00 44.86

MOTA	3690	0	LYS	482	69.638	4.752	0.155	1.00	45.23
ATOM	3691	N	PRO	483	68.749	6.234	-1.273	1.00	45.94
ATOM	3692	CD	PRO	483	68.518	6.880	-2.576	1.00	46.96
ATOM	3693	CA	PRO	483	68.099	6.983	-0.206	1.00	47.79
ATOM	3694	CB	PRO	483	67.542	8.200	-0.947	1.00	47.02
MOTA	3695	CG	PRO	483	67.269	7.666	-2.307	1.00	46.65
MOTA	3696	С	PRO	483	66.991	6.151	0.429	1.00	48.74
ATOM	3697	0	PRO	483	66.314	5.376	-0.251	1.00	48.01
ATOM	3698	N	LEU	484	66.858	6.268	1.742	1.00	49.91
ATOM	3700	CA	LEU	484	65.837	5.547	2.477	1.00	53.93
ATOM	3701	CB	LEU	484	66.433	4.883	3.720	1.00	50.17
ATOM	3702	CG	LEU	484	67.517	3.844	3.445	1.00	48.93
ATOM	3703	CD1	LEU	484	68.226	3.460	4.731	1.00	49.05
ATOM	3704	CD2	LEU	484	66.906	2.630	2.784	1.00	47.03
MOTA	3705	С	LEU	484	64.715	6.501	2.878	1.00	58.70
ATOM	3706	0	LEU	484	63.571	6.075	3.055	1.00	61.95
ATOM	3707	N	GLY	485	65.027	7.788	3.006	1.00	60.35
ATOM	3709	CA	GLY	485	63.998	8.737	3.397	1.00	64.00
MOTA	3710	C	\mathtt{GLY}	485	64.445	10.183	3.476	1.00	66.09
ATOM	3711	0	GLY	485	65.643	10.468	3.577	1.00	65.26
MOTA	3712	N	GLU	486	63.471	11.090	3.458	1.00	67.18
MOTA	3714	CA	GLU	486	63.733	12.525	3.508	1.00	68.69
ATOM	3715	CB	GLU	486	63.873	13.084	2.091	1.00	69.88
MOTA	3716	С	GLU	486	62.618	13.249	4.245	1.00	68.80
MOTA	3717	0	GLU	486	61.481	12.775	4.295	1.00	69.26
MOTA	3718	N	GLY	487	62.943	14.415	4.791	1.00	68.47
MOTA	3720	CA	GLY	487	61.960	15.188	5.520	1.00	67.56
MOTA	3721	C	GLY	487	62.373	16.635	5.634	1.00	66.71
MOTA	3722	0	GLY	487	63.040	17.172	4.747	1.00	66.48
ATOM	3723	N	ALA	488	61.979	17.265	6.735	1.00	67.22
ATOM	3725	CA	ALA	488	62.304	18.661	6.992	1.00	67.78
MOTA	3726	CB	ALA	488	61.637	19.121	8.283	1.00	68.97
MOTA	3727	С	ALA	488	63.817	18.830	7.085	1.00	67.38
MOTA	3728	0	ALA	488	64.413	18.597	8.141	1.00	67.14
ATOM	3729	N	PHE	489	64.429	19.155	5.946	1.00	66.22
ATOM	3731	CA	PHE	489	65.877	19.364	5.831	1.00	65.49
MOTA	3732	CB	PHE	489	66.277	20.699	6.467	1.00	66.11
ATOM	3733	С	PHE	489	66.749	18.207	6.368	1.00	64.07
ATOM	3734	0	PHE	489	67.924	18.399	6.731	1.00	61.56
ATOM	3735	N	GLY	490	66.171	17.005	6.349	1.00	60.79
MOTA	3737	CA	GLY	490	66.852	15.803	6.797	1.00	54.72
ATOM	3738	C	GLY	490	66.787	14.760	5.692	1.00	51.78
ATOM	3739	0	GLY	490	65.765	14.624	5.013	1.00	49.17
MOTA	3740	N	GLN	491	67.874	14.015	5.528	1.00	49.97
ATOM	3742	CA	GLN	491	68.000	12.984	4.504	1.00	48.06
MOTA	3743	CB	GLN	491	68.891	13.520	3.371	1.00	51.02
MOTA	3744	CG	GLN	491	69.286	12.518	2.289	1.00	56.00
MOTA	3745	CD	GLN	491	70.155	13.143	1.202	1.00	58.93
ATOM	3746	OE1	GLN	491	70.483	14.330	1.255	1.00	60.31
ATOM	3747	NE2	GLN	491	70.529	12.341	0.202	1.00	60.19
ATOM	3750	C	GLN	491	68.623	11.720	5.114	1.00	45.59
MOTA	3751	0	GLN	491	69.511	11.792	5.959	1.00	45.22
ATOM	3752	N	VAL	492	68.148	10.561	4.693	1.00	43.19
ATOM	3754	CA	VAL	492	68.676	9.304	5.193	1.00	41.54

							102					
		3755	CB	VAL	492	62.						
Α.	TOM :	3756	CG1	VAL	492	67.6		8.584	6.0	087	1.00	41.74
		3757	CG2	VAL	492			7.248			1.00	, -
A7	rom 3	758	C	VAL	492	67.2		9.463	7.2		1.00	
AT	rom 3	759	0	VAL		68.9	71 (8.424	3.9		1.00	44.07
AT	гом з	760	N	VAL	492	68.1	25 8	3.271	3.1		1.00	39.72
AT		762	CA	VAL	493	70.1	76 7	7.872	3.9			39.81
AT		763	CB		493	70.5	45 7	7.001	2.8		1.00	36.38
		764		VAL	493	71.58		.666	1.8		.00	35.88
AT		_	CG1	VAL	493	71.14		.069			.00	36.92
AT			CG2	VAL	493	72.97		.670	1.4		.00	36.64
· ATO				VAL	493	71.13		.689	2.46		.00	38.29
ATO				VAL	493	71.69			3.35		.00	36.03
ATO				LEU	494	70.94		.617	4.44		.00	36.57
			CA :	LEU	494	71.50	•	.637	2.57		.00	34.91
ATC			CB :	LEU	494	70.80	_	. 344	2.90		.00	36.04
ATO			CG]		494			. 244	2.09	4 1	.00	37.43
ATO		73 C	D1 1		494	71.31		814	2.26	_	.00	36.62
ATO		74 C	-		494	71.32	-	437	3.73		00	36.37
ATO	M 37	75 C			494	70.419	9 -0.	118	1.47		00	
ATO	M 37	76 O				72.967	73.	451	2.51	_	00	40.70
ATO	M 37'		_	_	194	73.308		160	1.560			37.08
ATON					195	73.839	2.	779	3.243		00	34.90
ATOM					195	75.246		830	2.918			37.18
ATOM					95	75.885		066				39.84
ATOM					95	75.949		578	3.541			39.29
ATOM		_			95	75.400	0.8		3.400			41.68
ATOM		_		LU 4	96	77.149	1.3		4.189			41.53
ATOM				LU 4	96	77.936			2.881			13.44
				U 4	96	78.328	0.2		3.297	1.0		12.86
ATOM				U 4	96	77.120	-0.6		2.101	1.0		4.63
ATOM					96	77.386	-1.1		1.320	1.0		3.31
ATOM			1 GL		96	76.494	-2.4		0.545	1.0		9.48
ATOM	3790	OE.	2 GL				-3.3		0.534	1.0		2.39
ATOM	3791	. С	GL			78.477	-2.5		0.053	1.0		2.15
ATOM	3792	0	GL			79.150	0.7	50 4	1.006	1.0	_	0.96
ATOM	3793	N	AL			79.889	1.56	58 3	3.455	1.0	_	
ATOM	3795	CA	ALA			79.267	0.4]		.280	1.00		0.81
ATOM	3796		AL			80.381	0.85		.096	1.00		0.79
ATOM	3797	C	ALA			79.888	1.24		.478	1.00		L.84
ATOM	3798	o	ALA			81.394	-0.28		.181			3.80
ATOM	3799	N	ILE			81.019	-1.44		.215	1.00		.72
ATOM	3801	CA				82.678	0.05		.183	1.00		.78
ATOM	3802		ILE			83.729	-0.95	-	.255	1.00		.03
ATOM	3803	CB	ILE		3	84.654	-0.89		. 455	1.00		.78
ATOM	3804	CG2	ILE	498		85.748	-1.95		.014	1.00	50	.57
ATOM		CG1	ILE	498		83.851	-1.103		119	1.00	51	.32
ATOM	3805	CD1	ILE	498		83.139			726	1.00	51	. 90
	3806	C	ILE	498		84.573	0.146		198	1.00		. 47
ATOM	3807	0	ILE	498		35.005	-0.754		511	1.00	48.	
	3808	N	GLY	499		34.754	0.359		805	1.00	47.	
	3810	CA	GLY	499			-1.829		271	1.00	49.	
ATOM	3811	С	GLY	499		35.563	-1.774	9.		1.00	53.	
ATOM	3812	0	GLY			5.076	-0.944	10.0		1.00		
	3813	N	LEU	499		5.885	-0.341			1.00	57.	
	3815	CA		500		3.768	-0.948	10.9			59.	
	3816	CB	LEU	500	8	3.193	-0.189	12.0	_	1.00	58.	
		-22	LEU	500	8	1.705	-0.519	12.1		1.00	57.	
SSSD/5514	45. v01						- 3-	-2.1	.u. j	1.00	55.	57

MOTA	3817	CG	LEU	500	80.789	0.036	11.086	1.00	54.81
ATOM	3818	CD1	LEU	500	79.361	-0.445	11.293	1.00	53.00
MOTA	3819	CD2	LEU	500	80.854	1.561	11.089	1.00	53.27
ATOM	3820	C	LEU	500	83.926	-0.466	13.333	1.00	58.15
MOTA	3821	0	LEU	500	84.461	-1.560	13.529	1.00	60.29
MOTA	3822	N	PRO	505	87.397	-6.022	10.511	1.00	77.18
ATOM	3823	CD	PRO	505	88.509	-6.651	11.242	1.00	78.26
MOTA	3824	CA	PRO	505	87.755	-4.660	10.097	1.00	75.62
MOTA	3825	CB	PRO	505	89.166	-4.487	10.669	1.00	75.77
MOTA	3826	CG	PRO	505	89.696	-5.884	10.715	1.00	77.07
ATOM	3827	C	PRO	505	87.709	-4.440	8.583	1.00	73.15
ATOM	3828	0	PRO	505	87.772	-3.308	8.105	1.00	72.63
ATOM	3829	N	ASN	506	87.595	-5.524	7.830	1.00	71.27
ATOM	3831	CA	ASN	506	87.518	-5.421	6.380	1.00	69.14
MOTA	3832	CB	ASN	506	88.577	-6.313	5.728	1.00	70.76
MOTA	3833	C	ASN	506	86.119	-5.840	5.940	1.00	67.30
ATOM	3834	0	ASN	506	85.834	-5.957	4.750	1.00	67.03
ATOM	3835	N	ARG	507	85.250	-6.064	6.921	1.00	65.27
ATOM	3837	CA	ARG	507	83.876	-6.479	6.669	1.00	62.86
ATOM	3838	CB	ARG	507	83.335	-7.267	7.864	1.00	65.45
MOTA	3839	C	ARG	507	82.991	-5.274	6.443	1.00	59.56
MOTA	3840	0	ARG	507	83.161	-4.247	7.100	1.00	59.70
ATOM	3841	N	VAL	508	82.057	-5.397	5.509	1.00	56.65
MOTA	3843	CA	VAL	508	81.135	-4.310	5.226	1.00	55.48
ATOM	3844	CB	VAL	508	80.850	-4.157	3.719	1.00	55.71
MOTA	3845	CG1	VAL	508	82.146	-3.962	2.962	1.00	58.18
MOTA	3846	CG2	VAL	508	80.096	-5.356	3.188	1.00	58.76
MOTA	3847	C	VAL	508	79.833	-4.537	5.979	1.00	53.10
MOTA	3848	0	VAL	508	79.352	-5.665	6.091	1.00	54.25
MOTA	3849	N	THR	509	79.282	-3.460	6.514	1.00	50.06
MOTA	3851	CA	THR	509	78.041	-3.512	7.260	1.00	45.70
MOTA	3852	CB	THR	509	78.256	-3.029	8.715	1.00	45.59
MOTA	3853	OG1	THR	509	79.395	-3.696	9.279	1.00	43.86
MOTA	3855	CG2	THR	509	77.028	-3.328	9.573	1.00	44.19
MOTA	3856	С	THR	509	77.064	-2.574	6.564	1.00	43.57
MOTA	3857	0	THR	509	77.416	-1.444	6.221	1.00	41.15
MOTA	3858	N	LYS	510	75.871	-3.073	6.268	1.00	42.96
MOTA	3860	CA	LYS	510	74.847	-2.253	5.640	1.00	41.91
MOTA	3861	CB	LYS	510	73.740	-3.144	5.091	1.00	44.74
MOTA	3862	CG	LYS	510	72.864	-2.461	4.069	1.00	51.83
MOTA	3863	CD	LYS	510	73.392	-2.645	2.659	1.00	55.00
ATOM	3864	CE	LYS	510	72.769	-3.879	2.020	1.00	58.36
ATOM	3865	NZ	LYS	510	73.069	-5.131	2.769	1.00	58.57
MOTA	3869	С	LYS	510	74.322	-1.367	6.789	1.00	40.74
MOTA	3870	0	LYS	510	73.909	-1.874	7.837	1.00	40.26
MOTA	3871	N	VAL	511	74.413	-0.052	6.624	1.00	37.21
MOTA	3873	CA	VAL	511	73.989	0.877	7.661	1.00	33.44
MOTA	3874	CB	LAV	511	75.227	1.515	8.362	1.00	34.53
MOTA	3875	CG1	VAL	511	76.100	0.436	9.014	1.00	31.98
MOTA	3876	CG2	VAL	511	76.048	2.322	7.358	1.00	34.82
MOTA	3877	С	LAV	511	73.134	1.989	7.087	1.00	31.34
MOTA	3878	0	VAL	511	73.025	2.130	5.871	1.00	31.33
MOTA	3879	N	ALA	512	72.485	2.748	7.961	1.00	30.70
MOTA	3881	CA	ALA	512	71.671	3.876	7.523	1.00	30.81

							-	-01				
		3882	CB	ALA	512	70						
		3883	C	ALA	512				379	8.206	1.0	0 29.85
		3884	0	ALA	512	72.4	453		L24	7.904		
		3885	N	VAL	513	73.(036	5.1	.97	8.996		
	MOTA	3887	CA	VAL		72.4	180	6.0		6.999		
Į		3888	CB		513	73.2	808	7.3	_	7.238		•
P		3889	CG1	VAL	513	74.3	58	7.5		6.223	_	
		890		VAL	513	75.1		8.7				
			CG2	VAL	513	75.2		6.3		6.547	1.00	
		891	C	VAL	513	72.3			_	5.223	1.00	28.70
		892	0	VAL	513	71.6		8.5		7.189	1.00	31.28
			N	LYS	514	72.22	30	8.82		.167	1.00	30.12
			CA	LYS	514	72.22	2.5	9.25		.321	1.00	31.03
			CB	LYS	514	71.43		10.47		-451	1.00	32.56
		897		LYS	514	70.88		10.63	5 9	.870	1.00	
ΑΊ	3E MO	398	~-	LYS		69.97	7	9.51		.326	1.00	34.31
AT	SE MO			LYS	514	69.51		9.77		. 753		38.25
AT	'OM 3 9				514	68.51		8.71		.230	1.00	47.74
AT		04 (LYS	514	67.22	6	8.75			1.00	51.60
AT		`		JYS	514	72.35	7	11.65		.468	1.00	58.53
AT			_		514	73.48	5	11.736	_	.137	1.00	30.29
AT			•	ET	515	71.86		12.50	_	628	1.00	28.14
		_	:A M	ET	515	72.643		12.580		320	1.00	30.67
AT(В м		515	73.435		13.747		920	1.00	29.94
ATO			G M	ET :	515	72.557		13.442		648	1.00	30.64
ATC		-	D M		515			13.038		464	1.00	32.16
ATC		L2 C1	E M		15	73.525		12.522	3.		1.00	
ATC		.3 C		`	15	74.015		10.933	3.		1.00	37.59
ATO	M 391	4 0				71.675		14.869				29.11
ATO	M 391		LE		15	70.462		14.664	6.5			29.71
ATO					16	72.212		16.060	6.4		1.00	30.04
ATO					16	71.381		17.206	6.1			29.56
ATO				_	16	72.093		18.508				30.76
ATO		_		_	16	72.396		18.724	6.5		: ۲۰۰۰	28.20
ATON	-				16	73.202		19.983	8.0		00	28.48
ATOM			2 LE	U 5:	L6	71.114	7	0.004	8.1			27.55
ATOM			LE	U 51	16	71.081		8.814	8.7			25.49
		_	LE	J 51	.6	71.728		7.225	4.6			0.97
ATOM		N	LYS			70.030		6.534	3.8	51 1		9.93
ATOM		CA	LYS			60.630		7.946	4.29			1.57
ATOM		CB	LYS			69.677		8.117	2.89	_		1.44
ATOM	3928	CG	LYS			68.169	1.	8.310	2.75			
MOTA	3929	CD	LYS			67.375	1	7.098	3.19			4.79
ATOM	3930	CE	LYS			66.148	16	5.888	2.34			8.42
ATOM	3931	NZ		_		65.087	17	7.950	2.58			5.52
ATOM	3935	C	LYS			63.901		7.740	1.69			3.77
ATOM	3936	0	LYS			70.457		377		_		5.38
ATOM	3937		LYS	517	,	70.892		.134	2.49		00 30	1.18
ATOM		N	SER	518		70.646		.594	3.37		00 27	.47
ATOM	3939	CA	SER	518		71.394			1.20			.13
	3940	CB	SER	518		71.518		.747	0.693	1.0		.11
ATOM	3941	OG	SER	518		0.242	20		-0.824	1.0		.45
ATOM	3943	C	SER	518	•	0.242		.567	-1.428			.51
ATOM	3944	0	SER	518		0.814	22	.103	1.073			
ATOM	3945	N	ASP			1.515	23.	.123	1.027			. 81
ATOM	3947	CA	ASP	519		9.540	22.	117	1.449		•	
ATOM	3948	CB		519	6	8.886	23.	354	1.836			
ATOM	3949	CG	ASP	519	6	7.473	23	421		1.0		
		CG	ASP	519	6	5.542			1.237	1.0		90
SSSD/55	145 001								1.771	1.0	0 34.	42
	VUI											

	700	
	. 220	2.333 1.00 35.58
2050 OD1 ASP 519	67.020 21.328	1 617 1.00 41.83
ATOM 3950 ODI 122	65.313 22.485	3 342 1.00 29.08
ATOM 3951 ODZ 1151	68.829 23.559	3 816 1.00 29.79
ATOM 3952 C 330	68.177 24.485	4 099 1.00 29.73
ATOM 3953 0 550	69.514 22.710	5 558 1.00 29.16
ATOM 3954 N 520	69.488 22.824	6.190 1.00 28.13
ATOM 3930 ATA 520	70.174 21.639	6 040 1.00 28.06
ATOM 3957 CB ALA 520	70.122 24.108	5 309 1.00 28.84
ATOM 3958 C 717 520	70.880 24.741	7 272 1.00 27.84
ATOM 3959 0	69.800 24.491	7 995 1.00 30.45
ATOM 3960 N THR 521	70.357 25.692	8 463 1.00 33.56
ATOM 3962 CR THR 521	69.254 26.635	9 520 1.00 36.27
ATOM 3963 CB THR 521	68.547 25.968	7 379 1.00 36.06
ATOM 3964 CG2 THR 521	68.275 27.074	9.048 1.00 30.04
ATOM 3966 CO2 mup 521	71.251 25.263	1 00 28 16
ATOM 3967 C THR 521	71.348 24.072	9.696 1.00 31.42
ATOM 3966 U GLU 522	71.876 26.241	10 832 1.00 36.94
ATOM 3969 K	72.745 25.978	11 299 1.00 44.74
ATOM 3971 CR GLU 522	73.404 27.282	12 450 1.00 58.34
ATOM 3972 CC GLU 522	74.414 27.130	- 12 009 1.00 64.50
ATOM 3973 CD GLU 522	75.769 26.579 76.798 27.26	$\frac{1}{2}$
ATOM 3974 OF GLU 522	, , , , , , , , , , , , , , , , , , , ,	1 11 452 1.00 70.40
ATOM 3975 OF GLI 522	7.5	= 11.969 1.00 34.02
ATOM 3970 011 522		2 12 684 1.00 31.11
ATOM 3977 0 CLII 522	, 2	12 097 1.00 32.53
ATOM 3970 TLYS 523	70.0	. 12 135 1.00 34.00
ATOM 3975 IN LYS 523		70 13.188 1.00 39.54
ATOM 5901 CP LYS 523	_	41 14.322 1.00 45.55
ATOM 3502 CG LYS 523		76 13.789 1.00 52.08
ATOM 3903		12 14.914 1.00 54.16
ATOM SOC CE LYS 52:	3 00	20 14 373 1.00 54·30
ATOM 5505 N7 1.YS 52	3 0 - 1 - 1	12 861 1.00 31.73
ATOM 5500 C TYS 52	3 05	13.788 1.00 31.15
ATOM SSSS 0 LYS 52	3	11.590 1.00 29.22
ATOM SOO N ASP 52	4 03	980 11.214 1.00 28.79
ATOM SSEA CA ASP 52	4 05	9.714 1.00 27.65
ATOM 3995 CB ASP 52	4 55 FD6 22.	396 9.286 1.00 33.00
2996 CG ASP 52	22	106 9.954 1.00 31.00
AUDM 3997 OD1 ASP 5.	24 00.500	120 8.270 1.00 30.01
NUM 3998 OD2 ASP 5	404 21	190 11.606 1.00 20.00
2999 C ASP 5	227 20	104 12.162 1.00 3313
ATOM 4000 O ASP 5	co2 21.	761 11.347 1.00 29.87
ATOM 4001 N LEU 5	70 073 21	.121 11.700 1.00 27
NUOM 4003 CA LEU 5	72.004 21	.997 11.282 1.00 24.00
TOW 4004 CB LEU	462 21	.433 11.593 1.00 2012
AMON ANDS CG LEU	-= 507 19	.979 11.098 1.00 231
ATOM 4006 CD1 LEU	525 75.520 22	.321 10.967 1.00 21.28
ATOM 4007 CD2 LEU	70.009 20	1.869 13.200 1.00 26.38
ATOM 4008 C LEU	525 72.50	9.777 13.653 1.00 26.09
ATOM TOO DEU	525 /5.25	13.956 1.00 29.72
ATOM 4005	520 721-	1 961 15.422 1.00 32.10
ATOM 4020	526 72101	2 209 15.939 1.00 33.43
ATOM 1012 CB SER	520 703 2	3.209 15.333 1.00 40.42 3.213 17.343 1.00 40.42
ATOM 4020 OG SER	526 71.793 2	₩ ₹ =
ATOM 4014 OG 5211		

								.00					
	ATOM	4016	C	SER	526	71							
	MOTA	4017	0	SER	526		572		. 728	15.	902	1.00	31.64
		4018	N	ASP	527	71.	869		.030	16.		1.00	0-1
A	MOTA	4020	CA	ASP	527	70.	454	20.	561	15.		1.00	5-
A	MOTA	4021	CB	ASP		69.4	492	19.	527	15.			
A	TOM .	4022	CG	ASP	527	68.1	L87		767	14.7		1.00	
A	TOM	4023	OD1		527	67.4	18		984	15.2	70	1.00	29.35
		1024	OD2	ASP	527	67.7	' 59		549			1.00	31.37
		025		ASP	527	66.4		21.		16.3		1.00	31.96
	7	026	C	ASP	527	70.0		18.		14.5		1.00	32.58
			0	ASP	527	69.8	54			15.2		1.00	28.82
	~	027	N	LEU	528	70.7	21	17.		16.0		1.00	29.65
		029	CA	LEU	528	71.3	~ <u>+</u>	17.9		14.1		1.00	29.29
			CB	LEU	528			16.6		13.75	94	1.00	29.94
			CG	LEU	528	71.78	30	16.6		12.33		1.00	
		032		LEU	528	72.31		15.2		11.84		1.00	26.45
AT	OM 4	033 (~	LEU		71.24	0	14.1		12.03		1.00	28.34
ATO	OM 4(~		528	72.75	6	15.3		10.37			27.16
ATO	OM 40		_		528	72.44	9	16.3		L4.77		1.00	25.91
ATO		36 1			528	72.61	7	15.1				1.00	29.72
ATO		_			529	73.22	4	17.3		5.17		1.00	28.98
ATC					529	74.30		17.13		5.16		00	30.15
ATO					529	75.188		18.38		6.13		.00	28.88
ATO					529	76.179		18.22		6.268		.00	26.91
ATO	*				29	75.960		10 6		7.423	3 1		24.82
ATO		~		LE 5	29	76.663		18.61		4.984		.00	23.98
			I	LE 5	29	73.709		19.93		4.973			28.33
ATO		_	I	_	29	74.172		16.79 		7.518	1		29.71
ATO			SI		30			15.88		3.193	1.	.00	29.19
ATON			A SE		30	72.672		L7.52	4 17	7.926			25.19
ATOM		8 CE			30	72.061		17.24	7 19	.214			26.84
ATOM		9 OG			30	70.948	1	.8.25		.521			31.46
ATOM		1 C	SE			70.045		8.363		.431			6.17
ATOM			SE			71.526		5.822		.248			7.58
ATOM	405					71.646	1	5.136		.270			0.05
ATOM	405		GL			70.972	1	5.357		.132	1.		9.61
ATOM			GL			70.458	1	3.999			1.		7.74
ATOM			GL		1	69.709		3.727		090	1.0		8.71
ATOM	4058		GL		1	69.147		2.319		789	1.(9.72
ATOM	4059		GLŢ		1	68.510	11	1.979		737	1.0		2.21
ATOM					1	68.026				414	1.0		3.88
ATOM	4060		GLU	53:		68.483		.846		281	1.0		.60
	4061	С	GLU	533	L	71.578	12	.833	14.		1.0		.70
ATOM	4062	0	GLU	53]		71.428		. 974	18.		1.0		. 91
ATOM	4063	N	MET	532		72.686	12	.007	19.	019	1.0		.46
ATOM	4065	CA	MET	532		72.000		.179	17.	567	1.0		.84
ATOM	4066	CB	MET	532		73.851		.296	17.6	548	1.00		.35
ATOM	4067	CG	MET	532		74.948		. 786	16.6		1.00		
ATOM	4068	SD	MET		-	6.299	12	.117	16.8		1.00		.41
ATOM	4069	CE	MET	532	7	7.503		675	15.6				
ATOM	4070	C		532	7	7.732		400	16.1		1.00		
ATOM	4071	0	MET	532	7	4.389		280			1.00	-	
ATOM	4072		MET	532	7	4.700	11	230	19.0		1.00		
3	4074	N	GLU	533	7	4.481	13.		19.6		1.00		74
3.00		CA	GLU	533	7.	4.985	10	704 E46	19.6		1.00	28.	
	4075	CB	GLU	533		5.182	13.		21.03	33]	1.00	29.	
	4076	CG	GLU	533	76	5.331	15.		21.42	23]	1.00	32.	23
ATOM	4077	CD	GLU	533	7-	7.656	15.6		20.65		00	34.4	 1 7
CCCD (= -	_			-	, ,	.056	14.9	37	20.77		.00	38.0	- <i>.</i>
SSSD/551	45. v01											-5.(

												_		
						1.00	14.7	80	21.903	3 1.0		39.75		
ATOM	4078	OEl	GLU	533			14.4	-	19.73	6 1.		38.75		
MOTA	4079	OE2	GLU	533		.192 .058	12.8	315	22.00	5 1.		31.55 30.63		
ATOM	4080	С	GLU	533		.521	12.		22.88	9 1.		30.63	1	
ATOM	4081	0	GLU	533	74	.750	12.	958	21.79	9 1.	00	31.31	-	
ATOM	4082	N	MET	534	72	700	12.	289	22.66	-	00	30.78) >	
ATOM	4084	CA	MET	534	71	.789	12.	672	22.31		00	31.2	s 5 PRT1	
MOTA	4085	CB	MET	534		348	12.	648	23.55		50	29.3	9 PRT1	
	4086	CG	MET	534	6:	9.453	12.	563	23.24		. 50			
MOTA	4087	SD	MET	534		7.688	14.	230	22.8		.50	26.9		-
MOTA MOTA	4088	CE	MET	534		7.290	10	773	22.5	60 1	.00	28.8		
	4089	C	MET	534	7	1.991		.083	23.5	68 1	.00	30.1	.0	
MOTA MOTA	4090	0	MET	534	7	2.053	10	.271	21.3	39 1	.00	29.1		
	4091	N	MET	535	7	2.149	8	.852	21.1	10 1	.00			
MOTA	4093	CA	MET	535		2.381		.551	19.6	17 1	.00			
MOTA	4094	CB	MET	535	_	72.546		.790	18.8	317 1	00			
MOTA MOTA			MET	535		71.281		.955	17.2	255	1.00		26	
			MET			71.255		.279	16.3	188	1.00		50	
MOTA MOTA			MET			71.336		3.388	21.	887	1.00		36	
ATOM			MET		•	73.612 73.626		7.287	22.		1.00			
MOTA		_	MET		-	74.640		9.233	21.	_	1.0			
ATOM			$\Gamma\lambda$			75.850		8.913	22.	649	1.0		.05	
OTA						76.934		9.954	22.	388	1.0		.80	
OTA						77.550		9.883	21.	004	1.0		.05	
ATO						78.534		1.01	7 20.	860	1.0		.83	
ATO						79.132	1	1.13	з 19.	.466	1.0		.32	
ATO	-			_		79.957		2.37	7 19	.440	1.0		.99	
ATO						75.550		8.83	4 24	.150	1.0		92	
ATC		11 C	Ľ,			75.920)	7.85	9 24	.806	1.0		81	
ATC		12 0	r;		_	74.837	,	9.82	6 24	.676	1.		5.37	
ATC		13 N		_	37	74.517	7	9.83	5 26	.090			1.32	
ATO		15 C			37 27	73.860)	11.15		.506			1.50	
ATO					37 37	74.82	В	12.33		.610			7.48	
AT					3 <i>1</i> 37	76.23		12.09		7.776		00 5	6.91	
ΤĄ				_	37	75.46		12.6		9.334		00 3	6.11	
				.— -	37	73.63		8.6		6.499		.00 3	8.54	
ΓA	OM 4:		_		537	73.84		8.0		7.548			3.69	
ΓA	OM 4	 –			538	72.65		8.3		5.661			31.62	
	rom 4				538	71.70)4	7.2	_	5.954		.00	28.21	
A.		121			538	70.49	92	7.3		4.974		.00	28.22	
A.				_	538	69.68	81	6.0		5.034			23.74	
A'					538	69.5	90		_	25.338		00	27.94	
A		127	CG1		538	68.4	87			24.344		1.00	31.07	
A		128	CD1	ILE ILE	538	72.3				26.008		1.00	33.13	
A		1129	C		538	71.9	52		-	26.860		1.00	29.52	
P	110	4130	0	ILE	539	73.2	39			25.09		1.00	28.40	
	MOTA	4131	N	GLY	539	73.8				25.09		1.00	30.21	
7		4133	CA	GLY	539	73.	111		_	24.28		1.00	29.66	
1	MOTA	4134	C	GLY	539	72.0	018		554	23.78		1.00	28.44	
	MOTA	4135	0	GLY	540	73.			.074	24.19		1.00	31.09	
	MOTA	4136	N	LYS	540	73.			.984	23.42		1.00	33.15	
	MOTA	4138	CA	LYS	540	74.	215		.089	22.89	75	1.00	39.54	
	MOTA	4139	CB	LYS	540	75.	116		.776	21.90	סנ	1.00	43.98	3
	MOTA	4140	CG	LYS	540		125	- 0	.175	21.3	49	1.00		
	MOTA	4141	CD	LYS	J-1 J									

		4142	CE	LYS	540								
		4143	NZ	LYS	540	77.0		0.562		349	1.00	50.79	
		4147	C	LYS	540	76.3		0.977		086	1.00	51.09	
		4148	0	LYS	540	72.0		0.087		059	1.00	32.78	
		4149	N	HIS	541	72.08		0.195	25.2	266	1.00	32.41	
		1151	CA	HIS	541	71.13		0.374	23.2		1.00	31.20	
		152	CB	HIS	541	70.08		1.304	. 23.5		1.00	31.53	
		153	CG	HIS	541	68.91		0.630	24.2		1.00	30.69	
		154	CD2	HIS	541	67.94		1.613	24.8		1.00	31.18	
		155	ND1		541	67.93		2.255	26.0		1.00	33.02	
	rom 4	157	CE1		541	66.88		2.123	24.1		L.00	30.56	
			NE2		541	66.26		3.037	24.8		.00	32.95	
			_		541	66.88		.140	26.0				
		161	_		541	69.59		.013	22.34			31.79	
		L62]		-	542	69.495		.404	21.27			32.72	
		64 (542	69.282	-3	.305	22.47			30.34	
AT		.65 (42	68.828		.131	21.35			32.32	
AT	OM 41	.66	_		42	68.637	- 5	.587	21.79			30.29	
AT	OM 41	67 C				67.560	-3.	.661	20.69			29.34	
AT(68 N			42	67.369	-3.	. 903	19.50			29.09	
ATO	OM 41				43	66.683	-3.	012	21.44	_		29.12	
ATC	OM 41				43	65.425		559	20.86	_	_	8.54	
ATC	M 41'			_	43	64.245	-3.	047	21.712			9.10	
ATO	M 417			_	43	64.253			21.900			9.69	
ATO	M 417					64.510			23.000			9.62	
ATO				_		64.020	-5.		20.828			1.63	
ATO				SN 54		65.299	-1.		20.532			8.66	
ATO				SN 54		64.207	-0.5		20.578			9.61	
ATO			II			66.432	-0.4		20.222			3.00	
ATON						66.466	0.9		L9.804			3.39	
ATOM						66.903	1.9		20.935	1.0		5.73	
ATOM						66.083	1.7		2.215	1.0	-	5.98	
ATOM						68.412	1.8		1.209	1.0	_	.04	
ATOM		-	l IL.			68.901	2.8		2.274	1.0		.30	
ATOM		-				67.463	1.0		8.639	1.0		.83	
ATOM	4188	_	IL			68.276	0.1		8.467	1.0		.20	
ATOM			ILI			67.307	2.0		7.771	1.0		.46	
ATOM	4191		ILE			68.223	2.20		5.641	1.00		.26	
ATOM	4192		ILE			67.647	3.19		5.585	1.00		.62	
ATOM	4193	CG1				68.726	3.59		1.562	1.00			
ATOM	4194	CD1	ILE		(56.453	2.56		.856	1.00		• •	
ATOM	4195	C	ILE		6	6.850	1.46		.875	1.00			
ATOM	4196	0	ILE			9.492	2.79		.267	1.00			
ATOM	4197	N	ILE	545	6	9.468	3.87		.846	1.00			
ATOM	4199		ASN	546	7	0.595	2.06			1.00			
ATOM	4200	CA	ASN	546	7	1.845	2.50		.164	1.00	29.		
АТОМ	4201	CB	ASN	546	7	2.580	1.309		.774	1.00	28.9	58	
ATOM	4202	CG	ASN	546	7	1.812	0.673			1.00	26.3	34	
ATOM		OD1	ASN	546	7.	1.634			.527	1.00	25.5	52	
ATOM	4203	ND2	ASN	546	7:		1.277 -0.542			1.00	28.8		
ATOM	4206	C	ASN	546	7:	2.810	3 200		318	1.00	26.5		
	4207	0	ASN	546		2.858	3.264		881	1.00	28.7		
ATOM	4208	N	LEU	547		3.578	3.041		675	1.00	29.2		
ATOM	4210	CA	LEU	547		.618	4.155		504	1.00	29.9		
ATOM	4211	CB	LEU	547	75	.075	4.936		834]	1.00	30.2		
CCC== :=				•	, 5	.0/5	6.081	17.		00	25.89		
SSSD/551	45. v01											-	

MOTA	4212	CG	LEU	547	76.161	7.034	17.232	1.00	27.73
ATOM	4213	CD1	LEU	547	75.670	7.851	16.033	1.00	27.38
MOTA	4214	CD2	LEU	547	76.545	7.966	18.345	1.00	29.14
ATOM ·	4215	C	LEU	547	75.811	4.004	16.567	1.00	32.22
MOTA	4216	0	LEU	547	76.256	3.291	17.471	1.00	33.38
MOTA	4217	N	LEU	548	76.317	4.005	15.335	1.00	32.12
ATOM	4219	CA	LEU	548	77.452	3.159	14.960	1.00	32.94
ATOM	4220	CB	LEU	548	77.103	2.310	13.740	1.00	29.97
MOTA	4221	CG	LEU	548	75.839	1.458	13.840	1.00	31.55
ATOM	4222	CD1	LEU	548	75.662	0.713	12.540	1.00	27.85
ATOM	4223	CD2	LEU	548	75.917	0.500	15.025	1.00	26.34
ATOM	4224	С	LEU	548	78.726	3.955	14.654	1.00	36.06
MOTA	4225	0	LEU	548	79.836	3.410	14.668	1.00	36.42
MOTA	4226	N	GLY	549	78.562	5.219	14.298	1.00	35.78
ATOM	4228	CA	GLY	549	79.713	6.042	13.987	1.00	36.22
ATOM	4229	С	GLY	549	79.267	7.376	13.433	1.00	35.30
MOTA	4230	0	GLY	549	78.062	7.646	13.362	1.00	33.46
ATOM	4231	N	ALA	550	80.232	8.206	13.042	1.00	34.94
ATOM	4233	CA	ALA	550	79.945	9.525	12.490	1.00	31.91
ATOM	4234	CB	ALA	550	79.588	10.495	13.613	1.00	30.54
ATOM	4235	C	ALA	550	81.128	10.077	11.715	1.00	31.58
MOTA	4236	0	ALA	550	82.281	9.832	12.080	1.00	31.23
ATOM	4237	N	CYS	551	80.818	10.812	10.643	1.00	31.13
MOTA	4239	CA	CYS	551	81.805	11.503	9.804	1.00	28.28
ATOM	4240	CB	CYS	551	81.621	11.180	8.316	1.00	27.27
ATOM	4241	SG	CYS	551	81.771	9.449	7.839	1.00	30.33
ATOM	4242	С	CYS	551	81.450	12.960	10.074	1.00	25.88
ATOM	4243	0	CYS	551	80.432	13.458	9.605	1.00	27.73
ATOM	4244	N	THR	552	82.214	13.586	10.954	1.00	25.35
ATOM	4246	CA	THR	552	81.988	14.967	11.353	1.00	26.79
ATOM	4247	CB	THR	552	82.051	15.092	12.899	1.00	27.76
ATOM	4248	OG1	THR	552	83.392	14.839	13.338	1.00	27.62
MOTA	4250	CG2	THR	552	81.119	14.086	13.575	1.00	29.17
MOTA	4251	C	THR	552	83.036	15.931	10.790	1.00	25.03
ATOM	4252	0	THR	552	82.825	17.137	10.746	1.00	25.34
ATOM	4253	N	GLN	553	84.174	15.385	10.381	1.00	27.34
ATOM	4255	CA	GLN	553	85.285	16.190	9.888	1.00	26.31
ATOM	4256	CB	GLN	553	86.601	15.639	10.468	1.00	25.05
MOTA	4257	CG	GLN	553	86.581	15.491	11.993	1.00	24.78
ATOM	4258	CD	GLN	553	86.382	16.823	12.709	1.00	25.40
MOTA	4259	OE1	GLN	553	87.175	17.748	12.546	1.00	33.74
ATOM	4260	NE2	GLN	553	85.338	16.920	13.516	1.00	25.61
MOTA	4263	C	GLN	553	85.390	16.274	8.379	1.00	27.08
MOTA	4264	0	GLN	553	85.083	15.318	7.669	1.00	28.76
ATOM	4265	N	ASP	554	85.804	17.438	7.899	1.00	28.63
ATOM	4267	CA	ASP	554	86.015	17.677	6.471	1.00	29.70
ATOM	4268	CB	ASP	554	87.335	17.050	6.051	1.00	29.73
ATOM	4269	CG	ASP	554	88.480	17.587	6.857	1.00	33.38
MOTA	4270	OD1	ASP	554	88.794	18.780	6.711	1.00	36.53
ATOM	4271	OD2	ASP	554	89.024	16.841	7.687	1.00	36.40
ATOM	4272	C	ASP	554	84.908	17.258	5.522	1.00	29.64
ATOM	4273	0	ASP	554	85.112	16.422	4.643	1.00	32.06
ATOM	4274	N	GLY	555	83.748	17.881	5.679	1.00	28.59
ATOM	4276	CA	GLY	555	82.620	17.579	4.825	1.00	26.85
				-	= :				

					7.70				
ATO		C	GLY	555 81					
ATC		0	~		.333	.7.434	5.607	7 00	
ATO		N	-	555 81	.319 ₁		6.834		25.30
ATO		CD			.229 _l	~ -	4.920	1.00	23.96
ATO:	M 4281	CA			.159 ₁			_	4.84
ATO	M 4282	CB		56 78			3.472	1.00 2	1.36
ATO		CG		56 ₇₈		-	5.550	1.00 2	5.26
ATOM	1 4284			56 79.			4.386		3.37
ATON		C		56 78.	_		3.398		4.44
ATOM	4200	0		56 79.	_		5.700	1.00 2	6.50
ATOM		N		⁵⁷ 78.			6.654		7.38
ATOM		CA	LEU 55	78.			.754		5.25
ATOM		CB	LEU 55	77.			.917		3.25
ATOM			LEU 55	7 76.		.217 10			.09
		CD1	LEU 55	7 78.0		.414 11	220		.35
ATOM	4292	CD2	LEU 55	, , ,		.733 12	^	.00 25	. 35
ATOM	4293	C :	LEU 55	.0.2		.340 12.			. 54
ATOM	4294	_	LEU 55	,,	.69 14.				. 91
ATOM	4295		TYR 558		60 14.				.06
ATOM	4297	~~		,	17 13.				. 05
ATOM		~		,,.0	18 11.			.00 29	
ATOM				, , . 0	13 10.			.00 28.	
ATOM	420-	-			59 11.		_	00 27.	
ATOM			YR 558	78.96	10.			00 31.	70
ATOM			YR 558	79.12	21 11.:			00 32.	
ATOM			YR 558	77.12	2 12.3		073 1.	00 32.	
ATOM		_	YR 558	77.27				00 30.	
ATOM			(R 558	78.28				00 29.	
ATOM	4	H T	R 558	78.45				00 33.2	
. 7 CD c	4307 C	\mathbf{T}	TR 558	76.84		_	53 1.0		
3.770	4308 0	TY	R 558	77.82		-	32 1.(
	4309 N	VA	L 559	75.60		02 10.6	47 1.0		
3	4311 CA	. VA	L 559	75.286	- • •	70 10.3	13 1.0		
	4312 CE			74 100			54 1.0		
	1313 CG	1 VA		74.102		32 12.32		_	
ATOM 4	1314 CG			73.802		36 13.60		•	
ATOM 4	315 C	VAI		74.456		31 12.68			
	316 0	VAI		74.911	8.77	2 11.13	_	_	
ATOM 4	317 N	ILE		73.834	8.53	6 10.59	_		
ATOM 4	319 CA	ILE		75.824	7.84				
ATOM 4	320 CB	ILE		75.638	6.46	5 10.96		–	
	321 CG2			77.012	5.82				
ATOM 4	322 CG1			76.819	4.468				
	323 CD1		560	77.793	6.74				
•	324 C		560	79.274	6.399				
3.500		ILE	560	74.917	5.644				
		ILE	560	75.404	5.044		1.00	29.17	
7.000		VAL	561	73.743	5.497		1.00	28.92	
3		VAL	561	72.957	5.129		1.00	28.60	
3 77 0		VAL	561	71.634	4.325		1.00	28.58	
70000		VAL	561		5.061	13.047	1.00	27.53	
ATOM 43		VAL	561	71.951	6.400	13.701	1.00		
ATOM 43	32 C	VAL	561	70.697	5.246	11.874	1.00	22.44	
ATOM 433		VAL		72.618	2.956	12.006		23.19	
ATOM 433	4 N	GLU	561 563	72.875	2.694	10.825	1.00	28.20	
ATOM 433		GLU	562	72.057	2.079	12.834	1.00	27.99	
ATOM 433			562	71.666	0.744		1.00	29.17	
	25	GLU	562	71.199	-0.086	12.399	1.00	28.96	
SSD/55145.	ν Ω 1					13.589	1.00	27.34	
-5115.	401								

MOTA	4338	CG	GLU	562	72.308	-0.331	14.583	1.00	30.12
MOTA	4339	CD	GLU	562	71.838	-1.075	15.808	1.00	32.29
ATOM	4340	OE1	GLU	562	72.526	-2.030	16.217	1.00	32.45
MOTA	4341	OE2	GLU	562	70.785	-0.702	16.362	1.00	30.16
MOTA	4342	С	GLU	562	70.580	0.794	11.340	1.00	29.79
ATOM	4343	0	GLU	562	69.690	1.653	11.386	1.00	29.75
MOTA	4344	N	TYR	563	70.684	-0.106	10.369	1.00	30.51
ATOM	4346	CA	TYR	563	69.735	-0.209	9.267	1.00	33.76
ATOM	4347	CB	$\mathbf{T}\mathbf{Y}\mathbf{R}$	563	70.494	-0.602	7.988	1.00	31.04
MOTA	4348	CG	TYR	563	69.624	-0.928	6.806	1.00	33.40
MOTA	4349	CD1	TYR	563	68.693	-0.019	6.340	1.00	33.07
MOTA	4350	CE1	TYR	563	67.908	-0.301	5.240	1.00	34.71
MOTA	4351	CD2	TYR	563	69.749	-2.141	6.147	1.00	34.61
MOTA	4352	CE2	TYR	563	68.970	-2.446	5.035	1.00	36.54
MOTA	4353	CZ	TYR	563	68.047	-1.518	4.589	1.00	36.83
ATOM	4354	OH	TYR	563	67.261	-1.805	3.501	1.00	38.81
MOTA	4356	C	TYR	563	68.655	-1.269	9.588	1.00	36.14
MOTA	4357	0	TYR	563	68.946	-2.365	10.023	1.00	37.70
MOTA	4358	N	ALA	564	67.406	-0.948	9.309	1.00	37.87
MOTA	4360	CA	ALA	564	66.276	-1.832	9.534	1.00	38.49
ATOM	4361	CB	ALA	564	65.278	-1.167	10.458	1.00	42.57
MOTA	4362	C	ALA	564	65.645	-2.153	8.179	1.00	39.65
ATOM	4363	0	ALA	564	64.796	-1.423	7.687	1.00	39.74
MOTA	4364	N	SER	565	66.039	-3.280	7.607	1.00	40.06
ATOM	4366	CA	SER	565	65.567	-3.699	6.295	1.00	40.67
ATOM	4367	CB	SER	565	66.267	-4.986	5.883	1.00	38.71
MOTA	4368	OG	SER	565	66.107	-5.964	6.889	1.00	41.35
ATOM	4370	C	SER	565	64.081	-3.884	6.106	1.00	42.17
ATOM	4371	0	SER	565	63.585	-3.741	4.992	1.00	44.25
ATOM	4372	N	LYS	566	63.360	-4.207	7.167	1.00	41.71
ATOM	4374	CA	LYS	566	61.928	-4.427	7.015	1.00	40.22
ATOM	4375	CB	LYS	566	61.525	-5.668	7.800	1.00	39.51
ATOM	4376	CG	LYS	566	62.202	-6.910	7.226	1.00	41.48
ATOM	4377	CD	LYS	566	62.113	-8.094	8.149	1.00	41.53
ATOM	4378	CE	LYS	566	62.710	-9.312	7.491	1.00	41.18
MOTA	4379	NZ	LYS	566	62.763	-10.458	8.438	1.00	46.17
ATOM	4383	С	LYS	566	61.007	-3.220	7.263	1.00	40.47
ATOM	4384	0	LYS	566	59.800	-3.367	7.486	1.00	42.68
MOTA	4385	N	GLY	567	61.584	-2.026	7.167	1.00	38.90
MOTA	4387	CA	GLY	567	60.826	-0.799	7.336	1.00	37.13
MOTA	4388	C	GLY	567	60.199	-0.592	8.694	1.00	36.72
MOTA	4389	0	GLY	567	60.644	-1.172	9.683	1.00	38.48
MOTA	4390	N	ASN	568	59.191	0.273	8.753	1.00	35.77
ATOM	4392	CA	ASN	568	58.518	0.549	10.015	1.00	35.36
ATOM	4393	CB	ASN	568	57.883	1.957	10.045	1.00	36.30
ATOM	4394	CG	ASN	568	56.635	2.088	9.169	1.00	38.06
ATOM	4395	OD1	ASN	568	55.623	1.421	9.383	1.00	38.66
ATOM	4396	ND2	ASN	568	56.686	3.010	8.221	1.00	37.29
ATOM	4399	C	ASN	568	57.504	-0.532	10.341	1.00	33.04
ATOM	4400	0	ASN	568	57.061	-1.265	9.461	1.00	32.10
ATOM	4401	N	LEU	569	57.142	-0.612	11.617	1.00	33.59
ATOM	4403	CA	LEU	569	56.199	-1.604	12.132	1.00	32.91
ATOM	4404	CB	LEU	569	56.045	-1.428	13.647	1.00	33.84
MOTA	4405	CG	LEU	569	55.088	-2.343	14.403	1.00	31.96
12 T O1-1	-2-200			202	23.000	2.543			0

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				ΈU	569	55.52	2 -3.79	7 14.2	16 1 0	0 22 44
				ΈU	569	55.08				
		08	_	EU	569	54.82			_	
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AT		10 N		RG	570	54.31				_
ATO				RG	570	52.999				
ATO		_		RG	570	52.659		_		
AT(-		RG	570	51.282		_		
ATO			D A	RG	570	51.203				
ATC			E AI	₹G	570	52.154				
ATC			Z AI	₹G	570	52.995				
ATC		19 M	H1 AF	₹G	570	53.016				_
ATO			H2 AF	≀G	570	53.804				
ATO		25 C	AF	2G	570	52.992				
ATO		6 0	AR	:G	570	52.145				
ATO		_	GL		571	53.971			• • •	
ATO		9 CA	A GL	U.	571	54.111				
ATO	M 443	0 CE	GL	U !	571	55.219	-1.400			37.51
ATO		1 CG	GL		571	54.945	-0.701	-		41.27
OTA		2 CD	GL		571	56.087	0.778			49.88
ATO		3 OE	1 GL		571	57.264	1.516		_	57.58
ATON	M 443	4 OE	2 GLI		71	55.804	1.122	5.636		60.59
ATON		5 C	GL		71	54.399	2.504	4.714		61.14
ATOM	1 443	6 0	GL		71	53.889	-2.896	7.228		36.24
ATOM			TYF		72	55.202	-3.716	6.459		34.22
ATOM	1 4439	CA	TYF		72	55.570	-3.238	8.232		35.98
ATOM	•	CB	TYF		72	56.526	-4.619	8.517		35.34
ATOM	4441	CG	TYR		72	56.959	-4.656	9.714	1.00	30.94
ATOM		CD	L TYR		72	58.009	-6.034	10.180	1.00	32.71
ATOM	4443	CE	LTYR		72	58.464	-6.714	9.547	1.00	32.33
ATOM	4444	CD2	TYR		72	56.369	-7.940	10.026	1.00	30.31
ATOM	4445	CE2			72	56.813	-6.626	11.303	1.00	33.43
ATOM	4446	CZ	TYR		72	57.864	-7.851	11.791	1.00	31.46
ATOM	4447	ОН	TYR		72	58.311	-8.502	11.148	1.00	33.99
ATOM	4449	C.	TYR			54.312	-9.706	11.640	1.00	36.30
MOTA	4450	0	TYR	57		54.121	-5.425	8.826	1.00	37.26
ATOM	4451	N	LEU	57		53.457	-6.530	8.314	1.00	36.91
ATOM	4453	CA	LEU	57			-4.850	9.665	1.00	36.82
ATOM	4454	CB	LEU	57		52.208 51.537	-5.476	10.075	1.00	35.56
ATOM	4455	CG	LEU	57			-4.629	11.165	1.00	34.03
ATOM	4456	CD1	LEU	57		52.238	-4.527	12.519	1.00	32.82
ATOM	4457	CD2	LEU	57		51.621	-3.423	13.377	1.00	28.95
ATOM	4458	C	LEU	57		52.168	-5.858	13.207	1.00	29.46
MOTA	4459	0	LEU	57		51.237	-5.658	8.915	1.00	34.56
ATOM	4460	N	GLN	57		50.670	-6.729	8.726	1.00	34.80
ATOM	4462	CA	GLN	57		51.030	-4.602	8.150	1.00	37.10
ATOM	4463	CB	GLN	57		50.101	-4.666	7.031	1.00	41.15
ATOM	4464	CG	GLN			49.875	-3.278	6.457		41.63
ATOM	4465	CD	GLN	574		49.089	-2.375	7.366		43.13
ATOM	4466	OE1	GLN	574		49.063	-0.959	6.860		47.77
ATOM	4467	NE2	GLN	574		49.655	-0.647	5.827		50.00
ATOM	4470	C	GLN	574		48.378	-0.086	7.582		49.67
ATOM	4471	0		574		50.529	~5.627	5.934		12.38
ATOM	4472	N	GLN	574		49.685	-6.284	5.318		44.56
	,2	**	ALA	575		51.835	-5.717			11.99
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MOTA	4474	CA	ALA	575	52.367	-6.608	4.676	1.00	41.29
MOTA	4475	CB	ALA	575	53.841	-6.325	4.446	1.00	40.43
MOTA	4476	C	ALA	575	52.186	-8.058	5.066	1.00	41.42
MOTA	4477	0	ALA	575	52.392	-8.949	4.249	1.00	43.65
ATOM	4478	N	ARG	576	51.815	-8.294	6.319	1.00	42.56
ATOM	4480	CA	ARG	576	51.642	-9.646	6.824	1.00	42.51
MOTA	4481	CB	ARG	576	52.676	-9.910	7.920	1.00	40.14
MOTA	4482	CG	ARG	576	54.100	-9.896	7.377	1.00	40.32
ATOM	4483	CD	ARG	576	55.172	-9.836	8.460	1.00	40.78
ATOM	4484	NE	ARG	576	56.513	-9.783	7.874	1.00	42.13
MOTA	4486	CZ	ARG	576	56.975	-8.785	7.120	1.00	40.73
ATOM	4487	NH1	ARG	576	56.215	-7.732	6.851	1.00	39.21
ATOM	4490	NH2	ARG	576	58.201	-8.846	6.622	1.00	37.62
ATOM	4493	C	ARG	576	50.242	-9.931	7.326	1.00	44.48
ATOM	4494	0	ARG	576	50.028	-10.869	8.098	1.00	46.84
ATOM	4495	N	ARG	577	49.275	-9.146	6.866	1.00	46.26
ATOM	4497	CA	ARG	577	47.893	-9.344	7.292	1.00	46.89
ATOM	4498	СВ	ARG	577	47.027	-8.170	6.845	1.00	46.16
ATOM	4499	CG	ARG	577	47.189	-6.939	7.696	1.00	44.93
ATOM	4500	CD	ARG	577	46.463	-5.766	7.080	1.00	44.60
MOTA	4501	NE	ARG	577	46.284	-4.683	8.039	1.00	45.05
ATOM	4503	cz	ARG	577	45.612	-3.565	7.793	1.00	45.95
ATOM	4504	NH1	ARG	577	45.052	-3.372	6.606	1.00	47.39
ATOM	4507	NH2	ARG	577	45.466	-2.655	8.749	1.00	45.49
ATOM	4510	C	ARG	577	47.334	-10.649	6.740	1.00	46.60
ATOM	4511	ō	ARG	577	47.478	-10.933	5.551	1.00	47.15
ATOM	4512	N	GLN	594	53.312	-14.007	7.967	1.00	63.97
ATOM	4514	CA	GLN	594	52.110	-14.068	8.799	1.00	63.06
ATOM	4515	CB	GLN	594	51.175	-15.183	8.319	1.00	64.16
ATOM	4516	C	GLN	594	52.501	-14.278	10.258	1.00	61.68
ATOM	4517	0	GLN	594	53.101	-15.292	10.619	1.00	60.95
ATOM	4518	N	LEU	595	52.140	-13.313	11.092	1.00	58.58
ATOM	4520	CA	LEU	595	52.470	-13.335	12.505	1.00	55.58
ATOM	4521	СВ	LEU	595	52.619	-11.902	13.020	1.00	54.05
ATOM	4522	CG	LEU	595	53.570	-11.074	12.153	1.00	56.23
ATOM	4523	CD1	LEU	595	53.496	-9.609	12.524	1.00	58.84
ATOM	4524	CD2	LEU	595	54.977	-11.596	12.301	1.00	55.93
ATOM	4525	C	LEU	595	51.480	-14.093	13.372	1.00	53.77
ATOM	4526	Ö	LEU	595	50.276	-14.046	13.139	1.00	54.31
MOTA	4527	N	SER	596	52.012	-14.780	14.377	1.00	51.04
ATOM	4529	CA	SER	596	51.206	-15.541	15.316	1.00	48.97
ATOM	4530	CB	SER	596	52.004	-16.737	15.834	1.00	48.89
ATOM	4531	OG	SER	596	52.945	-16.345	16.820	1.00	48.59
ATOM	4533	C	SER	596	50.853	-14.641	16.488	1.00	47.56
MOTA	4534	0	SER	596	51.470	-13.590	16.676	1.00	46.71
ATOM	4535	N	SER	597	49.888	-15.070	17.292	1.00	47.11
ATOM	4537	CA	SER	597	49.462	-14.315	18.461	1.00	47.88
		CB	SER	597	48.386	-15.084	19.229	1.00	50.66
MOTA	4538								
MOTA	4539	OG C	SER	597 597	47.574	-15.839	18.343	1.00	57.08
MOTA	4541	C	SER	597	50.666	-14.068	19.372	1.00	46.03
MOTA	4542	0	SER	597	50.735	-13.045	20.047	1.00	46.49
MOTA	4543	N	LYS	598	51.607	-15.007	19.399	1.00	46.08
MOTA	4545	CA	LYS	598	52.798	-14.844	20.229	1.00	46.33
MOTA	4546	CB	LYS	598	53.558	-16.163	20.384	1.00	46.67

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ATO	OM 45	547	CG	LYS	598							
ATO				LYS		V1.17			.623	1.00	49	.61
ATO				LYS	598	55.24			.668	1.00		.69
ATC					598	55.89	_		.026	1.00	53.	
ATO				LYS	598	54.89			.093	1.00		
ATO		_	_	LYS	598	53.70	6 -13.		.599	1.00	52.	
ATO				LYS	598	54.29	2 -12.		.311		45.	
ATO				ASP	599	53.78	0 -13.		. 264	1.00	44.	
ATO				ASP	599	54.59	8 -12.		. 513	1.00	44.	
ATO				ASP	599	54.52				1.00	43.	
		-		SP	599	55.288			001	1.00	44.	83
ATO				SP	599	56.228			560	1.00	48.	24
ATO		_	D2 A	SP	599	54.958			260	1.00	52.9	90
ATOM		-	. A	SP	599	54.120				1.00	51.4	13
ATON			A	SP	599	54.937	_		796	1.00	42.7	71
ATOM		55 ท	L	EU	600	52.803			059	1.00	45.0	00
ATOM	1 456	7 C		EU	600					1.00	37.6	
ATOM	1 456	8 C		EU	600	52.246	-		030	1.00	34.0	
ATOM	456			ΞŪ		50.747				1.00	34.0	
ATOM		_		ΞŪ	600	50.332	-10.0	68 16.2		1.00	33.1	
ATOM					600	48.814	~9.9	92 16.:		1.00		
ATOM					600	50.974	~9.0	12 15.3		1.00	37.3	
ATOM		_	LE		600	52.537	-9.45			00	25.6	
ATOM		_	LE		600	52.910	-8.29				34.5	
ATOM		_			601	52.415	-10.34				33.18	
ATOM					501	52.692	-9.96				34.24	
ATOM	4577				501	52.214	-11.03				35.80	
	4578			L (501	52.331	-10.48			.00	37.50)
MOTA	4579		2 VA	Le	01	50.766	-11.40	_			38.08	
ATOM	4580	_	VA	L e	01	54.198	-9.74				40.77	
ATOM	4581	_	VA.	L 6	01	54.634				.00	35.04	
ATOM	4582		SE		02	54.981	-8.85			.00	34.33	
ATOM	4584	CA	SE		02	56.421	-10.53				32.58	
MOTA	4585	CB	SEI		02	57.045	-10.42				86.01	
ATOM	4586	OG	SEF		02		-11.504				8.43	
ATOM	4588	C	SEF	_	02	58.453	-11.38		9 1.		3.36	
ATOM	4589	0	SER		02	56.809	-9.038		0 1.		5.21	
MOTA	4590	N	CYS		02	57.651	-8.363		4 1.		5.03	
ATOM	4592	CA	CYS	_		56.183	-8.614			-	4.15	
ATOM	4593	СВ	CYS)3	56.438	-7.294	19.14			4.04	
ATOM	4594	SG	CYS)3	55.543	-7.055	17.92			3.45	
ATOM	4595	C				55.653	-5.423	17.22				55
ATOM	4596	0	CYS	60		56.198	-6.211				2.19	PRT1
ATOM	4597		CYS	60		57.023	-5.316				2.79	
		N	ALA	60		55.088	-6.321				3.36	
	4599	CA	ALA	60	4	54.743	-5.358				1.31	
	4600	CB	ALA	60	4	53.321	-5.610				.36	
	4601	C	ALA	60	4	55.741	-5.394	22.483			.01	
	4602	0	ALA	60	4	56.050		23.128			.83	
	4603	N	TYR	60		56.212	-4.358	23.727		0 30	.89	
	4605	CA	TYR	60		57.189	-6.592	23.465			. 95	
	4606	СВ	TYR	60			-6.758	24.539		_	.34	
	4607	CG	TYR	60!		57.500	-8.236	24.737	1.0		.58	
ATOM 4	4608	CD1	TYR	605		58.640	-8.495	25.690	1.0		. 51	
	1609	CE1	TYR			58.511	-8.236	27.053	1.0		.50	
	1610	CD2		605		59.556	-8.507	27.943	1.00	_		
	611	CE2	TYR	605		59.841	-9.026	25.230	1.00		. 08	
•		ے ندب	TYR	605		60.896	-9.300	26.109	1.00			
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ATOM 4612 CZTYR 605 60.746 -9.042 27.464 1.00 37.56 ATOM 4613. OH TYR 605 61.776 -9.342 28.336 1.00 38.08 4615 С TYR 605 58.480 -6.006 24.191 1.00 32.42 **ATOM** 4616 TYR 605 58.975 -5.203 24.991 1.00 33.34 MOTA 0 GLN 606 -6.267 22.989 1.00 MOTA 4617 Ν 58.997 30.61 MOTA 4619 CA GLN 606 60.218 -5.643 22.474 1.00 31.12 MOTA 4620 CB GLN 606 60.499 -6.143 21.058 1.00 30.57 GLN 606 -7.568 21.008 1.00 33.90 **ATOM** 4621 CG 61.044 GLN -8.080 19.593 1.00 MOTA 4622 CD606 61.240 32.17 -7.652 18.883 1.00 MOTA 4623 OE1 GLN 606 62.155 32.55 1.00 -8.998 19.171 ATOM 4624 NE2 GLN 606 60.374 33.10 4627 GLN 22.487 1.00 MOTA С 606 60.157 -4.114 31.69 MOTA 4628 GLN 606 -3.453 22.910 1.00 0 61.111 31.18 MOTA N VAL 607 -3.564 22.020 1.00 4629 59.035 29.50 VAL 607 -2.122 22.000 1.00 MOTA 4631 CA 58.816 27.54 **ATOM** 4632 CB VAL 607 -1.751 21.306 1.00 57.454 26.79 CG1 VAL 607 -0.291 21.516 1.00 MOTA 4633 57.131 24.80 MOTA 4634 CG₂ VAL 607 57.505 -2.050 19.815 1.00 22.95 MOTA 4635 C VAL 607 58.827 -1.576 23.432 1.00 28.30 MOTA 4636 0 VAL 607 59.469 -0.548 23.705 1.00 28.32 ATOM ALA 1.00 4637 N 608 58.110 -2.247 24.340 27.21 **ATOM** 4639 CA ALA 608 58.061 -1.805 25.735 1.00 26.54 MOTA 4640 CB ALA 608 57.070 -2.649 26.550 1.00 26.70 MOTA 4641 С ALA 608 59.457 -1.850 26.368 1.00 25.97 MOTA 4642 0 ALA 608 59.802 -0.993 27.183 1.00 25.88 MOTA 4643 N ARG 609 60.250 -2.848 25.994 1.00 26.02 MOTA 4645 CA ARG 609 61.606 -2.977 26.512 1.00 30.44 MOTA 4646 CB ARG 609 62.234 -4.285 26.058 1.00 34.09 MOTA 4647 CG ARG 609 61.642 -5.516 26.682 1.00 39.24 MOTA 4648 CDARG 609 62.659 -6.615 26.615 1.00 42.75 MOTA NE ARG 609 63.405 -6.704 27.860 1.00 4649 45.52 -7.405 MOTA 4651 CZARG 609 64.525 28.019 1.00 46.24 MOTA ARG 609 -8.079 27.001 4652 NH1 65.055 1.00 41.48 ARG 609 -7.482 29.225 1.00 MOTA 4655 NH₂ 65.079 47.49 MOTA 4658 C ARG 609 62.478 -1.829 26.015 1.00 34.20 -1.255 MOTA 4659 О ARG 609 63.265 26.788 1.00 35.24 MOTA 4660 GLY 62.368 -1.528 24.717 1.00 N 610 33.25 ATOM 4662 CA GLY 610 -0.439 24.138 1.00 29.57 63.130 MOTA 4663 C GLY 610 62.802 0.814 24.908 1.00 29.31 MOTA 4664 0 GLY 610 63.695 1.543 25.335 1.00 27.46 MOTA 4665 N MET 611 61.507 1.020 25.147 1.00 31.07 MOTA 4667 CA MET 611 61.016 2.178 25.889 1.00 30.09 MOTA 4668 CB MET 611 59.493 2.280 25.782 1.00 29.51 MOTA 4669 CG MET 611 58.997 2.655 24.404 1.00 28.21 MOTA 4670 SD MET 611 59.760 4.175 23.787 1.00 29.00 MOTA 4671 CE MET 611 59.350 5.335 25.039 1.00 25.91 ATOM 4672 С MET 611 61.439 2.189 27.361 1.00 30.47 MOTA 4673 0 MET 611 61.734 3.242 27.919 1.00 29.43 MOTA 61.429 4674 N GLU 612 1.031 28.002 1.00 31.97 MOTA 4676 CA GLU 612 61.836 0.947 29.402 1.00 35.34 MOTA 4677 CB GLU 612 61.707 -0.490 29.904 1.00 36.17 **ATOM** CG GLU -0.729 31.278 1.00 4678 612 62.305 34.87 ATOM 4679 CD GLU 612 62.259 -2.185 31.705 1.00 32.68 GLU MOTA 4680 OE1 612 62.641 -3.070 30.904 1.00 35.01

		4681	OE2	GLU	612	61.0	4.0				
A	MOT	4682	C	GLU					32.858	1.00	36.56
A	TOM .	4683	0	GLU				.425	29.490	1.00	35.26
A	TOM 4	1684	N	TYR	613	-0.0		162	30.417	1.00	31.21
A'	TOM 4	1686	CA	TYR		0			28.491	1.00	36.10
A'	TOM 4	687	CB	TYR	613	65.49			28.440	1.00	
A.		688	CG		613	66.24			7.301	1.00	34.76
A7		689	CD1	TYR	613	67.70			7.284	1.00	31.15
		690	CE1	TYR	613	68.60	0 0.		8.207		34.28
		_		TYR	613	69.94			8.219	1.00	36.50
				TYR	613	68.17			6.366	1.00	38.20
			~-	TYR	613	69.52				1.00	32.99
	_			TYR	613	70.39			6.372	1.00	33.32
AT				ΓΥR	613	71.72			7.302	1.00	36.59
			C !	ľYR	613	65.58			7.333	1.00	35.73
AT) ;	ľYR	613	66.23			3.273	1.00	34.03
ATO	_		7 I	EU	614	64.916			9.075	1.00	35.26
ATO		'00 c	CA I	ŒU	614	64.945			7.250	1.00	31.78
ATO	OM 47	01 (CB I	ΈU	614				.998	1.00	29.50
ATO	OM 47	02 (EU	614	64.095	-		.775	1.00	28.26
ATC		03 C		EU	614	64.564			.422	1.00	31.29
ATC	M 47	04 C		EU	614	63.564	· - -	89 23	.321	1.00	28.09
ATO	M 47		. –			65.951					29.52
ATO			_		614	64.489	5.7		_		
ATO					614	65.108	6.7				32.49
ATO			_		615	63.431	5.23				31.73
ATO					615	62.906	5.87				33.06
ATO					615	61.598	5.19				35.16
ATO			AI		615	63.942	5.83				36.64
ATON		_	AI		515	64.065	6.80				35.36
ATOM		_	SE		516	64.690	4.73				86.80
ATOM	_	_		_	516	65.716	4.62				5.91
ATOM					16	66.287	3.19		40.		5.78
ATOM			SE	R 6	16	67.133	2.89	_			2.52
ATOM			SE	R 6	16	66.832	5.62		_	.00 2	9.64
			SE	R 6	16	67.556				.00 3	7.48
ATOM			LY	5 6	17	66.971	6.048			.00 3	8.76
ATOM			LYS	3 6	17	67.973	5.980				4.74
ATOM			LYS		17	68.540	6.93			.00 32	2.44
ATOM	4725	CG	LYS		17	69.330	6.520				2.94
ATOM	4726	CD	LYS		17	70.539	5.232	-			2.64
ATOM	4727	CE	LYS		L 7		5.402				3.45
ATOM	4728	NZ	LYS			71.252	4.091				.84
ATOM	4732	C	LYS			72.552	4.306	30.8	12 1.		.49
ATOM	4733	0	LYS			67.376	8.325	30.2			.29
ATOM	4734	N	LYS			67.909	9.188	29.5			
MOTA	4736	CA	LYS	61		66.245	8.528	30.9			. 95
ATOM	4737	CB		61		65.569	9.822	30.99			.87
ATOM	4738		LYS	61		66.512	10.868	31.58	_		.44
ATOM		CG	LYS	61		67.192	10.446	32.87			.44
ATOM	4739	CD	LYS	61		66.234	10.363	34.03			
ATOM	4740	CE	LYS	61		66.962	9.939				
	4741	NZ	LYS	618		66.070	10.032	35.31			
ATOM	4745	C	LYS	618		65.015		36.51		- •	82
ATOM	4746	0	LYS	618		64.557	10.327	29.66			
ATOM	4747	N	CYS	619		65.006	11.463	29.56			
ATOM	4749	CA	CYS	619			9.472	28.64		0 34.	
					,	54.525	9.848	27.32			
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MOTA	4750	CB	CYS	619	65.279	9.033	26.263	1.00	31.17
ATOM	4751	SG	CYS	619	64.816	9.306	24.541	1.00	30.02
ATOM	4752	С	CYS	619	63.004	9.701	27.149	1.00	30.45
ATOM	4753	0	CYS	619	62.418	8.649	27.388	1.00	29.24
MOTA	4754	N	ILE	620	62.359	10.798	26.800	1.00	30.14
MOTA	4756	CA	ILE	620	60.935	10.822	26.542	1.00	31.76
MOTA	4757	CB	ILE	620	60.268	12.040	27.193	1.00	31.26
MOTA	4758	CG2	ILE	620	58.799	12.116	26.774	1.00	31.66
MOTA	4759	CG1	ILE	620	60.392	11.957	28.712	1.00	29.71
MOTA	4760	CD1	ILE	620	60.016	13.236	29.396	1.00	27.40
MOTA	4761	С	ILE	620	60.864	10.961	25.023	1.00	31.86
ATOM	4762	0	ILE	620	61.384	11.920	24.465	1.00	32.70
MOTA	4763	N	HIS	621	60.249	9.986	24.366	1.00	31.70
MOTA	4765	CA	HIS	621	60.133	9.973	22.906	1.00	32.12
MOTA	4766	CB	HIS	621	59.708	8.578	22.430	1.00	29.61
ATOM	4767	CG	HIS	621	59.903	8.344	20.961	1.00	28.62
ATOM	4768	CD2	HIS	621	60.511	7.336	20.300	1.00	27.49
MOTA	4769	ND1	HIS	621	59.373	9.168	19.988	1.00	30.08
MOTA	4771	CE1	HIS	621	59.637	8.669	18.795	1.00	25.00
MOTA	4772	NE2	HIS	621	60.325	7.554	18.956	1.00	26.55
MOTA	4774	С	HIS	621	59.194	11.026	22.321	1.00	34.51
MOTA	4775	0	HIS	621	59.466	11.570	21.251	1.00	36.79
MOTA	4776	N	ARG	622	58.048	11.248	22.960	1.00	35.26
MOTA	4778	CA	ARG	622	57.068	12.239	22.490	1.00	34.68
MOTA	4779	CB	ARG	622	57.705	13.628	22.370	1.00	33.43
MOTA	4780	CG	ARG	622	58.285	14.135	23.674	1.00	31.52
MOTA	4781	CD	ARG	622	58.781	15.563	23.570	0.50	27.82
MOTA	4782	NE	ARG	622	59.216	16.050	24.876	0.50	28.82
MOTA	4784	CZ	ARG	622	60.362	15.715	25.463	0.50	30.41
MOTA	4785	NH1	ARG	622	61.215	14.891	24.860	0.50	31.15
MOTA	4788	NH2	ARG	622	60.640	16.168	26.680	0.50	30.83
MOTA	4791	C	ARG	622	56.283	11.891	21.213	1.00	34.71
MOTA	4792	0	ARG	622	55.289	12.544	20.912	1.00	35.58
MOTA	4793	N	ASP	623	56.719	10.884	20.459	1.00	34.90
ATOM	4795	CA	ASP	623	55.986	10.468	19.261	1.00	34.30
MOTA	4796	CB	ASP	623	56.443	11.212	17.994	1.00	36.76
MOTA	4797	CG	ASP	623	55.535	10.918	16.772	1.00	43.35
ATOM	4798	OD1	ASP	623	55.980	11.131	15.624	1.00	47.64
ATOM	4799	OD2	ASP	623	54.376	10.469	16.954	1.00	43.30
ATOM	4800	C	ASP	623	56.094	8.967	19.051	1.00	32.24
ATOM	4801	0	ASP	623	56.406	8.494	17.957	1.00	31.19
ATOM	4802	N	LEU	624	55.895	8.209	20.118	1.00	32.27
MOTA	4804	CA	LEU	624	55.964	6.759	20.005	1.00	33.18
MOTA	4805	CB	LEU	624	56.013	6.118	21.390	1.00	31.16
MOTA	4806	CG	LEU	624	56.019	4.592	21.452	1.00	32.74
ATOM	4807	CD1	LEU	624	57.257	4.020	20.765	1.00	30.64
ATOM	4808	CD2	LEU	624	55.974	4.177	22.904	1.00	34.51
ATOM	4809	C	LEU	624	54.738	6.274	19.217	1.00	35.18
ATOM	4810	0	LEU	624	53.589	6.511	19.612	1.00	35.72
ATOM	4811	N	ALA	625	54.997	5.632	18.084	1.00	32.37
ATOM	4813	CA	ALA	625	53.946	5.113	17.223	1.00	30.60
MOTA	4814	CB	ALA	625	53.447	6.205	16.298	1.00	25.26
MOTA	4815	C	ALA	625	54.618	4.020	16.427	1.00	29.87
MOTA	4816	0	ALA	625	55.839	3.978	16.378	1.00	32.01

AT(17 N		LA 626	53.834	3.16	3 15.77	9 1.0	0 20 40
ATO				LA 626	54.373				
ATC	- •	_		A 626	53.23]				
ATC					55.255				· · · - -
ATC					56.193	1.87			
ATC					54.935				
ATO					55.706	4.352			-, · · -
ATO					55.056				
ATO					54.894				
ATO					54.435	8.032			
ATO					53.987	8.878			
ATO					52.745	8.879			
ATO				•	51.822	8.094		-	
ATO					52.447	9.604			
ATON	_		AR		57.151	4.632	· ·	1.00	
ATON		_	ARO		58.058	4.687		1.00	30.79
ATON			ASI	√ 628	57.347	4.822	13.985	1.00	30.16
ATON	_				58.661	5.109	14.550	1.00	30.31
ATOM					58.587	6.257	15.549	1.00	28.50
ATOM				628	58.369	7.571	14.868	1.00	27.84
ATOM					58.893	7.796	13.782	1.00	31.41
ATOM ATOM				· — -	57.551	8.429	15.460	1.00	33.45
			ASN		59.352	3.919	15.169	1.00	28.53
ATOM			ASN		60.232	4.076	16.021	1.00	28.10
ATOM ATOM			VAL		58.887	2.733	14.803	1.00	28.64
ATOM			VAL		59.484	1.482	15.253	1.00	27.79
ATOM			VAL		58.475	0.577	15.983	1.00	28.30 25.38
ATOM				629	59.118	-0.753	16.284	1.00	23.38
ATOM				629	57.980	1.246	17.265	1.00	22.48
ATOM	4857 4858	_	VAL	629	59.925	0.810	13.949	1.00	28.69
ATOM	4859	O N	VAL	629	59.114	0.616	13.043	1.00	27.07
ATOM	4861	N	LEU	630	61.220	0.542	13.823	1.00	29.54
ATOM	4862	CA CB	LEU	630	61.749	-0.081	12.616	1.00	30.17
ATOM	4863	CG	LEU	630	62.999	0.659	12.142	1.00	29.62
ATOM	4864	CD1	LEU	630	62.831	2.180	12.035	1.00	29.14
ATOM	4865	CD1	LEU	630	64.121	2.795	11.579	1.00	29.83
ATOM	4866	CD2	LEU	630	61.693	2.543	11.086	1.00	32.59
ATOM	4867	0	LEU	630	62.036	-1.541	12.899	1.00	30.50
ATOM	4868	N	LEU VAL	630	62.290	-1.910	14.042	1.00	31.06
ATOM	4870	CA	VAL	631	61.966	-2.376	11.866	1.00	33.03
ATOM	4871	CB	VAL	631	62.174	-3.813	12.022	1.00	31.83
ATOM	4872	CG1	VAL	631	60.902	-4.605	11.582	1.00	29.48
ATOM	4873	CG2	VAL	631	61.017	-6.067		_	29.39
ATOM	4874	C	VAL	631	59.644	-3.984	12.196	_	25.38
ATOM	4875	0	VAL	631	63.379	-4.242	11.196	_	32.37
ATOM	4876	N		631	63.508	-3.865			33.57
ATOM	4878	CA	THR	632	64.285	-4.987	_		34.39
ATOM	4879	CB	THR	632	65.504	-5.453	. .	_	35.84
ATOM	4880	OG1	THR	632	66.659	-5.685			33.11
ATOM	4882	CG2	THR	632	66.328				34.88
ATOM	4883	CG2	THR	632	66.922				28.85
ATOM	4884	0	THR	632	65.272				37.63
	4885	N	THR	632	64.195	-7.347		_	37.20
-		14	GLU	633	66.289	-7.163			39.78
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ATOM	4887	CA	GLU	633	66.182	-8.379	8.794	1.00	43.30
ATOM	4888	CB	GLU	633	67.437	-8.590	7.933	1.00	46.66
MOTA	4889	CG	GLU	633	67.336	-9.729	6.876	1.00	51.37
MOTA	4890	CD	GLU	633	66.490	-9.404	5.622	1.00	54.30
MOTA	4891	OE1	GLU	633	65.859	-8.327	5.523	1.00	55.85
MOTA	4892	OE2	GLU	633	66.460	-10.256	4.710	1.00	55.95
MOTA	4893	С	GLU	633	65.919	-9.592	9.677	1.00	42.72
MOTA	4894	0	GLU	633	65.360	-10.582	9.222	1.00	45.10
MOTA	4895	N	ASP	634	66.287	-9.494	10.949	1.00	42.83
ATOM	4897	CA	ASP	634	66.075	-10.585	11.884	1.00	43.03
ATOM	4898	CB	ASP	634	67.324	-10.809	12.743	1.00	49.02
MOTA	4899	CG	ASP	634	68.539	-11.240	11.916	1.00	55.95
MOTA	4900	OD1	ASP	634	68.462	-12.292	11.237	1.00	59.10
MOTA	4901	OD2	ASP	634	69.568	-10.525	11.943	1.00	59.41
ATOM	4902	C	ASP	634	64.848	-10.340	12.751	1.00	41.75
MOTA	4903	0	ASP	634	64.737	-10.873	13.847	1.00	42.79
MOTA	4904	N	ASN	635	63.937	-9.508	12.257	1.00	42.51
MOTA	4906	CA	ASN	635	62.686	-9.186	12.939	1.00	42.53
MOTA	4907	CB	ASN	635	61.768	-10.417	12.992	1.00	45.07
MOTA	4908	CG	ASN	635	61.483	-10.985	11.624	1.00	46.54
MOTA	4909	OD1	ASN	635	60.868	-10.336	10.786	1.00	49.77
MOTA	4910	ND2	ASN	635	61.949	-12.192	11.383	1.00	49.29
MOTA	4913	С	ASN	635	62.801	-8.577	14.331	1.00	40.51
MOTA	4914	0	ASN	635	61.939	-8.800	15.187	1.00	41.80
ATOM	4915	N	VAL	636	63.844	-7.795	14.561	1.00	37.98
ATOM	4917	CA	VAL	636	64.016	-7.164	15.856	1.00	33.92
ATOM	4918	CB	LAV	636	65.517	-7.005	16.195	1.00	32.21
MOTA	4919	CG1	VAL	636	65.697	-6.284	17.530	1.00	31.40
MOTA	4920	CG2	VAL	636	66.169	-8.367	16.242	1.00	30.93
ATOM	4921	C	VAL	636	63.349	-5.797	15.811	1.00	31.85
MOTA	4922	0	VAL	636	63.531	-5.061	14.849	1.00	33.47
MOTA	4923	N	MET	637	62.525	-5.492	16.807	1.00	31.69
ATOM	4925	CA	MET	637	61.860	-4.194	16.879	1.00	31.44
ATOM	4926	CB	MET	637	60.642	-4.241	17.820	1.00	34.97
ATOM	4927	CG	MET	637	59.559	-5.264	17.455	1.00	36.80
ATOM	4928	SD	MET	637	58.860	-5.048	15.803	1.00	35.45
MOTA	4929	CE	MET	637	59.030	-6.709	15.116	1.00	32.12
MOTA	4930	C	MET	637	62.874	-3.209	17.454	1.00	31.86
MOTA	4931	0	MET	637	63.512	-3.496	18.479	1.00	29.47
ATOM	4932	N	LYS	638	62.985	-2.041	16.820	1.00	30.87
MOTA	4934	CA	LYS	638	63.915	-0.994	17.244	1.00	29.66
ATOM	4935	CB	LYS	638	65.161	-0.983	16.349	1.00	27.51
ATOM	4936	CG	LYS	638	66.171	-2.059	16.691	1.00	27.29
ATOM	4937	CD	LYS	638	67.370	-1.984	15.781	1.00	28.55
ATOM	4938	CE	LYS	638	68.409	-3.029	16.150	1.00	24.75
ATOM	4939	NZ	LYS	638	68.964	-2.785	17.498	1.00	25.59
ATOM	4943	C	LYS	638	63.283	0.383	17.215	1.00	27.72
ATOM	4944	0	LYS	638	62.918	0.869	16.146	1.00	27.66
ATOM	4945	N	ILE	639	63.163	1.004	18.387	1.00	26.21
ATOM	4947	CA	ILE	639	62.597	2.343	18.501	1.00	26.27
ATOM	4948	CB	ILE	639	62.580	2.862	19.965	1.00	26.52
MOTA	4949	CG2	ILE	639	61.896	4.206	20.017	1.00	21.50
ATOM	4950	CG1	ILE	639	61.918	1.854	20.926	1.00	25.70
MOTA	4951	CD1	ILE	639	60.496	1.494	20.599	1.00	25.62

А	TOM 4	1952	a								
		1953	C	ILE	639		05 3.:	288 17	.718	1 00	
		954	0	ILE	639			— ·	. 906	1.00	29.56
			N	ALA	640	62.89			.857	1.00	27.74
		956		ALA	640	63.62				1.00	27.91
		957		ALA	640	63.37			042	1.00	28.79
	_ ·	958		ALA	640	63.16			563	1.00	26.74
			0	ALA	640	62.08	_			1.00	28.91
			N.	ASP	641	64.00			956.	1.00	28.67
	_		CA :	ASP	641	63.70	_			1.00	28.25
		963	CB 2	ASP	641	62.52			296	1.00	30.80
		964 (CG 1	ASP	641	62.869				1.00	33.44
		965 (_	ASP	641					1.00	38.01
AT		966 (_	ASP	641	64.002			574]	1.00	42.41
AT	OM 49	67 (_	SP	641	62.006			160 1	L.00	41.74
ATO	OM 49	68 0		SP	641	63.501				00	29.07
ATO	OM 49	69 N		HE	642	62.847				.00	28.42
ATO	_					64.138	-	18.6		.00	29.69
ATO	OM 49		_		642	64.036		4 20.0		.00	29.62
ATO	OM 49		-		642	64.347	7.65	6 20.8		.00	27.18
ATC		_	_		642	65.702	7.05			.00	
ATO		_			542	66.848	7.55	9 21.2		.00	23.96
ATO					542	65.828	5.97	4 19.7		.00	23.66
ATO					542	68.090	6.99				24.08
ATO					42	67.069	5.40				23.02
ATO				_	42	68.200	5.90				23.20
ATO			PH	_	42	64.948	10.075				21.68
ATO		_	PH		42	64.755	10.664				32.99
ATO			GL	_	43	65.940	10.396				32.10
ATON				_	43	66.869	11.463				34.66
ATOM			GL	_	43	66.639	12.755				35.29
ATOM			GL	_	43	67.464	13.666	_	_		39.13
	•	_	LE	U 6	44	65.520	12.850		_		39.83
ATOM			LE	J 64	44	65.202	14.043		_		2.26
ATOM			LE	J 64	14	63.935	13.843				6.25
ATOM			LEU	J 64	14	63.911	12.839	16.91			4.59
ATOM			l LEC	J 64	4	62.653		15.76		00 4	3.00
ATOM			LEU	64	4	65.119	13.068	14.94		00 4	2.61
ATOM		_	LEU			65.037	13.016	14.889			5.65
ATOM		0	LEU			64.391	15.298	18.578			9.59
ATOM	4995	N	ALA			65.585	15.281	19.623			1.90
ATOM	4997	CA	ALA	64		65.495	16.401	18.080		0 5:	2.08
ATOM	4998	CB	ALA	_		66.414	17.677	18.777		0 54	1.71
ATOM	4999	C	ALA				18.699	18.124			1.38
ATOM	5000	0	ALA	64		64.053	18.184	18.790			5.44
ATOM	5001	N	ASP	652		63.534	18.582	19.832	1.0		.69
ATOM	5003	CA	ASP	652		52.389	21.543	14.759	1.0		.74
ATOM	5004	CB	ASP			51.207	21.745	13.934	1.00	_	.83
ATOM	5005	CG	ASP	652		51.601	21.995	12.472	1.00	_	
ATOM	5006	OD1		652		50.398	22.241	11.569	1.00	_	.22 .95
ATOM	5007	OD2	ASP	652		49.354	22.715	12.065	1.00		
ATOM	5008		ASP	652		50.497	21.956	10.357			.71
ATOM	5009	C	ASP	652		50.321	20.514	14.042	1.00		. 02
ATOM		0	ASP	652		50.568	19.495	13.394	1.00		.11
ATOM	5010	N	TYR	653		49.272	20.628		1.00		. 96
	5012	CA	TYR	653		48.348	19.524	14.849	1.00		. 57
ATOM	5013	CB	TYR	653		47.274	19.914	15.064	1.00		68
CCC						- · -		16.088	1.00	76.	85
SSSD/55	145. v01										

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ATOM	5014	CG	TYR	653	47.771	19.995	17.519	1.00	79.55
MOTA	5015	CD1	TYR	653	46.983	20.567	18.518	1.00	80.89
MOTA	5016	CE1	TYR	653	47.438	20.648	19.836	1.00	83.02
MOTA	5017	CD2	TYR	653	49.032	19.503	17.874	1.00	80.87
MOTA	5018	CE2	TYR	653	49.496	19.578	19.183	1.00	81.70
MOTA	5019	CZ	TYR	653	48.698	20.152	20.160	1.00	83.09
ATOM	5020	OH	TYR	653	49.165	20.243	21.451	1.00	83.73
MOTA	5022	C	TYR	653	47.685	19.038	13.787	1.00	75.03
ATOM	5023	0	TYR	653	47.232	17.897	13.711	1.00	75.97
ATOM	5024	N	TYR	654	47.679	19.885	12.767	1.00	73.85
MOTA	5026	CA	TYR	654	47.039	19.538	11.507	1.00	73.32
MOTA	5027	CB	TYR	654	46.276	20.750	10.972	1.00	71.97
MOTA	5028	CG	TYR	654	45.259	21.276	11.954	1.00	70.94
ATOM	5029	CD1	TYR	654	45.659	21.801	13.185	1.00	71.41
ATOM	5030	CE1	TYR	654	44.733	22.234	14.121	1.00	73.60
MOTA	5031	CD2	TYR	654	43.899	21.206	11.680	1.00	71.81
MOTA	5032	CE2	TYR	654	42.956	21.642	12.610	1.00	74.81
ATOM	5033	CZ	TYR	654	43.380	22.152	13.832	1.00	74.84
MOTA	5034	OH	TYR	654	42.457	22.571	14.769	1.00	76.60
MOTA	5036	C	TYR	654	47.975	18.967	10.446	1.00	73.82
ATOM	5037	0	TYR	654	47.545	18.671	9.329	1.00	74.25
MOTA	5038	N	LYS	655	49.249	18.806	10.784	1.00	74.04
MOTA	5040	CA	LYS	655	50.195	18.256	9.827	1.00	75.41
MOTA	5041	CB	LYS	655	51.626	18.680	10.164	1.00	78.45
MOTA	5042	CG	LYS	655	52.647	18.198	9.151	1.00	83.01
MOTA	5043	CD	LYS	655	54.062	18.589	9.537	1.00	87.72
MOTA	5044	CE	LYS	655	55.076	17.813	8.703	1.00	91.45
ATOM	5045	NZ	LYS	655	56.489	18.133	9.074	1.00	94.17
ATOM	5049	C	LYS	655	50.075	16.736	9.832	1.00	75.50
ATOM	5050	0	LYS	655	50.245	16.092	10.872	1.00	75.90
ATOM	5051	N	LYS	656	49.750	16.173	8.672	1.00	75.26
ATOM	5053	CA	LYS	656	49.597	14.730	8.533	1.00	74.97
ATOM	5054	CB	LYS	656	48.723	14.406	7.323	1.00	75.40
ATOM	5055	CG	LYS	656	47.266	14.753	7.519	1.00	76.87
ATOM	5056	CD	LYS	656	46.489	14.535	6.239	1.00	80.75
MOTA	5057	CE	LYS	656	45.001	14.655	6.483		83.60
ATOM	5058	NZ	LYS	656	44.236	14.637	5.204	1.00	87.14
ATOM	5062	C	LYS	656	50.939	14.016	8.414	1.00	74.58
ATOM	5063	0	LYS	656	51.904	14.578	7.897	1.00	75.01
ATOM	5064	N	GLY	660	49.137	9.764	5.736	1.00	59.18
ATOM	5066	CA	GLY	660	48.106	10.781	5.848	1.00	56.19
ATOM	5067	C	GLY	660	47.407	10.761	7.192	1.00	55.31
ATOM	5068	0	GLY	660	46.289 48.059	11.263	7.328	1.00	56.96
ATOM	5069	N CA	ARG	661		10.163	8.183	1.00	53.02
ATOM	5071	CA	ARG	661	47.493	10.083	9.527	1.00	49.80
ATOM	5072	CB	ARG	661	47.944	8.799	10.229	1.00	51.79 50.59
ATOM	5073 5074	CG	ARG	661	47.683	7.523	9.450	1.00	
ATOM		CD	ARG	661	47.822	6.323	10.367	1.00	53.68
ATOM ATOM	5075 5077	NE CZ	ARG ARG	661 661	47.714 47.928	5.044 3.863	9.665 10.236	1.00 1.00	52.66 51.73
ATOM	5077	NH1	ARG	661	48.264	3.863	10.236	1.00	50.23
ATOM	5078	NH1	ARG	661	47.800	2.751	9.528	1.00	52.58
ATOM	5081	C	ARG	661	47.800	11.297	10.346	1.00	44.80
ATOM	5085	0	ARG	661	48.865	11.297	9.986	1.00	43.61
AION	2003	_	-M/G	00 T	-U.00J	xx. //	٥٠,١٥٥	±. 00	

							_	.02					
	ATOM	5086	N	LEU	662								
	MOTA	5088	CA	LEU	662				. 528	11.4	53	1.00	40 5.
	MOTA	5089	CB	LEU				12.	654	12.3		1.00	40.74
	ATOM	5090	CG	LEU	662			13.	415	12.6		1.00	37.88
	ATOM	5091	CD1	LEU	662	-5.,	515		074	11.4			36.19
	ATOM	5092	CD2	LEU	662	(045		278	11.83		1.00	35.32
ž	ATOM	5093	C	LEU	662	46.2	217		383	11.15		1.00	31.05
7	MOTA	5094	0		662	48.1		12.		13.62	_	1.00	34.37
Į		5095	N	LEU	662	47.5		11.		14.41		1.00	35.34
		5096	CD	PRO	663	49.4	41	12.				.00	33.06
		5097		PRO	663	50.3	75	13.1		13.84		.00	36.39
	`	5098	CA	PRO	663	50.1	58	12.1		12.86	8 1	.00	37.57
	_			PRO	663	51.5	16	12.7		15.05		.00	36.39
				PRO	663	51.72	28			14.88		.00	36.98
				PRO	663	49.47		12.6		13.40		.00	38.48
				PRO	663	49.69		12.4		16.37	1	.00	35.47
			N 7		664	48.64		11.8	41 1	7.392		.00	35.08
			CA v		664			13.5		6.362		.00	34.28
			CB /		564	47.95	т.	13.9	31 1	7.583			
	OM 5	106 c	·		664	47.03	8	15.18	31 1	7.376			34.43
		L07 C			64	47.88	5	16.40		7.160			36.92
AT	OM 51	L08 C			64	46.09	1	14.98		6.186	1.		37.55
AT	OM 51	.09 0		-	64	47.13	7	12.74		3.120			38.28
AT		10 N		-		46.908		12.64		3.318	1.		33.03
AT			_	-	65 65	46.803	3	11.80		7.236	1.	-	34.62
ATO	OM 51		_		65	46.040)	10.63		.614	1.0		32.47
ATO	OM 51	-			65	45.456	5	9.95		.370	1.(30.71
ATC				-	65	44.324		10.77		.3/0	1.0		9.59
ATO					55	43.927		10.334		.768	1.0		9.64
ATO						42.664		11.056		.367	1.0		1.86
ATO					55	42.296		10.720		.899	1.0	0 3	0.42
ATO		_	LY		5	46.801	•	9.644		.486	1.0	0 2	6.50
ATO			LY		5	46.230				498	1.0		2.23
ATO		_	TR	P 66	6	48.080		8.659		955	1.0		0.04
ATO			TR	P 66	6	48.886		9.915		748	1.0		1.38
ATO	_		TR	66	6	50.204		9.068		619	1.00	_	3.32
ATOM	_		TRI	66	5	50.078		8.682		945	1.00		.07
			TRI			49.531		7.530		006	1.00		.26
ATOM			TRE			49.630		7.559	16.	684	1.00		.07
ATOM			TRE			49.030		5.257	16.		1.00		.71
ATOM			TRP	666		48.982		3.569	15.8		1.00		.56
ATOM		NE1	TRP			50.473		5.238	18.2		1.00	-	. 97
ATOM	5134	CZ2	TRP	666		50.206		.469	17.1		1.00		.9/
ATOM	5135	CZ3	TRP	666		49.190	5	.929	14.8		1.00	27.	. 38
ATOM	5136		TRP	666		48.548	8	.248	14.5		1.00	27.	. 22
ATOM	5137	С	TRP			48.658		. 934	14.1			30.	14
ATOM	5138	0	TRP	666		49.203		.802	20.9		.00	26.	
ATOM	5139	N		666		49.688	9	.202	21.8		.00	33.	84
ATOM	5141	CA	MET	667	4	48.905	11	.099	20.9		.00	32.	82
ATOM	5142	CB	MET	667	4	19.180	11	960		_	.00	35.	
ATOM	5143		MET	667		9.150	13	423	22.06		.00	37.	
ATOM	5143	CG	MET	667	5	0.487	13.	975	21.64		.00	41.9	
ATOM		SD	MET	667	5	0.384			21.22		.00	48.4	
ATOM	5145	CE	MET	667	5	0.711	15.	728	20.91		.00	55.3	
	5146	C	MET	667		8.294	75.	745	19.18	3 1.	.00	49.2	
ATOM	5147	0	MET	667		7.066	11.		23.28	9 1.	00	38.9	
ATOM	5148	N	ALA	668	-± ∕1 :	_	11.	699	23.18	31.	00	39.1	
CCC- '-				_	-4	0.733	11.	824	24.45	_	00	38.7	
SSSD/55	145. v01									•		50.7	4

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37.82 1.00 25.727 11.728 48.231 38.49 668 1.00 ALA 26.857 CA 5150 11.527 MOTA 49.224 38.16 668 1.00 25.891 ALA CB 5151 13.051 MOTA 47.497 37.21 668 1.00 ALA 25.363 С 5152 14.072 MOTA 47.937 39.78 668 1.00 ALA 26.644 0 MOTA 5153 13.062 46.383 40.08 669 1.00 PRO 27.367 N 5154 11.931 MOTA 45.785 1.00 40.68 669 PRO 26.858 CD 5155 14.281 MOTA 45.598 669 1.00 42.15 PRO 27.782 CA 5156 13.806 MOTA 44.474 42.56 669 1.00 PRO 27.446 CB 5157 12.352 MOTA 44.346 42.69 669 1.00 PRO CG 27.484 5158 15.432 MOTA 46.398 42.14 669 1.00 PRO С 27.019 5159 16.566 MOTA 46.320 669 1.00 43.21 PRO 0 28.532 5160 15.153 MOTA 47.168 670 44.62 1.00 GLU 29.160 N 5161 16.211 MOTA 47.956 44.95 670 GLU 30.429 1.00 CA 5163 15.719 MOTA 48.651 45.54 670 1.00 GLU 30.197 CB 14.782 5164 MOTA 49.824 42.72 GLU 670 1.00 30.079 CG 5165 13.332 MOTA 49.422 41.43 670 GLU 1.00 30.066 CD 5166 12.481 MOTA 50.332 44.44 670 1.00 GLU 30.015 OE1 5167 13.036 MOTA 48.212 670 44.88 1.00 GLU 28.195 OE2 5168 16.772 MOTA 48.993 45.08 670 1.00 GLU 28.194 С 5169 17.968 MOTA 49.248 44.75 670 1.00 GLU 27.358 5170 0 15.908 MOTA 49.565 45.92 671 1.00 ALA26.392 N 5171 MOTA 16.323 50.573 44.10 671 1.00 ALA25.766 CA 5173 15.095 MOTA 51.256 47.96 671 1.00 ALA 25.314 CB 5174 17.193 MOTA 49.944 671 49.16 1.00 ALA 24.894 С 18.192 5175 MOTA 50.526 49.84 671 24.917 1.00 ALA 0 5176 16.836 MOTA 48.729 50.74 672 1.00 LEU 23.881 5177 17.554 MOTA 47.989 53.20 672 1.00 LEU 23.289 CA 5179 16.619 MOTA 46.926 55.26 672 1.00 LEU 22.004 CB 5180 16.989 MOTA 46.184 672 57.12 1.00 LEU 20.856 5181 CG 17.155 MOTA 47.153 1.00 672 52.86 LEU 21.680 5182 CD1 15.895 45.203 MOTA 672 1.00 50.79 LEU 24.408 CD2 5183 18.826 MOTA 47.327 50.95 672 1.00 LEU 23.736 С 5184 19.855 MOTA 47.302 52.07 672 1.00 LEU 25.618 0 5185 18.751 MOTA 46.792 54.39 673 1.00 PHE 26.226 N 5186 19.884 MOTA 46.111 51.21 673 1.00 PHE 27.019 CA 5188 19.396 MOTA 44.892 1.00 48.49 673 PHE 26.186 CB 5189 18.656 MOTA 43.871 673 47.79 26.646 1.00 PHE CG 5190 17.473 MOTA 43.304 49.04 673 PHE 1.00 5191 CD1 24.949 19.149 MOTA 43.470 47.90 PHE 673 1.00 5192 CD2 25.888 16.789 MOTA 42.349 673 1.00 49.71 PHE CE1 24.182 5193 18.473 MOTA 42.511 46.86 673 1.00 PHE 24.655 CE2 5194 17.288 MOTA 41.952 673 1.00 58.25 PHE 27.123 CZ5195 20.741 MOTA 47.007 673 60.52 1.00 PHE 27.034 С 21.971 5196 MOTA 47.000 673 59.63 1.00 PHE 27.983 5197 0 20.094 MOTA 47.784 62.11 ASP 674 1.00 28.905 5198 N 20.815 MOTA 48.652 63.81 674 ASP 1.00 30.307 CA 5200 20.196 MOTA 48.568 66.46 674 1.00 ASP 30.791 CB 5201 20.015 MOTA 47.143 66.70 674 ASP 31.247 1.00 5202 CG 18.901 MOTA 46.815 68.77 674 ASP 1.00 30.722 OD1 5203 20.981 MOTA 46.354 63.36 674 ASP 1.00 28.482 OD2 5204 20.852 MOTA 50.119 64.11 674 1.00 ASP 29.310 C 21.175 5205 MOTA 50.979 62.94 674 1.00 ASP 27.228 0 5206 20.486 MOTA 50.410 60.75 675 1.00 ARG 26.706 5207 N 20.456 MOTA 51.789 675 ARG 5209 CA MOTA

							-01				
	MOTA	5210	CB	ARG	675		~-				
	MOTA	5211	CG	ARG	675	52.2		1.874	26.360		60.56
	MOTA	5212	CD	ARG	675	51.4 51.9		2.560	25.261	1.00	63.67
		5213	NE	ARG	675	53.3		3.970	24.964		66.99
		5215	CZ	ARG	675	54.06		980	24.337	1.00	69.34
		5216	NH1	ARG	675	53.63		.068	24.173	1.00	68.48
		5219	NH2	ARG	675	55.25		.254	24.590	1.00	65.81
		5222	C	ARG	675	52.75		.965	23.593	1.00	68.76
		5223 5224	0		675	53.93			27.700	1.00	58.06
		226	N		676	52.22			27.766	1.00	59.30
			CA		676	52.99			28.483	1.00	55.62
			~		576	52.15			29.489	1.00	54.09
					576	52.749			30.765	1.00	52.69
			~		76	52.049	19.		31.629 31.540	1.00	49.38
AT					76	51.306	19.		32.845	1.00	53.15
AT		.			76	53.468	16.		8.953	1.00	57.79
AT	OM 52	233 1			76	52.668	15.		8.730	1.00	53.83
ATO					77	54.773	16.6		8.745	1.00	54.87
ATO		_			77 77	55.343	15.4		8.236	1.00 1.00	51.76
ATO					, , 77	56.232	15.7	722 2	7.031	_	49.42
ATC				YR 6		55.466	16.1	.81 25	~ ~ ~ -		51.33 56.22
ATO			E1 T	YR 67		55.158	17.5	29 25			56.22 56.12
ATO	_		D2 T	YR 67		54.491 55.078	17.9	60 24	1.479	_	56.18
ATO ATO				(R 67		54.411	15.2		823		88.13
ATO				R 67	7	54.125	15.6		.679		7.65
ATO			f TY	TR 67	7	53.504	17.0		.512		8.23
ATON		-	TY		7	56.136	17.45 14.73			.00 6	1.71
ATOM			TY			56.983	15.33			00 4	6.46
ATOM			TH			55.818	13.46			.00 4	8.65
ATOM						56.498	12.66				1.73
ATOM			THI 1 THI	_		55.680	12.59				9.83
MOTA				, •		54.462	11.86				L.78
ATOM			THE			55.342	13.98				5.77
ATOM		_	THE			56.661	11.24	2 30.	~		.84
ATOM	5256		HIS			56.258	10.91	7 28.			.46 .51
ATOM	5258		HIS			57.264	10.388	30.			.36
ATOM	5259		HIS			57.423 58.348	9.003		457 1.		.91
ATOM	5260	_	HIS	679		59.761	8.294		139 1.		. 05
ATOM ATOM	5261	CD2	HIS	679	ě	50.453	8.798	-	104 1.		. 68
ATOM	5262 5264		HIS	679	6	0.632	9.569		278 1.	00 37.	89
ATOM	5264 5265	CE1	HIS	679	6	1.803	8.507 9.071			00 37.	49
ATOM	5267	NE2	HIS	679	6	1.721	9.722	30.6		00 39.	
ATOM	5268	C	HIS	679	5	6.032	8.376	31.7		00 39.	81
ATOM	5269	O N	HIS	679		5.771	7.458	30.4		0 36.	76
ATOM	5271	CA	GLN	680	5.	5.126	8.908	29.66			16
ATOM	5272	CB	GLN	680	5.	3.754	8.407	31.26 31.33			
ATOM	5273	CG	GLN GLN	680	53	3.069	8.815	32.64			
ATOM	5274	CD	GLN	680	53	3.645	8.128	33.88		-	
ATOM	5275	OE1	GLN	680	53	3.676	6.595	33.78	_		
	5276	NE2	GLN	680 680	52	.669	5.925	33.99			
MOTA	5279	C	GLN	680 680	54	.846	6.043	33.46	4 1.00		
				500	52	.927	8.842	30.12			
SSD/551	4501								4.00	37.5	4

185

MOTA	5280	0	GLN	680	51.950	8.185	29.765	1.00	37.93
ATOM	5281	N	SER	681	53.282	9.961	29.504	1.00	36.38
MOTA	5283	CA	SER	681	52.563	10.367	28.306	1.00	38.05
ATOM	5284	CB	SER	681	52.857	11.819	27.940	1.00	41.41
MOTA	5285	OG	SER	681	54.239	12.069	27.938	1.00	42.92
MOTA	5287	C	SER	681	52.991	9.421	27.178	1.00	37.92
ATOM	5288	0	SER	681	52.205	9.148	26.263	1.00	37.21
ATOM	5289	N	ASP	682	54.237	8.932	27.248	1.00	34.77
MOTA	5291	CA	ASP	682	54.750	7.972	26.267	1.00	31.99
MOTA	5292	CB	ASP	682	56.243	7.683	26.481	1.00	31.08
ATOM	5293	CG	ASP	682	57.165	8.638	25.721	1.00	33.63
ATOM	5294	OD1	ASP	682	58.386	8.503	25.920	1.00	32.35
ATOM	5295	OD2	ASP	682	56.707	9.500	24.930	1.00	29.46
MOTA	5296	C	ASP	682	53.969	6.672	26.457	1.00	31.54
MOTA	5297	0	ASP	682	53.675	5.971	25.493	1.00	29.94
MOTA	5298	N	VAL	683	53.677	6.334	27.712	1.00	30.48
MOTA	5300	CA	VAL	683	52.913	5.126	28.023	1.00	32.94
MOTA	5301	CB	VAL	683	52.731	4.939	29.572	1.00	33.94
MOTA	5302	CG1	VAL	683	51.635	3.905	29.872	1.00	32.71
MOTA	5303	CG2	VAL	683	54.042	4.474	30.209	1.00	27.41
MOTA	5304	C	VAL	683	51.545	5.164	27.299	1.00	32.27
MOTA	5305	0	VAL	683	51.106	4.158	26.733	1.00	30.54
MOTA	5306	N	TRP	684	50.902	6.332	27.282	1.00	32.57
MOTA	5308	CA	TRP	684	49.616	6.477	26.600	1.00	32.76
MOTA	5309	CB	TRP	684	49.060	7.895	26.765	1.00	33.67
MOTA	5310	CG	TRP	684	47.855	8.210	25.891	1.00	38.22
ATOM	5311	CD2	TRP	684	46.503	8.435	26.328	1.00	39.96
MOTA	5312	CE2	TRP	684	45.734	8.735	25.177	1.00	39.59
MOTA	5313	CE3	TRP	684	45.869	8.416	27.578	1.00	39.26
MOTA	5314	CD1	TRP	684	47.842	8.373	24.528	1.00	39.02
ATOM	5315	NE1	TRP	684	46.576	8.687	24.096	1.00	38.42
ATOM	5317	CZ2	TRP	684	44.362	9.011	25.240	1.00	36.62
ATOM	5318	CZ3	TRP	684	44.502	8.691	27.641	1.00	40.70
MOTA	5319	CH2	TRP	684	43.766	8.982	26.475	1.00	40.57
MOTA	5320	С	TRP	684	49.819	6.158	25.125	1.00	31.98
ATOM	5321	0	TRP	684	49.066	5.367	24.557	1.00	32.43
MOTA	5322	N	SER	685	50.859	6.748	24.529	1.00	29.63
MOTA	5324	CA	SER	685	51.195	6.531	23.119	1.00	28.62
MOTA	5325	CB	SER	685	52.457	7.296	22.751	1.00	24.72
MOTA	5326	OG	SER	685	52.323	8.664	23.072	1.00	30.04
MOTA	5328	С	SER	685	51.414	5.055	22.825	1.00	27.91
ATOM	5329	0	SER	685	51.022	4.555	21.767	1.00	28.60
MOTA	5330	N	PHE	686	52.063	4.372	23.763	1.00	27.96
ATOM	5332	CA	PHE	686	52.333	2.947	23.662	1.00	27.03
MOTA	5333	CB	PHE	686	53.163	2.499	24.868	1.00	25.79
ATOM	5334	CG	PHE	686	53.440	1.029	24.890	1.00	26.25
MOTA	5335	CD1	PHE	686	54.252	0.451	23.923	1.00	27.32
MOTA	5336	CD2	PHE	686	52.839	0.208	25.841	1.00	26.22
ATOM	5337	CE1	PHE	686	54.464	-0.930	23.900	1.00	25.87
ATOM	5338	CE2	PHE	686	53.046	-1.170	25.828	1.00	24.37
MOTA	5339	CZ	PHE	686	53.856	-1.740	24.854	1.00	26.42
ATOM	5340	C	PHE	686	51.003	2.160	23.596	1.00	28.82
MOTA	5341	0	PHE	686	50.912	1.129	22.914	1.00	26.74
MOTA	5342	N	GLY	687	49.991	2.636	24.324	1.00	29.52



							т.	00				
		5344	CA	GLY	687							
7	ATOM	5345	C	GLY	687	10.0			982 24	.302	1.00	י איז ריי
Į	MOTA	5346	0	GLY		0		2.		.896	1.00	,
7	MOTA	5347	N	VAL	687	47.4		1.0		.414	1.00	
<i>2</i> 4		5349	CA		688	48.2		3.:		.238		
A		5350		VAL	688	47.7	77			.879	1.00	00
		5351		VAL	688	47.8	00	4.8		.424	1.00	
		352		VAL	688	47.2	11	4.9		.020	1.00	27.24
	marr	353		VAL	688	46.99	90	5.6			1.00	28.29
			_	VAL	688	48.61		2.4		404	1.00	26.96
		354		VAL	688	48.08		1.8		951	1.00	28.49
				LEU	689	49.90)5			024	1.00	28.84
	-		CA]	EU	689	50.80		2.3		252	1.00	27.99
			CB I	ĿΕŪ	689	52.26	0	1.5		461	1.00	26.14
			CG I	ΈU	689	53.36		1.6			1.00	27.31
		360 (CD1 I	ŒU	689			1.0			1.00	26.60
		361 (CD2 L	EU	689	54.68		1.76		175	1.00	28.19
AT	OM 53	62 (_		689	53.56		-0.40)1 19.		1.00	25.55
AT	OM 53	63 (689	50.362		0.05	3 19.6		1.00	
AT	OM 53	64 N	_		690	50.37		-0.68	6 18.6		1.00	26.48
ATO	OM 53		_			49.953		-0.34	4 20.8		1.00	27.06
AT(67 C			690	49.465		-1.70			1.00	28.55
ATO		_			590	49.070)	-1.88			1.00	29.16
ATC	OM 53			-	590	50.114		-2.08				31.40
ATC					590	49.427		-2.02			1.00	31.49
ATC					590	50.821		-3.41			1.00	34.09
ATO			LE		90	48.240		-1.958			1.00	30.84
ATO			LE	_	90	48.088		-3.023	_		1.00	26.51
ATO	,		TR	_	91	47.376		0.954				25.15
ATO				P 6	91	46.169		1.049			1.00	28.51
ATO		_		P 6	91	45.332						29.56
				P 6	91	43.992		0.227				28.91
ATO				P 6:	91	43.718		0.169	-			30.95
ATON			2 TRI		91	42.337		0.556	17.40			29.87
ATOM			3 TRI			44.505		0.367	17.18			31.97
ATOM		L CD:	1 TRE					1.049	16.35			7.72
ATOM		NE:	L TRE			42.796		0.231	19.29			0.68
ATOM		CZ2				41.797		0.111	18.35			3.68
ATOM		CZ3				41.729	(0.652	15.96	_		9.42
ATOM						43.906	ב	327	15.154			
ATOM			TRP	69		42.523	1	.129	14.969	•		7.13
MOTA	5388	0	TRP			46.564	- 1	.289	17.856		-	9.18
ATOM	5389		GLU			45.996		.156	17.194			3.78
ATOM		CA		69:		47.564	-0	.543	17.380		_	7.64
ATOM	5392	CB	GLU	692		48.078	-0	.669	16.018			9.83
ATOM	5393	CG	GLU	692		49.267		.262	15.790			3.08
ATOM	5394		GLU	692		48.945		. 735	15.680			.40
ATOM	5395	CD	GLU	692	;	50.183		.561		1.		.45
ATOM		OE1	GLU	692	'	50.938		886	15.369	1.0		.47
ATOM	5396	OE2	GLU	692	!	50.413			16.320	1.0		.66
	5397	С	GLΰ	692		18.563		875	14.182	1.0		. 44
ATOM	5398	0	GLU	692		18.385		082	15.761	1.0		.07
ATOM	5399	N	ILE	693		9.244		612	14.665	1.0		.18
ATOM	5401	CA	ILE	693				663	16.746	1.0		
ATOM	5402	CB	ILE	693		9.754		024	16.608	1.0		
MOTA	5403	CG2	ILE	693		0.632	-4.	443	17.828	1.0		
ATOM	5404	CG1	ILE	693		1.037	-5.	907	17.706	1.0		
				0 3 3	5	1.907	-3.		17.890	1.0		
SSSD/55	145 001								·	4.0	0 26.	99

ATOM	5405	CD1	ILE	693	52.663	-3.747	19.194	1.00	25.37
ATOM	5406	C	ILE	693	48.603	-5.023	16.452	1.00	29.21
MOTA	5407	0	ILE	693	48.568	-5.807	15.512	1.00	27.89
ATOM	5408	N	PHE	694	47.623	-4.942	17.336	1.00	31.33
ATOM	5410	CA	PHE	694	46.523	-5.888	17.279	1.00	34.41
ATOM	5411	CB	PHE	694	45.958	-6.114	18.687	1.00	35.37
ATOM	5412	CG	PHE	694	46.978	-6.717	19.621	1.00	35.60
		CD1	PHE	694	47.606	-5.942	20.586	1.00	37.23
ATOM	5413								
ATOM	5414	CD2	PHE	694	47.424	-8.024	19.426	1.00	35.59
ATOM	5415	CE1	PHE	694	48.669	-6.460	21.333	1.00	36.39
ATOM	5416	CE2	PHE	694	48.484	-8.546	20.170	1.00	35.34
MOTA	5417	CZ	PHE	694	49.110	-7.762	21.118	1.00	35.71
MOTA	5418	C	PHE	694	45.481	-5.715	16.176	1.00	34.41
MOTA	5419	0	PHE	694	44.623	-6.579	15.982	1.00	34.48
MOTA	5420	N	THR	695	45.617	-4.637	15.404	1.00	33.03
MOTA	5422	CA	THR	695	44.742	-4.379	14.263	1.00	31.81
MOTA	5423	CB	THR	695	44.113	-2.957	14.278	1.00	29.75
MOTA	5424	OG1	THR	695	45.142	-1.961	14.218	1.00	30.72
MOTA	5426	CG2	THR	695	43.254	-2.759	15.524	1.00	29.40
MOTA	5427	C	·THR	695	45.596	-4.533	13.011	1.00	31.44
ATOM	5428	0	THR	695	45.153	-4.241	11.906	1.00	33.00
MOTA	5429	N	LEU	696	46.832	-4.987	13.209	1.00	31.24
ATOM	5431	CA	LEU	696	47.799	-5.199	12.134	1.00	31.36
ATOM	5432	СВ	LEU	696	47.421	-6.418	11.291	1.00	33.53
ATOM	5433	CG	LEU	696	47.270	-7.741	12.042	1.00	33.00
ATOM	5434	CD1	LEU	696	47.010	-8.838	11.052	1.00	35.50
ATOM	5435	CD2	LEU	696	48.515	-8.061	12.830	1.00	36.09
ATOM	5436	C	LEU	696	48.066	-3.976	11.249	1.00	30.84
ATOM	5437	0	LEU	696	48.135	-4.067	10.024	1.00	28.23
ATOM	5438	N	GLY	697	48.302	-2.839	11.890	1.00	31.54
ATOM	5440	CA	GLY	697	48.591	-1.632	11.141	1.00	33.87
ATOM	5441	C	GLY	697	47.375	-0.765	10.924	1.00	32.77
ATOM	5442	0	GLY	697	47.322	0.042	9.994	1.00	33.90
ATOM	5443	N	GLY	698	46.392	-0.921	11.797	1.00	33.29
ATOM	5445	CA	GLY	698	45.187	-0.122	11.681	1.00	32.66
		C	GLY	698	45.408	1.368	11.877	1.00	30.57
ATOM	5446								27.36
ATOM	5447	0	GLY	698	46.336	1.803	12.553 11.285	1.00	30.92
ATOM	5448	N	SER	699	44.517	2.148		1.00	
MOTA	5450	CA	SER	699	44.552	3.595	11.376	1.00	32.19
MOTA	5451	СВ	SER	699	44.062	4.202	10.058	1.00	34.24
MOTA	5452	OG	SER	699	44.019	5.616	10.123	1.00	38.67
MOTA	5454	С	SER	699	43.644	4.014	12.538	1.00	31.81
MOTA	5455	0	SER	699	42.431	3.759	12.525	1.00	31.39
ATOM	5456	N	PRO	700	44.228	4.597	13.594	1.00	31.82
MOTA	5457	CD	PRO	700	45.645	4.842	13.919	1.00	28.82
MOTA	5458	CA	PRO	700	43.353	4.992	14.697	1.00	31.31
MOTA	5459	CB	PRO	700	44.345	5.341	15.809	1.00	31.31
ATOM	5460	CG	PRO	700	45.552	5.800	15.061	1.00	30.41
MOTA	5461	C	PRO	700	42.484	6.170	14.295	1.00	31.19
ATOM	5462	0	PRO	700	42.899	7.021	13.510	1.00	29.93
ATOM	5463	N	TYR	701	41.235	6.144	14.736	1.00	32.69
ATOM	5465	CA	TYR	701	40.291	7.223	14.445	1.00	32.54
ATOM	5466	CB	TYR	701	40.650	8.416	15.323	1.00	34.47
MOTA	5467	CG	TYR	701	40.512	8.141	16.794	1.00	39.16
	5-0,			-					·

A	TOM 5	468	CD1	mvr.						
		469	CE1	TYR				433 17.	683 ₁	.00 44.31
		470	CD2	TYR		5		241 19.		
		471		TYR	701		21 7.	642 17.		
		472		TYR	701	95.1	47 7.	447 18.		
		473		TYR	701	-0.10	54 7.	750 19.		.00 45.05
				TYR	701	٠,٠,٠	19 7.5	590 20.		.00 47.24
			_	TYR	701	-0.21	.5 7.6	555 12.9		00 52.18
				TYR	701	40.37	'9 8.8			00 30.56
		`		PRO	702	39.92	8 6.7			00 29.73
AT				PRO	702	39.65	9 5.2			00 30.38
AT				PRO	702	39.84	7 7.0			00 30.22
ATO		_ '		PRO	702	39.69	3 5.7			
ATO			_	RO	702	39.00	7 4.8			43.03
ATO		_		RO	702	38.72	2 8.0		• •	
ATO			_	RO	702	37.55	7 7.8		~ ~	
ATC				LY	703	39.100	9.1			50
ATC		_		LY	703	38.154	10.13		_	· · · - -
ATO			•	LY	703	37.893	11.16			
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ATO			- · ·	AL	704	38.579				_
ATO				A L	704	38.416	11.95			
ATO		_			704	38.582				
ATO			31 V.		704	38.522	12.19			
ATO		_			704	37.506	10.14			
ATON			VA		704	39.430	13.08			
ATON			VA		704	40.634	12.86			· · · =
ATOM			PR	_	705	38.957	14.30			
ATOM					705	37.594	14.692			
ATOM					705	39.875	15.443			
ATOM					705	39.053	16.495			
ATOM					705	37.647	16.187			
ATOM			PRO		705	40.280	15.879			
ATOM		-	PRO		05	39.651	15.490			
ATOM			VAI		06	41.322	16.697			
ATOM		-	VAL		06	41.852	17.176			1 0
ATOM	5508		VAL		06	42.923	18.261			
ATOM	5509	CG1			06	43.577	18.618	16.017		39.01
ATOM	5510	CG2			06	43.961	17.786	13.673	1.00 1.00	40.33
ATOM	5511	0	VAL		06	40.826	17.716	15.895	1.00	38.61
ATOM	5512	N	VAL		06	40.823	17.319	17.065	1.00	35.65
ATOM	5514	CA	GLU		07	39.955	18.605	15.426	1.00	33.55
ATOM	5515	CB	GLU		7	38.941	19.220	16.278	1.00	36.74
ATOM	5516	C	GLU	70		38.129	20.242	15.482	1.00	37.20
ATOM	5517		GLU	70		38.014	18.188	16.900		38.98
ATOM	5518	0	GLU	70		37.634	18.295	18.074	1.00	38.46
ATOM	5520	N	GLU	70		37.681	17.170	16.115	1.00	39.04
ATOM	5521	CA	GLU	70		36.802	16.105	16.571	1.00	37.81
ATOM	5522	CB	GLU	70		36.316	15.289	15.378	1.00	37.70
ATOM		CG	GLU	70		35.459	16.091	14.413	1.00	40.73
ATOM	5523 5524	CD	GLU	70		34.235	16.677	15.084	1.00	43.44
ATOM	5524 5525	OE1	GLU	70		33.629	16.007	15.084	1.00	51.52
ATOM	5525	OE2	GLU	708	3	33.882	17.824	14.732	1.00	50.14
ATOM	5526 5527	C	GLU	708		37.506	15.223	17.588	1.00	59.46
	5527	0	GLU	708	3	36.897	14.782	18.567	1.00	36.53
SSSD/55	145. v01							±0.36/	1.00	36.80

ATOM	5528	N	LEU	709	38.799	14.993	17.376	1.00	35.69
MOTA	5530	CA	LEU	709	39.584	14.179	18.301	1.00	35.48
MOTA	5531	CB	LEU	709	41.039	14.044	17.830	1.00	34.84
ATOM	5532	CG	LEU	709	41.921	13.250	18.802	1.00	32.41
MOTA	5533	CD1	LEU	709	41.608	11.787	18.674	1.00	30.10
MOTA	5534	CD2	LEU	709	43.378	13.514	18.560	1.00	29.93
ATOM	5535	C	LEU	709	39.568	14.842	19.673	1.00	35.58
ATOM	5536	0	LEU	709	39.377	14.177	20.694	1.00	35.43
MOTA	5537	N	PHE	710	39.792	16.150	19.686	1.00	36.79
MOTA	5539	CA	PHE	710	39.800	16.918	20.927	1.00	40.58
ATOM	5540	CB	PHE	710	39.944	18.413	20.637	1.00	42.55
MOTA	5541	CG	PHE	710	41.308	18.808	20.162	1.00	46.38
ATOM	5542	CD1	PHE	710	42.392	17.942	20.313	1.00	47.29
MOTA	5543	CD2	PHE	710	41.515	20.050	19.580	1.00	47.93
ATOM	5544	CEl	PHE	710	43.659	18.312	19.892	1.00	51.21
ATOM	5545	CE2	PHE	710	42.781	20.435	19.155	1.00	50.89
ATOM	5546	CZ	PHE	710	43.859	19.562	19.312	1.00	53.31
ATOM	5547	C	PHE	710	38.517	16.676	21.694	1.00	40.14
ATOM	5548	0	PHE	710	38.543	16.446	22.898	1.00	39.86
MOTA	5549	N	LYS	711	37.399	16.705	20.977	1.00	41.02
MOTA	5551	CA	LYS	711	36.101	16.479	21.584	1.00	38.66
MOTA	5552	CB	LYS	711	34.985	16.803	20.580	1.00	40.75
MOTA	5553	CG	LYS	711	33.601	16.727	21.181	1.00	46.99
MOTA	5554	CD	LYS	711	32.522	17.174	20.218	1.00	50.71
ATOM	5555	CE	LYS	711	31.163	16.733	20.739	1.00	52.53
MOTA	5556	NZ	LYS	711	30.041	17.194	19.884	1.00	57.76
MOTA	5560	C	LYS	711	35.990	15.046	22.120	1.00	38.06
MOTA	5561	0	LYS	711	35.535	14.831	23.250	1.00	36.29
MOTA	5562	N	LEU	712	36.431	14.066	21.330	1.00	38.10
MOTA	5564	CA	LEU	712	36.392	12.662	21.764	1.00	38.69
MOTA	5565	CB	LEU	712	36.914	11.714	20.672	1.00	37.19
ATOM	5566	CG	LEU	712	36.070	11.436	19.424	1.00	34.73
MOTA	5567	CD1	LEU	712	36.814	10.453	18.524	1.00	35.54
MOTA	5568	CD2	LEU	712	34.709	10.872	19.818	1.00	30.90
MOTA	5569	С	LEU	712	37.230	12.472	23.021	1.00	39.62
ATOM	5570	0	LEU	712	36.843	11.745	23.940	1.00	39.44
MOTA	5571	N	LEU	713	38.398	13.101	23.044	1.00	40.10
ATOM	5573	CA	LEU	713	39.279	12.999	24.199	1.00	42.81
ATOM	5574	CB	LEU	713	40.606	13.716	23.924	1.00	41.70
ATOM	5575	CG	LEU	713	41.495	13.040	22.868	1.00	41.86
MOTA	5576	CD1	LEU	713	42.742	13.862	22.607	1.00	37.19
ATOM	5577	CD2	LEU	713	41.873	11.647	23.340	1.00	41.17
MOTA	5578	С	LEU	713	38.577	13.566	25.437	1.00	43.18
MOTA	5579	0	LEU	713	38.479	12.889	26.457	1.00	44.79
MOTA	5580	N	LYS	714	38.004	14.760	25.312	1.00	42.75
MOTA	5582	CA	LYS	714	37.301	15.389	26.425	1.00	43.70
MOTA	5583	CB	LYS	714	36.842	16.796	26.043	1.00	44.69
MOTA	5584	CG	LYS	714	38.001	17.746	25.836	1.00	47.92
MOTA	5585	CD	LYS	714	37.543	19.171	25.583	1.00	55.01
ATOM	5586	CE	LYS	714	38.733	20.077	25.238	1.00	59.44
MOTA	5587	NZ	LYS	714	39.773	20.132	26.320	1.00	60.10
MOTA	5591	C	LYS	714	36.127	14.557	26.940	1.00	43.94
MOTA	5592	0	LYS	714	35.843	14.551	28.140	1.00	44.20
MOTA	5593	N	GLU	715	35.477	13.819	26.046	1.00	43.29

	MOTA	5595	CA	GLU	715	24.3	50				
		5596	CB	GLΰ	715		_		26.435	1.00	42.29
		5597	CG	GLU	715	33.4		.682 2	5.225	1.00	
		5598		GLU	715	32.9		.916 2	4.522	1.00	
	TOM 5	599		GLU	715	32.0		566 2	3.332	1.00	55.01
A'	TOM 5	600		GLU	715	32.3		605 2	2.596	1.00	58.09
		601		GLU	715	30.99		251 2	3.136	1.00	55.83
A'	rom 5	602	_	3LU	715	34.80		665 2	7.064	1.00	
. A7	гом 5	603	`	LY		33.98			7.421	1.00	41.07
AT	OM 5	605		FLY	716	36.11			7.182	1.00	38.01
ΓA	OM 5			LY	716	36.64			7.770	1.00	41.11
		'	_ `	LY	716	36.51	0 9.		5.847	1.00	39.69
		-	_	IS	716	36.56	2 7.		290	1.00	39.64
AT					717	36.35	9 9.3		.554		36.71
AT				IS	717	36.21	5 8.3		.541	1.00	41.95
AT				IS	717	35.85	9 8.9		.183	1.00	43.32
AT		-		IS	717	35.813	7.9		.060	1.00	43.38
ATO		-		IS	717	34.802	7.1		.596	1.00	44.79
ATO		-		IS	717	36.912	7.6		. 285	1.00	44.64
ATO			_		717	36.584	6.7			1.00	46.21
ATC			E2 H)		717	35.307	6.4			1.00	46.21
ATO					717	37.485	7.4			1.00	45.55
ATO					717	38.581	8.0			1.00	43.90
ATO			AR	_	718	37.304				1.00	45.45
ATO					718	38.387	5.20				43.44
ATO			-		718	38.500	4.36				42.68
ATO					18	38.844	5.16				41.00
ATO					18	40.214	5.82	•			40.09
ATON					18	40.658	6.54				41.06
ATON					18	40.521	7.86				39.51
ATOM		_		-	18	39.940	8.60				39.90
ATOM	,			-	18	41.024	8.44				6.48
ATOM			ARG		18	38.080	4.30				2.06
ATOM			ARG		18	36.911	4.00				3.91
ATOM			MET		19	39.113	3.933				4.40
ATOM			MET		19	38.928	3.079				2.56
ATOM			MET	71	.9	40.219	2.964				2.82
ATOM			MET	71	.9	40.595	4.221				2.59
ATOM	5643 5644		MET	71	.9	42.093	4.079				1.15
ATOM	5645		MET	71	9	43.323	3.949			00 44	1.11
ATOM		C	MET	71	9	38.460	1.694				L.33
ATOM	5646	0	MET	71	9	38.822	1.216				.74
ATOM	5647	N	ASP	72	0	37.635	1.075				. 56
ATOM	5649	CA	ASP	72		37.090	-0.265	20.58			.50
ATOM	5650	CB	ASP	720)	36.077	-0.660	20.82			.51
	5651	CG	ASP	720		34.811	0.181	19.73		00 48	.60
ATOM	5652	OD1	ASP	720		34.678		19.74		00 53	.03
ATOM	5653	OD2	ASP	720		33.943	1.082	20.61		00 59	.61
ATOM	5654	C	ASP	720		38.177	-0.067	18.88		0 50	. 58
ATOM	5655	0	ASP	720	-	39.235	-1.329	20.82			. 64
ATOM	5656	N	LYS	721	-	37.876	-1.172	20.19	9 1.0		
ATOM	5658	CA	LYS	721		88.784	-2.436	21.487			
ATOM	5659	CB	LYS	721		8.278	-3.565	21.555		0 42.	
ATOM	5660	CG	LYS	721		9.000	~4.565	22.587		0 42.	
MOTA	5661	CD	LYS	721	3	8.445	-5.888	22.570	1.0	0 47.	
CCC= :				-	3	V.145	-6.805	23.628	1.00		
SSSD/55	145. v01										

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MOTA 5662 CE LYS 721 38.450 -8.246 23.163 1.00 54.96 NZ LYS 721 24.282 1.00 59.67 MOTA 5663 38.165 -9.190 С LYS 721 38.825 20.182 1.00 43.05 MOTA 5667 -4.215 LYS 721 37.779 19.625 1.00 46.08 MOTA 5668 0 -4.577 PRO 722 19.601 1.00 5669 N 40.025 -4.348 43.22 ATOM PRO 722 20.067 1.00 MOTA 5670 CD 41.337 -3.872 43.52 PRO 722 40.139 18.275 1.00 **ATOM** 5671 CA -4.968 41.04 1.00 MOTA 5672 CB PRO 722 41.631 -4.856 17.965 40.87 PRO 18.764 MOTA 5673 CG 722 42.074 -3.682 1.00 42.22 PRO 18.346 1.00 MOTA 5674 C 722 39.726 -6.427 39.64 MOTA 5675 0 PRO 722 39.730 -7.023 19.425 1.00. 37.12 ATOM 5676 N SER 723 39.311 -6.982 17.212 1.00 40.36 MOTA 5678 CA SER 723 38.947 -8.389 17.158 1.00 41.41 ATOM 5679 CB SER 723 38.205 -8.707 15.865 1.00 38.26 MOTA 5680 OG SER 723 39.049 -8.520 14.749 1.00 43.87 ATOM 5682 С SER 723 40.294 -9.102 17.191 1.00 41.54 ATOM 5683 0 SER 723 41.284 -8.575 16.703 1.00 40.90 ASN 724 -10.300 17.750 1.00 MOTA 5684 N 40.338 44.89 ATOM ASN 724 -11.019 17.853 1.00 5686 CA 41.598 48.14 ATOM ASN 724 -11.202 16.476 1.00 5687 CB 42.256 52.43 15.715 MOTA CG ASN 724 41.682 -12.374 1.00 5688 57.29 MOTA 5689 OD1 ASN 724 41.637 -13.492 16.225 1.00 61.96 MOTA 5690 ND2 ASN 724 41.218 -12.125 14.500 1.00 60.91 ASN 724 18.811 1.00 ATOM 5693 С 42.509 -10.255 48.17 MOTA 5694 0 ASN 724 43.648 -9.918 18.495 1.00 49.88 1.00 47.12 MOTA 5695 N CYS 725 41.960 -9.935 19.973 ATOM 5697 CA CYS 725 -9.238 21.010 1.00 46.17 42.686 CYS 725 -7.717 ATOM 5698 CB 42.569 20.862 1.00 44.83 5699 CYS 725 -6.813 22.159 1.00 MOTA SG 43.459 42.51 С CYS 725 42.017 -9.697 22.294 1.00 45.78 ATOM 5700 725 ATOM 5701 CYS 40.803 -9.642 22.423 1.00 44.83 0 ATOM 5702 N THR 726 42.810 -10.224 23.212 1.00 45.63 ATOM 5704 CA THR 726 42.289 -10.711 24.482 1.00 45.47 THR 726 43.351 25.217 1.00 MOTA 5705 CB -11.545 45.93 25.786 MOTA 5706 OG1 THR 726 44.307 -10.651 1.00 45.04 THR 24.233 1.00 ATOM 5708 CG2 726 44.061 -12.495 42.99 THR 726 -9.545 MOTA 5709 С 41.858 25.359 1.00 45.73 THR 726 25.216 MOTA 5710 0 42.368 -8.445 1.00 46.91 ASN 727 -9.789 26.257 1.00 MOTA 5711 N 40.914 45.93 ASN 727 27.141 1.00 MOTA 5713 CA 40.448 -8.736 47.85 MOTA 5714 CB ASN 727 39.300 -9.237 28.022 1.00 54.88 MOTA 5715 CG ASN 727 39.629 -10.544 28.731 1.00 65.11 ASN 727 **ATOM** 5716 OD1 40.737 -10.734 29.229 1.00 70.58 ATOM 5717 ND2 ASN 727 38.681 -11.472 28.735 1.00 69.68 ATOM 5720 C ASN 727 41.591 -8.212 27.999 1.00 44.18 ATOM ASN 727 41.594 -7.047 28.390 1.00 5721 0 41.35 GLU 728 MOTA 5722 N 42.572 -9.073 28.260 1.00 42.82 ATOM 5724 CA GLU 728 43.725 -8.713 29.071 1.00 42.37 GLU 728 -9.952 29.379 1.00 MOTA 5725 CB 44.573 43.09 **ATOM** 5726 CG GLU 728 45.806 -9.654 30.245 1.00 48.30 **ATOM** GLU 728 46.643 -10.889 30.568 1.00 50.11 5727 CD 29.668 **ATOM** 5728 OE1 GLU 728 46.867 -11.732 1.00 47.98 MOTA OE2 GLU 728 47.085 -11.010 31.733 1.00 51.69 5729 GLU 728 44.551 -7.652 28.356 1.00 39.57 ATOM 5730 С

	ATOM	5731	0	~;								
	ATOM	5732	O N	GLU	_	44.8	52	-6.6	05 20	000	_	
		5734	N	LEU		44.8		-7.9	_	. 933	1.00	92.50
	_	5735	CA	LEU	729	45.6		-6.9		.089	1.00	-,.50
		5736	CB	LEU	729	46.0		-7.62		.274	1.00	
		5737	CG	LEU	729	47.1		-8.67		.935	1.00	
			CD1	LEU	729	47.10		-9.55	-	.001	1.00	
	`	5738	CD2	LEU	729	48.50				766	1.00	35.69
	_	5739	C	LEU	729	44.88		-8.01		174	1.00	37.72
		740	0	LEU	729	45.46		-5.67		050	1.00	35.52
			N	TYR	730	43.56		-4.59			1.00	33.96
		743	CA	TYR	730	42.76		-5.77			1.00	32.90
			CB	TYR	730	-2.70		4.59			1.00	32.41
			CG	TYR	730	41.33		4.98		398	1.00	32.16
			CD1	TYR	730	40.44	_	3.787	7 25.]		1.00	34.93
	COM 5	747		TYR	730	40.769		2.827	24.2		1.00	
	'OM 5	748 (ΓΥR	730	39.962	? -	1.716	23.9		1.00	32.49
AT		~		TYR		39.282	: <u> </u>	3.605			1.00	32.80
AT	OM 57				730	38.465		2.496				33.45
AT	OM 57				730	38.814	- 3	1.557			1.00	34.81
ATO		'53 C			730	38.009	- (0.465			00	34.06
ATO		54 0	_		730	42.767	- 3	3.788	27.1		.00	36.66
ATO		_		_	730	42.837		2.558	27.08		.00	33.48
ATC	DM 57		_ ••		731	42.698		.466	28.24		.00	34.94
ATO			_		731	42.724		.755	20.24		.00	35.29
ATO					731	42.465		.709	29.52		.00	38.38
ATO					731	41.048		.264	30.69		.00	42.01
ATO			-		31	39.785		.965	30.70		.00	53.67
ATO					31	39.828		.688	30.83		.00	62.97
ATO			ME	T 7	31	44.073			32.64			61.83
ATON			ME	T 7	31	44.160		.049	29.67			34.52
ATOM		_	ME	T 7	32	45.118		958	30.23			33.23
ATOM		_		T 7:	32	46.445		669	29.13			33.93
ATOM			ME	T 73	32	47.506		065	29.168			36.26
			ME	T 73	32	48.935		995	28.565			5.56
ATOM			ME'			50.186		418	28.643	1.		5.26
ATOM			ME			50.480	-4.		28.001			0.46
ATOM		_	MET			46.369	-5.		29.415	1.(6.88
ATOM	, 2	-	MET				-1.		28.389	1.0	_	4.75
ATOM	5773	N	MET			46.827	-0.		28.873	1.0	_	5.49
ATOM	5775		MET			45.741	-1.7		27.213	1.0		4.63
MOTA	5776	CB	MET			45.571	-0.5	566	26.413	1.0	_	2.79
ATOM	5777	CG	MET		_	44.787	-0.8	353	25.130	1.0	_	3.16
MOTA	5778	SD	MET	733		45.544	4.0	01	24.047	1.0		
MOTA	5779	CE	MET	733		44.421	-1.9	90 2	22.670	1.0		2.32
ATOM	5780	C	MET	733		45.155	-3.4		22.068	1.0		.66
MOTA	5781	0	MET			14.789	0.4	52 2	7.229	1.00	-	.47
ATOM	5782	N	ARG	733		15.176	1.6		7.318			. 94
ATOM	5784	CA		734		3.679	0.0		7.818	1.00		. 72
ATOM	5785	CB	ARG	734	-	2.854	0.9		8.621	1.00		. 73
ATOM	5786	CG	ARG	734	4	1.586	0.19			1.00		.41
ATOM	5787		ARG	734		_	-0.33		9.095	1.00		.42
ATOM		CD	ARG	734		0.256	0.78		7.950	1.00	34.	
ATOM	5788 5780	NE	ARG	734	3.	9.416	1.74		7.043	1.00	37.	70
ATOM	5790 5701	CZ	ARG	734		8.092			7.750	1.00	43.	
ATOM	5791	NH1	ARG	734	3,	7.439	1.66	_	7.844	1.00	46.	
ATOM	5794	NH2	ARG	734	37	7.420	0.66		7.268	1.00	48.	
CCCD/==	~				J.	- 140	2.57	⊥ 28	.530	1.00	44.	
SSSD/551	145. v01											

ATOM	5797	С	ARG	734	43.660	1.458	29.793	1.00	32.12
ATOM	5798	0	ARG	734	43.492	2.610	30.180	1.00	35.37
ATOM	5799	N	ASP	735	44.566	0.646	30.327	1.00	33.75
MOTA	5801	CA	ASP	735	45.438	1.076	31.433	1.00	36.72
MOTA	5802	CB	ASP	735	46.379	-0.055	31.857	1.00	42.71
MOTA	5803	CG	ASP	735	45.722	-1:052	32.774	1.00	47.31
ATOM	5804	OD1	ASP	735	46.124	-2.241	32.720	1.00	50.99
MOTA	5805	QD2	ASP	735	44.824	-0.646	33.552	1.00	48.45
MOTA	5806	C	ASP	735	46.291	2.251	30.972	1.00	34.25
ATOM	5807	0	ASP	735	46.376	3.286	31.648	1.00	34.31
ATOM	5808	N	CYS	736	46.927	2.064	29.816	1.00	31.85
ATOM	5810	CA	CYS	736	47.780	3.077	29.204	1.00	29.93
MOTA	5811	CB	CYS	736	48.413	2.545	27.921	1.00	24.97
MOTA	5812	SG	CYS	736	49.504	1.159	28.180	1.00	31.35
ATOM	5813	C	CYS	736	46.994	4.325	28.885	1.00	31.62
MOTA	5814	0	CYS	736	47.562	5.416	28.823	1.00	30.73
ATOM	5815	N	TRP	737	45.680	4.174	28.711	1.00	35.03
ATOM	5817	CA	TRP	737	44.812	5.308	28.395	1.00	36.35
MOTA	5818	CB	TRP	737	43.808	4.927	27.297	1.00	36.43
MOTA	5819	CG	TRP	737	44.451	4.487	26.010	1.00	34.34
MOTA	5820	CD2	TRP	737	43.914	3.565	25.052	1.00	34.81
MOTA	5821	CE2	TRP	737	44.852	3.461	23.999	1.00	33.92
MOTA	5822	CE3	TRP	737	42.730	2.816	24.980	1.00	33.06
ATOM	5823	CD1	TRP	737	45.659	4.890	25.514	1.00	35.19
MOTA	5824	NE1	TRP	737	45.907	4.279	24.309	1.00	35.00
MOTA	5826	CZ2	TRP	737	44.644	2.633	22.886	1.00	33.45
MOTA	5827	CZ3	TRP	737	42.527	1.991	23.876	1.00	32.92
MOTA	5828	CH2	TRP	737	43.480	1.909	22.844	1.00	30.45
ATOM	5829	C	TRP	737	44.080	5.895	29.609	1.00	37.23
ATOM	5830	0	TRP	737	43.047	6.551	29.474	1.00	37.44
MOTA	5831	N	HIS	738	44.624	5.681	30.798	1.00	41.45
ATOM	5833	CA	HIS	738	44.006	6.208	32.008	1.00	41.52
MOTA	5834	CB	HIS	738	44.675	5.635	33.258	1.00	41.23
MOTA	5835	CG	HIS	738	43.925	5.924	34.522	1.00	43.31
ATOM	5836	CD2	HIS	738	43.618	7.096	35.126	1.00	41.58
MOTA	5837	ND1	HIS	738	43.338	4.935	35.279	1.00	44.22
MOTA	5839	CE1	HIS	738	42.693	5.487	36.294	1.00	46.62
MOTA	5840	NE2	HIS	738	42.848	6.798	36.223	1.00	43.99
MOTA	5842	С	HIS	738	44.118	7.726	32.015	1.00	41.75
ATOM	5843	0	HIS	738	45.179	8.268	31.731	1.00	40.84
MOTA	5844	N	ALA	739	43.025	8.405	32.352	1.00	42.47
MOTA	5846	CA	ALA	739	43.004	9.873	32.398	1.00	44.58
ATOM	5847	CB	ALA	739	41.629	10.361	32.825	1.00	48.19
MOTA	5848	С	ALA	739	44.081	10.467	33.317	1.00	45.12
MOTA	5849	0	ALA	739	44.653	11.510	33.020	1.00	45.66
MOTA	5850	N	VAL	740	44.262	9.852	34.481	1.00	46.64
MOTA	5852	CA	VAL	740	45.278	10.273	35.453	1.00	46.78
MOTA	5853	CB	VAL	740	44.867	9.893	36.888	1.00	47.74
MOTA	5854	CG1	VAL	740	45.919	10.372	37.890	1.00	49.35
MOTA	5855	CG2	VAL	740	43.515	10.495	37.211	1.00	47.89
ATOM	5856	C	VAL	740	46.601	9.573	35.121	1.00	45.24
MOTA	5857	0	VAL	740	46.754	8.362	35.347	1.00	45.01
MOTA	5858	N	PRO	741	47.588	10.335	34.637	1.00	43.46
MOTA	5859	CD	PRO	741	47.536	11.794	34.437	1.00	43.51

ATOM	5860	CA	PRO	74.						
ATOM	5861	CB		741	-0.5		9.804	34.26	c	
ATOM	5862	CG	PRO	741	10.7	01 1	1.070			
ATOM	5863	C	PRO	741	48.6		.010	33.94		
ATOM	5864		PRO	741	49.5	_	.936	33.42	_	42.81
ATOM		0	PRO	741	50.24			35.32		47.45
	5865	N	SER	742	49.39	-	.950	34.994		45.12
ATOM	5867	CA	SER	742	49.00	-	.280	36.601	1.00	48.78
ATOM	5868	CB	SER	742	49.99		.532	37.703	1.00	
MOTA	5869	OG	SER	742	49.84	5 9	.317	39.012		48.76
ATOM	5871	C	SER		48.48	2 9	.488	39.373		51.11
ATOM	5872	0	SER	742	49.37	6 7	150	37.867		53.50
ATOM	5873	N	GLN	742	49.93	26.	283	38.539	_	47.77
ATOM	5875	CA		743	48.19		962			47.31
ATOM	5876		GLN	743	47.51	-	689	37.284	1.00	47.57
ATOM	5877	CB	GLN	743	46.004			37.384	1.00	47.14
ATOM			GLN	743	45.438			37.531	1.00	50.16
		CD	GLN	743	46.239		447	38.871	1.00	54.69
ATOM	5879	OE1		743	46.235		964	40.051	1.00	57.62
	5880	NE2	~	743	46.898		196 .	40.749	1.00	
	5883	~			46.202	7.:		10.268		59.09
ATOM		_		743	47.816	4.7		36.212	1.00	59.45
ATOM		- `		743	47.365	3.6		6.182		44.41
			-	744	48.515	5.3			1.00	44.39
3		· ·		744	48.902	4.5		5.212	1.00	42.87
			RG 7	44	49.350	5.3		4.046	1.00	41.45
3				44	48.316			2.883	7 ^ ~	37.34
3.000	^ ~ -		RG 7	44	48.854	6.3		2.412		32.30
7.000	891 N	E A	RG 7	44	47.921	7.2		1.270		31.37
	893 C		RG 7	44	47.321	8.2		0.946		36.76
ATOM 5	394 N	H1 AI		44	48.271	9.49	92 30	0.543	_	
ATOM 5	397 NI		•	44	49.553	9.81			-	9.88
ATOM 5	900 C	AF			47.330	10.40				9.94
ATOM 5	01 0	AR		14	50.068	3.61			1.00 g	9.12
ATOM 55	02 N				50.813	3.94		40-		1.40
3	03 CD	PR			50.203	2.44		_		2.84
7 0000					49.345	1.73	-		1.00 4	0.11
ATOM 59					51.332	1.60	_		L.00 39	9.91
ATOM 59			0 74	5	51.019		-	.266 1		3.58
_		PRO	74:	5	50.250	0.26		.605 1		4.46
		PRO	74	5	52.640	0.645		377 1		.41
- 05,		PRO	745	5	52.634	2.202				.73
ATOM 59		THE			52.634	3.027				
ATOM 591		THR			53.753	1.843	34.			.71
ATOM 591	2 CB	THR			55.050	2.328	33.	.		.90
ATOM 591					56.085	2.380	35.			. 77
ATOM 591					56.296	1.059	35.			. 85
ATOM 591					55.605	3.302	20.		.00 33.	
ATOM 591	_	THR	746		55.544	1.327	36.		00 32.	17
ATOM 591	_	THR	746	ĩ	55.026		32.8		00 32.	69
·		PHE	747	5	6.538	0.213	32.7		00 31.	
3.55		PHE	747	-	7.093	1.708	32.0	66 1.		
ATOM 592		PHE	747	-	P 12:	0.782	31.0	83 1.		
ATOM 5922	CG	PHE	747		8.121	1.472	30.1			
ATOM 5923	CD1	PHE			7.504	2.287	29.0	• •	• .	
ATOM 5924		PHE	747		6.772	1.666	28.0			
ATOM 5925			747	5	7.609	3.667	29.0			
ATOM 5926	CE2	PHE	747	5	6.170	2.407			_	
ATOM 5927		PHE	747	5	7.001	4.413	27.10		0 24.3	
-2. 332/	CZ	PHE	747		5.276		28.09		0 29.2	
SSSD/55145. v(- · U	3.776	27.10	3 1.0		
- 2220/33145, v(T								/	-

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ATOM	5928	C	PHE	747	57.714	-0.413	31.782	1.00	31.92
ATOM	5929	0	PHE	747	57.727	-1.514	31.243	1.00	32.46
MOTA	5930	N	LYS	748	58.233	-0.199	32.986	1.00	33.47
MOTA	5932	CA	LYS	748	58.816	-1.302	33.733	1.00	35.57
ATOM	5933	CB	LYS	748	59.468	-0.800	35.026	1.00	39.42
MOTA	5934	CG	LYS	748	60.083	-1.923	35.861	1.00	46.49
MOTA	5935	CD	LYS	748	60.817	-1.407	37.103	1.00	50.69
MOTA	5936	CE	LYS	748	61.253	-2.574	37.999	1.00	52.57
MOTA	5937	NZ	LYS	748	62.072	-2.129	39.155	1.00	56.45
MOTA	5941	C	LYS	748	57.700	-2.318	34.028	1.00	35.58
MOTA	5942	0	LYS	748	57.898	-3.526	33.871	1.00	34.72
MOTA	5943	N	GLN	749	56.522	-1.818	34.411	1.00	35.59
MOTA	5945	CA	GLN	749	55.369	-2.684	34.692	1.00	38.20
MOTA	5946	CB	GLN	749	54.154	-1.872	35.162	1.00	42.73
MOTA	5947	CG	GLN	749	54.264	-1.171	36.499	1.00	49.30
ATOM	5948	CD	GLN	749	53.060	-0.282	36.761	1.00	53.13
MOTA	5949	OE1	GLN	749	53.194	0.915	37.023	1.00	52.71
ATOM	5950	NE2	GLN	749	51.873	-0.856	36.644	1.00	58.54
ATOM	5953	C	GLN	749	54.954	-3.392	33.409	1.00	36.16
ATOM	5954	0	GLN	749	54.745	-4.605	33.393	1.00	36.67
ATOM	5955	N	LEU	750	54.801	-2.609	32.342	1.00	35.83
ATOM	5957	CA	LEU	750	54.381	-3.117	31.037	1.00	34.49
MOTA	5958	CB	LEU	750	54.324	-1.988	30.004	1.00	32.49
ATOM	5959	CG	LEU	750	53.206	-0.958	30.188	1.00	31.94
ATOM	5960	CD1	LEU	750	53.411	0.230	29.267	1.00	30.45
MOTA	5961	CD2	LEU	750	51.859	-1.610	29.933	1.00	29.30
ATOM	5962	C	LEU	750	55.294	-4.214	30.559	1.00	33.87
ATOM	5963	0	LEU	750	54.828	-5.208	30.027	1.00	34.72
ATOM	5964	N	VAL	751	56.598	-4.038	30.759	1.00	36.12
ATOM	5966	CA	VAL	751	57.585	-5.045	30.363	1.00	34.50
ATOM	5967	CB	VAL	751	59.054	-4.532	30.559	1.00	31.96
ATOM	5968	CG1	VAL	751	60.052	-5.646	30.308	1.00	30.24
MOTA	5969 5970	CG2 C	VAL VAL	751 751	59.342 57.349	-3.386	29.604	1.00	28.02
MOTA MOTA	5970 5971	0	VAL	751 751		-6.321	31.182	1.00	36.11
ATOM	5972	N	GLU	751 752	57.333 57.107	-7.422 -6.165	30.638 32.479	1.00	36.45 37.83
ATOM	5974	CA	GLU	752 752	56.869	-7.326	33.331	1.00	
ATOM	5975	CB	GLU	752 752	56.800	-6.910	34.804	1.00	41.47 43.03
MOTA	5976	CG	GLU	752 752	58.122	-6.305	35.263	1.00	52.52
ATOM	5977	CD	GLU	752 752	58.251	-6.176	36.761	1.00	57.18
ATOM	5978	OE1	GLU	752 752	58.600	-5.068	37.233	1.00	58.11
ATOM	5979	OE2	GLU	752	58.032	-7.191	37.461	1.00	61.59
ATOM	5980	C	GLU	752 752	55.623	-8.097	32.890	1.00	40.16
ATOM	5981	0	GLU	752 752	55.689	-9.308	32.642	1.00	39.75
ATOM	5982	N	ASP	753	54.524	-7.376	32.696	1.00	40.06
ATOM	5984	CA	ASP	753	53.275	-7.982	32.264	1.00	39.73
ATOM	5985	CB	ASP	753	52.157	-6.947	32.247	1.00	41.00
ATOM	5986	CG	ASP	753	51.668	-6.591	33.640	1.00	45.17
ATOM	5987	OD1	ASP	753 753	51.753	-7.468	34.543	1.00	49.78
ATOM	5988	OD2	ASP	753 753	51.733	-5.439	33.829	1.00	45.51
ATOM	5989	C C	ASP	753 753	53.396	-8.595	30.890	1.00	39.64
ATOM	5990	0	ASP	753 753	52.955	-9.720	30.674	1.00	41.84
ATOM	5991	Ŋ	LEU	754	53.998	-7.861	29.960	1.00	37.75
ATOM	5993	CA	LEU	754 754	54.161	-8.358	28.603	1.00	38.16
T 701.1	د ر ر د	1		,	J-4 . 2 U 2	0.550	20.005	1.00	50.10

		100
ATOM 5994	CB LEU	754 54.664 7.05-
ATOM 5995	00	75.4 27.664 1 00 05
ATOM 5996	GD:	33.552 -6.270 27 307
ATOM 5997	CD2	54.141 -5.062 26 500 36.64
ATOM 5998	0	754 52.459 -6.968 36.465
ATOM 5999	,	55.070 -9.561 20 571
ATOM 6000	N	54.905 -10.451 27.740
ATOM 6002	~-	56.014
ATOM 6003		55 56.930 -10 728 20 724 1.00 39.19
ATOM 6004		55 57.956 -10.462 25.594 1.00 40.87
ATOM 6005		55 59.128 -11.415 -1.00 45.11
		55 59 750 30.652 1.00 48 64
· •	OD2 ASP 75	55 59 422 24.012 31.711 1.00 54 27
	C ASP 75	55 56 000
ATOM 6008	O ASP 75	21.952 29.947 1.00
ATOM 6009	N ARG 75	29.289 1 00 25
ATOM 6011	CA ARG 75	55.232 -11.771 30.955 1 00
ATOM 6012	CB ARG 75	6 -12.817 31.437 1 00 40 00
ATOM 6013	CG ARG 756	33.5/3 -12.316 32.663
ATOM 6014	/56	32.435 -13.217 32 120
7/17/07/4	NTD 3	51.791 -12.631 34 380 42.12
AMOM		51.353 -11.247 34 196 42.33
ATION	7777	50.295 -10.891 32 460
ATOM	TITO 3.5	49.549 -11.818 32.055
ATION	,	49.998 -9.605 33.305
ATOM SOCI	-210 /36	53.362 -13 275 -3 1.00 48.92
ATOM Sees	-40 /36	53 247 30.364 1.00 40 19
ATOM COOL		53 600 30.110 1.00 42 24
3 770	A ILE 757	51 706 -29./1/ 1.00 38 10
7/17/03/4	/5/	50 953 28.683 1.00 38 40
T MOL-	G2 ILE 757	49 952 28.187 1.00 36 55
3	G1 ILE 757	50 216 27.105 1.00 34 67
ATOM 6032 CI	D1 ILE 757	49 554 29.364 1.00 34 65
ATOM 6033 C	ILE 757	-9.423 29.048 1.00
ATOM 6034 O	ILE 757	27.500 1.00 30
ATOM 6035 N	VAL 758	31.709 -14.360 27.025 1.00 33.19
ATOM 6037 CA	VAL 758	33.492 -12.996 27.061 1.00
ATOM 6038 CB		34.161 -13.645 25.937 1 00 to
ATOM 6039 CG		33.382 -13.052 25.682 1 00 45
ATOM 6040 CG		30.308 -13.855 24.621 1 00 11.72
ATOM 6041 C	VAL 758	33.491 -11.619 25.229 1 00
ATOM 6042 O		54.299 -15.133 26 231 7 00
ATOM 6043 N		54.045 -15.971 25.360 -1.00 47.11
ATOM 6045 CA		54.695 -15.446 37.464
ATOM 6046 CB		54.879 -16.820 27 000
ATOM CO	ALA 759	55.423 -16.830 20 227
ATOM COLD	ALA 759	53.568 -17.500 17.00 50.11
ATION 55	ALA 759	53.520 -10.715 27.850 1.00 54.72
ATIOM TO T	LEU 760	52.496 -16.003 -1.348 1.00 58.64
A TION	LEU 760	51 104 28.329 1.00 54 84
ATTOM SEE	LEU 760	50 330 1- 28.343 1.00 55 87
ATOM 6053 CG	LEU 760	50.875 -17.034 29.459 1.00 56.85
ATOM 6054 CD1	LEU 760	17.165 30.885 1 00 55
ATOM 6055 CD2	LEU 760	49.991 -16.392 31.849 1 00 55 55
ATOM 6056 C		30.959 -18.631 31.289 1 00 57
ATOM 6057 O		50.454 -17.546 27.013 1.00 57.78
ATOM 6058 N		49.262 -17.859 26.944
	THR 761	51.151 -17.134 35 056
SSSD/55145. v01		25.956 1.00 58.71

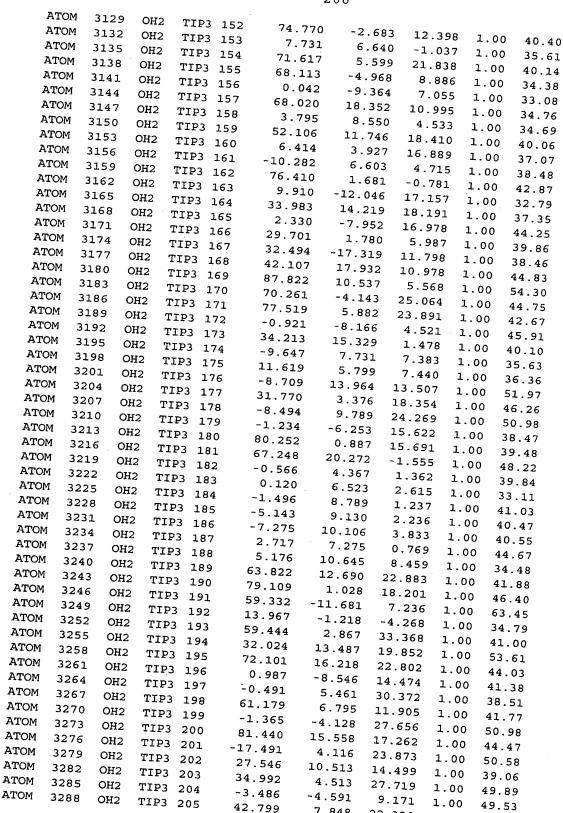
	- 04
	50.541 -17.025 24.630 1.00 59.04
NEOM 6060 CA 111K	020 -15.657 23.971 1.00 50.1-
THR 6061 CB THR 761	50 207 -14.610 24.775 1.00 50.55
NEOM 6062 OG1 THR 761	50.212 -15.584 22.590 1.00 53.02
PUCM 6064 CG2 THR /61	F1 049 -18.138 23.721 1.00 60.11
2004 6065 C THR /61	50 255 -18,295 23.530 1.00 02.50 DPT2
THR 761	-8.976 20.202 0.50 57.05 PPT2
ATOM 6067 SG CYS 1603	12.109 23.281 0.50 30.25 TPT2
A HOM 6068 CG MET 534	69.311 12.958 24.867 0.50 42.66 FRI2
ATOM 6069 SD MET 534	69.286 12.083 25.804 0.50 43.27 PRT2
NEOM 6070 CE MET 534	70.335 -7.949 16.446 0.50 36.47 FRID
ATOM 6071 SG CYS 603	704 25.061 2.660 1.00 24.53
ATOM 2676 OH2 TIP3 1	3 992 15.898 1.00 33.00
TTP3 2	10.717 10.596 1.00 20.20
ATOM 2679 OH2 TIP3 3 ATOM 2682 OH2 TIP3 3	20.056 7.685 1.00 20.25
NTOM 2685 OH2 TIP3 4	75 073 16.616 6.785 1.00 20.15
2688 OH2 TIP3 5	9.502 1.00 33.05
ATTOM 2691 OH2 TIP3 6	53 012 11.060 24.263 1.00 35.55
NTOM 2694 OH2 TIP3 /	51.913 22.524 1.00 26.63
amow 2697 OH2 TIP3 8	4.614 32.443 1.00 25.05
2700 OH2 TIP3 9	72.169 4.735 13.281 1.00 22.02
NTOM 2703 OH2 TIP3 10	17 110 5.543 22.764 1.00 41.00
ATOM 2706 OH2 TIP3 11	41.110 8.857 21.555 1.00 36.99
ATOM 2709 OH2 TIP3 12	73.115 74.465 -2.607 28.883 1.00 30.17
2712 OH2 TIP3 13	76 944 13.287 23.954 1.00 52.5
2715 OH2 TIP3 14	70.062 17.048 18.200 1.00 32.00
ATOM 2718 OH2 TIP3 15	22 066 11,657 15.958 1.00 25.02
ATOM 2721 OH2 TIP3 16	0.095 1.00 20.00
ATOM 2724 OH2 TIP3 17	20 259 -0.001 5.000 1.00 37.25
AMOM 2727 OH2 TIP3 18	5 442 2.705 19.077 1.00 25.05
ATOM 2730 OH2 TIP3 19	07.009 6.166 4.885 1.00 23.03
ATOM 2733 OH2 TIP3 20	24.242 -1.725 16.911 1.00 32.22
ATOM 2736 OH2 TIPS 21	2.428 27.861
ATOM 2739 OH2 TIP3 22	-0.704 -11.834 30·V ² 3 0.0
ATOM 2742 OH2 TIP3 23	-5 993 -1.757 1.00 23
ATOM 2745 OH2 T1P3 24	27 516 7.803 15.070 1.00 35.78
7 TOM 2748 OH2 TIP3 25	27 574 0.146 6.004 -
NUM 2751 OH2 TIP3 26	27.119 -12.972 27.844 1.00 45.00
70M 2754 OH2 T1P3 27	20, 439 -17,074 13.203 1.00 30.20
ATOM 2757 OH2 T1P3 20	20 706 14.393 7.969 1.00 32.20
ATOM 2760 OH2 TIPS 25	-2.338 -3.424 11.295 21.00 37.83
ATOM 2763 OH2 1200	35.086 -4.130 18.030 1.00 23.69
ATOM 2766 OH2 T1P3 31	20 455 17.922 9.507
ATOM 2769 OH2 T1P3 32	m rao 3.619 10.000
ATTOM 2772 OH2 T1P3 33	5.290 11.280 1.00
2775 OH2 TIP3 34	20 210 -8.799 20.244
ATOM 2778 OH2 T1P3 35	6.195 3.150 13.803 1.00 31.33
ATOM 2781 OH2 T1P3 30	21 998 2.830 0.154 1.5
ATOM 2784 OH2 TIP3 37	19.915 2.023 -3.939 1.00 32.67
ATOM 2787 OH2 T1P3 30	62 242 2.604 32.859 1.00 33.55
ATOM 2790 OH2 TIP3 35	$\frac{3}{21}$ $\frac{231}{231}$ $\frac{-7.063}{21.003}$ $\frac{-3.900}{21.003}$ $\frac{1.00}{25.003}$
2793 OH2 TIP3 40	1 -15.809 8.838 22.610 1.00 50.62
ATOM 2796 OH2 TIP3 4.	2 40.120 2.154 8.433 1.00 37.85
ATOM 2799 OH2 T1P3 4	2 11.128 -0.045 1.00 37.00
ATOM 2802 OH2 TIP3 4	3 25.0
• • • • • • • • • • • • • • • • • • •	

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ATOM 2805 OH2 TIP3 4	
ATOM 2808 OVO	9,030 17 300 -
ATOM 2811 OVD	87.772 18.919 10.505 1.00 29.79
ATOM 222 11P3 4	5 74 504 77 10.595 1.00 48 44
7.TOM 0112 11P3 4	$7 29.365 \frac{200}{1.00} 1.00 39.19$
7.TOM 0012 T1P3 48	3 66 406 20.707 10.560 1.00 34 71
0112 11193 46	6.826 15.051 1 00 22 22
ATOM 2823 OH2 TIP3 50	21.441 5.731 1.00 22.25
ATOM 2826 OH2 TID2 51	2.912 3.173 1.00 20.05
ATOM 2829 OH2 TIP3 52	19.496 5.141 4 007
ATOM 2832 OVO	67.492 3.490 10.002 1.00 28.88
ATOM 2835 OVO	34.791 5.413 24 707
ATOM 2839 OVE -	34.787 -16 010 1.00 40.16
ATOM 2015	59.972 7.450 25 1.00 39.46
ATOM 2012 11P3 56	~7 130 27.8/U 1.00 31 56
11P3 57	54 000 -1.696 6.345 1.00 42 00
ATOM 2847 OH2 TIP3 58	11.953 25.360 1 00 40
ATOM 2850 OH2 TIP3 50	6.686 16.740 1 00 46
ATOM 2853 OH2 TIDE CO.	73.750 20.885 19.041
AIOM 2856 OUR man-	3.431 -8.270 -8.270 -8.270
ATOM 2859 OV2 777	37.904 10.790 5 612
ATOM 2862 OTTO	29.982 -9.545 1 300
ATOM 2005 PT	66.918 1 757 1.303 1.00 39.11
ATOM 2012 11P3 64	49.117 1 210 34.68
ATTOM 000 112 11P3 65	41 246 12.227 1.00 34 31
7 TOM 25 TIP3 66	10 755 10 29.033 1.00 34 55
IIP3 67	1.167 1 00 40
ATOM 2877 OH2 TIDE CO	-4.327 21.439 1 00 3-
ATOM 2880 OH2 TIDE CO	16.267 13.265 1 00 55 00
ATOM 2883 OH2 TIP3 70	0.111 4.362 3.445
ATOM 2886 OV2	73.131 18.780 22 620
ATOM 2889 OTTO	-7.949 -3.409 24 953 1.00 40.20
ATOM 2892 OVA	66.379 -4.621 28 422 - 35.49
ATOM 222 11P3 73	21.506 -20 711 4 225 4.00 45.46
ATOM SOCIETIES 74	59.539 -6.865 4.815 1.00 52.46
ATOM 2225	16 565 4.928 1.00 48 87
ATOM 2001	-15 235 T -3.008 1.00 51.80
0112 1101 77	32 936 4.428 1.00 29 13
0112 11113 70	2.785 13.213 1 00 27
ATOM 2910 OH2 TID2 70	-2.768 10.996 1 00 22 22
ATOM 2913 OH2 TIP3 80	2.354 5.447 1 00 22
ATOM 2916 OH2 TID2 01	2.434 21.950 1.00 22.53
ATOM 2919 OH2 TIP3 82	27.374 3.628 6 163 7 7
ATOM OCCU	-8.708 6.263 9.533 1.00 34.06
ATOM OFF	1.500 -1.935 9 721
7 TOM 000	-4.825 -3 133 C 27.61
ATOM 222-	17.513 2 020 0.984 1.00 33.50
ATOM 2021 OH2 TIP3 86	20 200 - 1.966 1.00 24 27
ATOM 2012 11P3 87	2.920 1.00 26 15
ATOM 2937 OH2 TIP3 88	-2.158 22.213 1 00 05
ATOM 2940 OH2 TTP3 PQ	-6.185 -1.553 1 00
ATOM 2943 OH2 TIP3 90	10.670 -15.654 6.839 1 00 25
ATOM 2946 OH2 TID2 07	4.107 -12.003 11 805 1 33.36
ATOM 2949 OUR 7777	6.238 0.927 3.340 33.92
ATOM 2275	-13.563 1.438 5.472
ATOM 2955 OV2 777	15.707 -7.454 0.702 1.00 27.86
ATOM 2070	-1.856 -5.303 0.106 1.00 26.69
ATOM 2001	12 654
ATOM 22 11P3 96	69 774 27 -4.474 1.00 31 32
ATOM 2964 OH2 TIP3 97	27.363 2.127 1.00
	24.036 -13.192 0.040
SSSD/55145. v01	0.040 1.00 48.53

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		3 -4.625		.00 31.9	
ATOM 2967 OH2 TIP3		3	3.487 1	00 38.9	
TTP3	99 10.51	·	4.342 1	00 30.6	
TTP3	100 -9.49		10.514	L.00 36.0	
ATOM DOTO TIP3	101 73.05	· -	30.608	1.00 29.3	. 8
ATOM 2570 OUS TIP3	102 -3.15	·	11.792	1.00 47.8	10
TTP3	103 36.63			1.00 24.0)3
ATOM 2005 ONO TTP3	104 21.4		19.432	1.00 53.	
ATOM 2500 OUS TIPS	105 31.2		22.266	1.00 51.	
ATOM 2500	106 5.6		17.464	1.00 35.	
ATOM 2332	107 -13.1		-1.042	1.00 27.	83
ATOM 2007 OH2 TIP3	108 26.6		18.172	1.00 30.	90
AIOM 255	109 24.1		3.558	1.00 33.	82
AIOM SOOT ONE TIPE	110 -1.9	12 (17	33.196	1.00 54.	
ATOM 5005 TTP	3 111 59.5		1.991	1.00 37.	
ATOM SOCI ON TIP	3 112 4.3		0.958	1.00 29	
ATOM 3000 TTP	3 113 8. ³		25.812	1.00 38	
ATOM SOLE ON TTP	3 114 75.		14.189		.24
ATOM JOES ONS TIP	3 115 48.		9.146		.85
AIOM SOLI ONO TIP			12.964		.83
ATOM SOLL ON TIE	3 117 83.	·	-3.252		.78
ATOM SOCIA					.32
ATOM SOCIO OTO TIT		600		1.00 33	.73
AIOM SOOT ON TI					.72
ATOM SOUT OTT TT					2.37
AIOM SOUT			_		5.80
ATOM SOUP		10			5.12
ATOM SOLE ONS TT		·			1.90
ATOM SOLE OTO TT		. 1. / 2			4.83
ATOM SOLO	13			1.00 3	5.46
AIOM SOSS ONO TI	F J	- 75	_	1.00 3	5.43
AIOM SOUT	.FJ IIV	,		1.00 4	0.68
ATOM 3057 OH2 13				1.00	4.99
ATOM 3063 OH2 T	113				12.31
ATOM 3066 OH2 T	113	• • • • • • • • • • • • • • • • • • • •		3 1.00	58.71
ATOM 3069 OH2 T	113	• •		8 1.00	36.75
ATTOM 3072 OH2 T				9 1.00	52.90
ATOM 3075 OH2 T	113			5 1.00	37.81
ATOM 3078 OH2 T		3.354 15.0 5.717 11.2	51 9.06	_	35.18
ATOM 3081 OH2 7	.1.5	2.951 -2.4	69 2.07		22.07
ATOM 3084 OH2		75.645 3.4	86 20.52		38.01
2087 OH2	TITO	13.237 7.4	12 -2.64		33.50
ATOM 3090 OH2	1 1 2 2 -	11.262 -9.9	70 0.9		26.14
ATOM 3093 OH2	1110	59.480 10.7	772 14.09	98 1.00	52.08
ATOM 3096 OH2		13.869 -16.2	121 3.9		40.06
ATOM 3099 OH2	1113	-6.407 -3.4	413 16.6		44.38
ATOM 3102 OH2	TIP3 143	25.667 -12.	645 3.4		48.28
ATOM 3105 OH2	TIP3 144	16.282 10.	641 6.4		40.94
ATOM 3108 OH2	1113		861 7.0		39.45
ATOM 3111 OH2	TIP3 146		569 1.8		27.35
ATOM 3114 OH2	TIP3 147	44.809 7.	627 11.6	70 1.00	35.65
ATOM 3117 OH2	TIP3 148		459 16.5	1.00	37.21
ATOM 3120 OH2	TIP3 149	2.941 -7	.118 -1.		38.43
ATOM 3123 OH2	TIP3 150		.086 20.	704 1.00	42.80
ATOM 3126 OH2	TIP3 151	J			



7.848

22.320

1.00

43.50

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ATOM	3291	OH2	TIP3	206	52.728	11.884	21.811	1.00	39.98
MOTA	3294	OH2	TIP3	207	26.706	14.069	19.833	1.00	46.68
MOTA	3297	OH2	TIP3	208	-7.154	8.907	6.444	1.00	42.83
MOTA	3300	OH2	TIP3	209	86.648	5.606	16.034	1.00	51.15
ATOM	3303	OH2	TIP3	210	54.879	15.840	20.379	1.00	50.23
MOTA	3306	OH2	TIP3	211	51.417	19.473	22.691	1.00	48.35
MOTA	3309	OH2	TIP3	212	20.102	6.924	7.085	1.00	38.15
ATOM	3312	OH2	TIP3	213	28.991	1.941	-3.570	1.00	47.39
MOTA	3315	OH2	TIP3	214	26.505	2.386	-4.633	1.00	46.48
MOTA	3318	OH2	TIP3	215	36.482	2.810	18.521	1.00	46.26
MOTA	3321	OH2	TIP3	216	16.941	-20.504	14.128	1.00	49.74
MOTA	3324	OH2	TIP3	217	28.572	-14.448	6.157	1.00	49.13
MOTA	3327	OH2	TIP3	218	31.380	1.471	-1.998	1.00	43.02
MOTA	3330	OH2	TIP3	219	10.065	-16.338	15.455	1.00	42.75
ATOM	3333	OH2	TIP3	220	7.350	-11.974	5.652	1.00	55.35
MOTA	3336	OH2	TIP3	221	-12.328	14.547	10.986	1.00	51.29
ATOM	3339	OH2	TIP3	222	11.186	9.609	-1.388	1.00	37.68
MOTA	3342	OH2	TIP3	223	11.389	12.276	-1.400	1.00	46.93
MOTA	3345	OH2	TIP3	224	34.202	13.069	-1.161	1.00	41.79
MOTA	3348	OH2	TIP3	225	31.303	17.822	7.853	1.00	48.21
MOTA	3351	OH2	TIP3	226	36.875	11.804	-2.106	1.00	59.03
MOTA	3354	OH2	TIP3	227	35.134	3.048	11.020	1.00	50.41
ATOM	3357	OH2	TIP3	228	63.950	13.409	26.627	1.00	43.40
MOTA	3360	OH2	TIP3	229	36.367	6.116	15.221	1.00	57.79
MOTA	3363	OH2	TIP3	230	90.606	4.355	6.342	1.00	47.53
MOTA	3366	OH2	TIP3	231	50.038	-11.673	10.767	1.00	56.90
MOTA	3369	OH2	TIP3	232	60.196	-10.144	16.590	1.00	51.61
MOTA	3372	OH2	TIP3	233	18.021	-21.179	7.008	1.00	49.93
MOTA	3375	OH2	TIP3	234	66.236	-1.218	30.583	1.00	39.55
MOTA	3378	OH2	TIP3	235	74.959	18.928	20.659	1.00	38.04
MOTA	3381	OH2	TIP3	236	-2.816	10.082	3.187	1.00	49.31
MOTA	3384	OH2	TIP3	237	5.894	-3.410	25.289	1.00	35.55
MOTA	3387	OH2	TIP3	238	35.784	6.047	12.543	1.00	41.96
MOTA	3390	OH2	TIP3	239	-5.400	16.537	14.180	1.00	43.13
ATOM	3393	OH2	TIP3	240	46.589	-11.622	26.970	1.00	43.71
MOTA	3396	OH2	TIP3	241	6.199	6.592	13.797	1.00	46.51
ATOM	3399	OH2	TIP3	242	-3.777	-5.158	20.907	1.00	42.08
ATOM	3402	OH2	TIP3	243	1.969	-3.711	-0.282	1.00	37.38
MOTA	3405	OH2	TIP3	244	86.200	11.629	22.877	1.00	56.51
MOTA	3408	OH2	TIP3		10.557	7.565	5.514	1.00	47.58
MOTA	3411	OH2	TIP3	246	4.802	8.149	2.136	1.00	50.70
MOTA	3414	OH2	TIP3	247	64.590	-8.128	20.596	1.00	43.65
MOTA	3417	OH2	TIP3	248	11.346	-17.840	13.283	1.00	47.64
MOTA	3420	OH2	TIP3	249	42.116	-6.808	14.953	1.00	53.79
MOTA	3423	OH2	TIP3	250	2.745	-4.054	22.128	1.00	60.88
MOTA	3426	OH2	TIP3	251	71.999	1.177	-2.124	1.00	47.90
ATOM	3429	OH2	TIP3	252	50.328	-3.210	33.068	1.00	57.01
MOTA	3435	OH2	TIP3	253	57.838	9.337	11.631	1.00	52.55
MOTA	3438	OH2	TIP3	254	43.373	20.489	30.490	1.00	51.97
MOTA	3441	OH2	TIP3	255	67.045	16.529	15.793	1.00	49.02
MOTA	3444	OH2	TIP3	256	87.509	21.566	5.114	1.00	54.21
MOTA	3447	OH2	TIP3	257	21.060	10.052	-9.215	1.00	60.32
MOTA	3450	OH2	TIP3	258	11.827	2.450	27.951	1.00	54.26
MOTA	3453	OH2	TIP3	259	64.788	-0.418	3.563	1.00	50.94

ATOM 3459 OH2 TIP3 261 25.605 -8.106 27.287 1.00 62.1 ATOM 3462 OH2 TIP3 262 -18.804 10.886 12.628 1.00 55.2 ATOM 3468 OH2 TIP3 263 30.652 11.349 16.201 1.00 50.4 ATOM 3471 OH2 TIP3 265 29.720 9 106 18.465 1.00 53.2	ATOM ATOM	3462 OH2 3465 OH2 3468 OH2	TIP3 261 TIP3 262 TIP3 263 TIP3 264	25.605 -18.804 30.652 22.350	10.886 11.349 -16.098	27.287 12.628 16.201 -2.742	1.00 1.00 1.00	62.8 52.8 55.2 50.4 53.2
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TABLE 2

Atom		Atom	A.A	A.A	х	Y	Z	occ	В	
No.		Type	Type	No.						
ATOM	1	N	GLU	1464	-13.425	16.769	8.973	1.00	61.21	
ATOM	3	CA	GLU	1464	-12.536	16.852	7.821	1.00	59.70	
MOTA	4	CB	GLU	1464	-11.383	17.829	8.085	1.00	60.05	
MOTA	5	C	GLU	1464	-11.998	15.478	7.427	1.00	57.11	_
ATOM	6	0	GLU	1464	-12.134	15.076	6.274	1.00	59.75	
ATOM	7	N	LEU	1465	-11.406	14.749	8.368	1.00	52.21	
MOTA	9	CA	LEU	1465	-10.871	13.424	8.062	1.00	46.72	
MOTA	10	CB	LEU	1465	-10.102	12.844	9.249	1.00	44.98	
MOTA	11	CG	LEU	1465	-8.608	13.123	9.384	1.00	46.11	
ATOM	12	CD1	LEU	1465	-8.338	14.592	9.663	1.00	51.13	
MOTA	13	CD2	LEU	1465	-8.064	12.286	10.512	1.00	4.99	
MOTA	14	C	LEU	1465	-12.000	12.475	7.700	1.00	44.16	
ATOM	15	0	LEU	1465	-13.101	12.577	8.239	1.00	44.04	
MOTA	16	N	PRO	1466	-11.760	11.580	6.732	1.00	42.53	
ATOM	17	CD	PRO	1466	-10.535	11.534	5.913	1.00	41.30	
ATOM	18	CA	PRO	1466	-12.740	10.591	6.269	1.00	41.16	
MOTA	19	CB	PRO	1466	-12.134	10.111	4.959	1.00	41.48	
ATOM	20	CG	PRO	1466	-10.658	10.213	5.220	1.00	41.30	
MOTA	21	C	PRO	1466	-12.906	9.441	7.261	1.00	41.31	
MOTA	22	0	PRO	1466	-11.929	8.936	7.816	1.00	41.05	
MOTA	23	N	GLU	1467	-14.145	9.044	7.500	1.00	41.02	
MOTA	25	CA	GLU	1467	-14.428	7.960	8.427	1.00	42.42	
MOTA	26	CB	GLU	1467	-15.931	7.904	8.712	1.00	47.98	
MOTA	27	CG	GLU	1467	-16.565	9.238	9.105	1.00	52.79	
MOTA	28	CD	GLU	1467	-17.998	9.093	9.606	1.00	54.21	
MOTA	29	OE1	GLU	1467	-18.474	7.949	9.741	1.00	58.90	
MOTA	30	OE2	GLU	1467	-18.650	10.120	9.879	1.00	55.90	
ATOM	31	С	GLU	1467	-13.972	6.628	7.837	1.00	40.93	
MOTA	32	0	GLU	1467	-14.061	6.426	6.620	1.00	44.32	
MOTA	33	N	ASP	1468	-13.473	5.731	8.689	1.00	35.10	
MOTA	35	CA	ASP	1468	-13.024	4.404	8.256	1.00	31.82	
ATOM	36	CB	ASP	1468	-11.507	4.358	7.992	1.00	30.65	
MOTA	37	CG	ASP	1468	-11.025	3.002	7.440	1.00	29.93	
MOTA	38	OD1	ASP	1468	-11.689	1.958	7.603	1.00	29.63	
MOTA	39	OD2	ASP	1468	-9.945	2.974	6.835	1.00	33.63	
MOTA	40	C	ASP	1468	-13.394	3.441	9.369	1.00	31.81	
ATOM	41	0	ASP	1468	-12.618	3.209	10.302	1.00	31.91	
MOTA	42	N	PRO	1469	-14.569	2.819	9.247	1.00	29.68	
MOTA	43	CD	PRO	1469	-15.482	2.963	8.097	1.00	28.33	
ATOM	44	CA	PRO	1469	-15.100	1.863	10.220	1.00	31.80	
ATOM	45	CB	PRO	1469	-16.352	1.331	9.510	1.00	32.51	
ATOM	46	CG	PRO	1469	-16.783	2.496	8.656	1.00	27.41	
MOTA	47	C	PRO	1469	-14.146	0.731	10.590	1.00	30.44	
MOTA	48	0	PRO	1469	-14.272	0.135	11.654	1.00	30.02	
MOTA	49	N	ARG	1470	-13.198	0.442	9.704	1.00	31.06	
MOTA	51	CA	ARG	1470	-12.240	-0.636	9.917	1.00	31.86	
ATOM	52	CB	ARG	1470	-11.386	-0.860	8.660	1.00	31.36	
ATOM	53	CG	ARG	1470	-12.107	-1.437	7.448	1.00	33.08	

3.000									
ATO		CD		_	-11.148	-1.588	6.248	3 1.00	31.08
ATO:		NE	ARG		-10.540	-0.310	5.891		
ATO		CZ	ARG		-9.656	-0.135			
ATO		NH:		-	-9.260	-1.164			
ATO		NH2	2 ARG	1470	-9.155	1.074			
ATO		С	ARG	1470	-11.290	-0.436		_	-
ATO		0	ARG	1470	-10.820	-1.410			
ATO		N	TRP	1471	-11.031	0.814			31.84
ATO		. CA	TRP	1471	-10.063	1.090			
ATON		CB	TRP	1471	-8.816	1.677			
ATON		CG	TRP	1471	-8.173	0.725	10.941		30.15
ATOM		CD2	TRP	1471	-7.288	-0.329	11.315		29.54
ATOM	1 72	CE2	TRP	1471	-6.913	-0.992	10.132		31.07
ATOM	1 73	CE3	TRP	1471	-6.762	-0.768	12.536		34.41
ATOM	1 74	CD1	TRP	1471	-8.309	0.660	9.587	1.00	29.46
ATOM	75	NE1	TRP	1471	-7.557	-0.371	9.089		30.20
ATOM	77	CZ2	TRP	1471	-6.042	-2.085	10.135	1.00	33.09
ATOM	78	CZ3	TRP	1471	-5.897	-1.853	12.540	1.00	31.68
ATOM	79	CH2	TRP	1471	-5.541	-2.494	11.347	1.00	29.65
ATOM	80	C	TRP	1471	-10.477	2.019	13.620	1.00	30.18
ATOM	81	0	TRP	1471	-9.782	2.108		1.00	29.94
MOTA	82	N	GLU	1472	-11.573	2.737	14.631 13.416	1.00	30.00
ATOM	84	CA	GLU	1472	-12.051	3.706		1.00	29.06
ATOM	85	CB	GLU	1472	-13.312	4.386	14.380	1.00	28.62
MOTA	86	CG	GLU	1472	-13.641	5.733	13.849	1.00	29.16
ATOM	87	CD	GLU	1472	-12.676	6.848	14.529	1.00	30.74
ATOM	88	OE1	GLU	1472	-12.090	6.799	14.156	1.00	30.05
ATOM	89	OE2	GLU	1472	-12.511	7.784	13.057	1.00	31.32
MOTA	90	C	GLU	1472	-12.327	3.159	14.961	1.00	30.26
ATOM	91	0	GLU	1472	-12.969	2.125	15.767 15.916	1.00	28.70
ATOM	92	N	LEU	1473	-11.810	3.842	16.781	1.00	31.01
ATOM	94	CA	LEU	1473	-12.054	3.451	18.161	1.00	27.38
ATOM	95	CB	LEU	1473	-10.763	3.073	18.899	1.00	29.61
ATOM	96	CG	LEU	1473	-10.923	2.756	20.403	1.00	28.56
MOTA	97	CD1	LEU	1473	-11.485	1.354	20.403	1.00	30.06
ATOM	98	CD2	LEU	1473	-9.595	2.876		1.00	28.42
ATOM	99	C	LEU	1473	-12.617	4.714	21.115 18.764	1.00	28.15
ATOM	100	0	LEU	1473	-12.179	5.814		1.00	31.81
MOTA	101	N	PRO	1474	-13.670	4.591	18.407	1.00	33.00
ATOM	102	CD	PRO	1474	-14.488	3.400	19.596	1.00	31.45
MOTA	103	CA	PRO	1474	-14.261	5.774	19.859	1.00	31.72
MOTA	104	CB	PRO	1474	-15.400	5.176	20.226	1.00	31.23
ATOM	105	CG	PRO	1474	-15.815	4.005	21.048	1.00	29.01
ATOM	106	С	PRO	1474	-13.217	6.444	20.247	1.00	29.09
ATOM	107	0	PRO	1474	-12.447		21.120	1.00	33.36
ATOM	108	N	ARG	1475	-13.188	5.765	21.808	1.00	36.40
ATOM	110	CA	ARG	1475	-12.228	7.770	21.112	1.00	33.67
ATOM	111	CB	ARG	1475	-12.433	8.498	21.924	1.00	33.96
ATOM	112	CG	ARG	1475	-12.433	9.991	21.735	1.00	35.31
ATOM	113	CD	ARG	1475		10.405	20.333	1.00	40.10
ATOM	114	NE			-12.060	11.906	20.145		42.98
ATOM	116	CZ			-11.785	12.194	18.737		42.91
ATOM	117	NH1		1475 1475	-10.578	12.443	18.253		41.30
ATOM	120	NH2			-9.529		19.064		41.88
			- 440	±3/3	-10.413	12.567	16.943	1.00	40.98

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ATOM 124 O ARG 1475 -11.240 8.046 24.061 1.00 33 ATOM 125 N ASP 1476 -13.479 7.920 23.928 1.00 36 ATOM 127 CA ASP 1476 -13.479 7.581 25.335 1.00 36 ATOM 128 CB ASP 1476 -15.112 7.629 25.741 1.00 36 ATOM 129 CG ASP 1476 -15.930 6.480 25.163 1.00 46 ATOM 130 OD1 ASP 1476 -15.438 5.706 24.322 1.00 46 ATOM 131 OD2 ASP 1476 -15.438 5.706 24.322 1.00 46 ATOM 132 C ASP 1476 -13.023 6.232 25.724 1.00 36 ATOM 133 O ASP 1476 -13.023 6.232 25.724 1.00 36 ATOM 133 O ASP 1476 -13.023 6.232 25.724 1.00 36 ATOM 134 N ARG 1477 -12.564 5.475 24.732 1.00 36 ATOM 136 CA ARG 1477 -11.961 4.171 24.993 1.00 36 ATOM 137 CB ARG 1477 -12.269 3.212 23.852 1.00 36 ATOM 138 CG ARG 1477 -13.716 2.939 23.640 1.00 25 ATOM 140 NE ARG 1477 -14.498 3.342 25.918 1.00 36 ATOM 142 CZ ARG 1477 -14.498 3.342 25.918 1.00 36 ATOM 143 NH1 ARG 1477 -14.498 3.342 25.918 1.00 36 ATOM 143 NH1 ARG 1477 -14.498 3.342 25.918 1.00 36 ATOM 146 NH2 ARG 1477 -14.500 1.794 27.549 1.00 36 ATOM 149 C ARG 1477 -14.950 4.025 28.062 1.00 36 ATOM 150 O ARG 1477 -9.777 3.281 25.455 1.00 36 ATOM 151 N LEU 1478 -9.923 5.466 24.984 1.00 36 ATOM 151 N LEU 1478 -9.923 5.466 24.984 1.00 36 ATOM 153 CA LEU 1478 -8.493 5.663 25.076 1.00 36 ATOM 155 CG LEU 1478 -8.493 5.663 25.076 1.00 36 ATOM 156 CD1 LEU 1478 -8.493 5.663 25.076 1.00 36 ATOM 157 CD2 LEU 1478 -8.493 5.663 25.076 1.00 36 ATOM 156 CD1 LEU 1478 -8.493 5.663 25.076 1.00 36 ATOM 157 CD2 LEU 1478 -6.581 6.137 23.284 1.00 36 ATOM 157 CD2 LEU 1478 -8.6280 4.650 23.161 1.00 24 ATOM 158 C LEU 1478 -8.6280 4.650 23.161 1.00 24 ATOM 159 O LEU 1478 -8.581 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.581 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.581 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.581 6.505 26.295 1.00 36 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -	O ARG 1475 -11.240 8.046 24.061 1.00 37.10 N ASP 1476 -13.479 7.920 23.928 1.00 36.47 CA ASP 1476 -13.632 7.581 25.335 1.00 37.24 CB ASP 1476 -15.112 7.629 25.741 1.00 39.66 CG ASP 1476 -15.438 5.706 24.322 1.00 47.52 OD1 ASP 1476 -15.438 5.706 24.322 1.00 47.52 OD2 ASP 1476 -17.098 6.349 25.568 1.00 48.06 C ASP 1476 -13.034 5.856 26.898 1.00 40.09 N ARG 1477 -12.564 5.475 24.732 1.00 34.34 CA ARG 1477 -11.961 4.171 24.993 1.00 31.59 CG ARG 1477 -12.269 3.212 23.852 1.00 31.59 CG </th
ATOM 125 N ASP 1476 -13.479 7.920 23.928 1.00 36 ATOM 127 CA ASP 1476 -13.632 7.581 25.335 1.00 36 ATOM 128 CB ASP 1476 -15.112 7.629 25.741 1.00 36 ATOM 129 CG ASP 1476 -15.930 6.480 25.163 1.00 46 ATOM 130 OD1 ASP 1476 -15.438 5.706 24.322 1.00 46 ATOM 131 OD2 ASP 1476 -15.438 5.706 24.322 1.00 46 ATOM 131 OD2 ASP 1476 -13.023 6.232 25.724 1.00 36 ATOM 132 C ASP 1476 -13.023 6.232 25.724 1.00 36 ATOM 133 O ASP 1476 -13.034 5.856 26.898 1.00 46 ATOM 134 N ARG 1477 -12.564 5.475 24.732 1.00 36 ATOM 136 CA ARG 1477 -11.961 4.171 24.993 1.00 36 ATOM 137 CB ARG 1477 -12.269 3.212 23.852 1.00 36 ATOM 138 CG ARG 1477 -14.314 2.342 24.875 1.00 36 ATOM 140 NE ARG 1477 -14.498 3.342 25.918 1.00 36 ATOM 140 NE ARG 1477 -14.498 3.342 25.918 1.00 36 ATOM 143 NH1 ARG 1477 -14.498 3.342 25.918 1.00 36 ATOM 144 NH2 ARG 1477 -14.490 4.025 28.062 1.00 36 ATOM 145 NH2 ARG 1477 -10.452 4.266 25.153 1.00 36 ATOM 149 C ARG 1477 -9.777 3.281 25.445 1.00 36 ATOM 150 O ARG 1477 -9.777 3.281 25.445 1.00 36 ATOM 151 N LEU 1478 -9.923 5.466 24.984 1.00 36 ATOM 155 CG LEU 1478 -8.493 5.663 25.076 1.00 36 ATOM 156 CD1 LEU 1478 -6.581 6.137 23.284 1.00 36 ATOM 156 CD LEU 1478 -6.581 6.137 23.284 1.00 36 ATOM 157 CD2 LEU 1478 -6.581 6.137 23.284 1.00 36 ATOM 159 O LEU 1478 -6.581 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -6.581 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.508 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -6.580 4.650 23.161 1.00 36 ATOM 159 O LEU 1478 -6.581 6.599 28.491 1.00 36 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 163 CB VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36	N ASP 1476 -13.479 7.920 23.928 1.00 36.47 CA ASP 1476 -13.632 7.581 25.335 1.00 37.24 CB ASP 1476 -15.112 7.629 25.741 1.00 39.66 CG ASP 1476 -15.930 6.480 25.163 1.00 42.38 OD1 ASP 1476 -15.438 5.706 24.322 1.00 47.52 OD2 ASP 1476 -13.023 6.349 25.568 1.00 48.06 C ASP 1476 -13.023 6.232 25.724 1.00 36.93 O ASP 1476 -13.034 5.856 26.898 1.00 40.09 N ARG 1477 -12.564 5.475 24.732 1.00 34.34 CA ARG 1477 -11.961 4.171 24.993 1.00 32.47 CB ARG 1477 -12.269 3.212 23.852 1.00 31.59 CG ARG 1477 -14.314 2.342 24.875 1.00 30.65 NE ARG 1477 -14.314 2.342 24.875 1.00 30.65 NE ARG 1477 -14.498 3.342 25.918 1.00 31.37 CZ ARG 1477 -14.498 3.342 25.918 1.00 31.37 CZ ARG 1477 -14.498 3.342 25.918 1.00 32.81 NH1 ARG 1477 -14.822 3.055 27.174 1.00 32.81 NH1 ARG 1477 -14.950 4.025 28.062 1.00 31.74 C ARG 1477 -10.452 4.266 25.153 1.00 33.13 O ARG 1477 -9.777 3.281 25.445 1.00 33.55 N LEU 1478 -9.923 5.466 24.984 1.00 33.56 CB LEU 1478 -8.493 5.663 25.076 1.00 34.98 CG LEU 1478 -8.493 5.663 25.076 1.00 34.98 CG LEU 1478 -6.581 6.137 23.284 1.00 31.11 CD1 LEU 1478 -6.581 6.137 23.284 1.00 31.11 CD1 LEU 1478 -6.580 4.650 23.161 1.00 28.80 C LEU 1478 -6.581 6.137 23.284 1.00 31.11 CD1 LEU 1478 -6.280 4.650 23.161 1.00 28.80 C LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -6.428 6.839 21.940 1.00 28.80
ATOM 127 CA ASP 1476 -13.632 7.581 25.335 1.00 33 ATOM 128 CB ASP 1476 -15.112 7.629 25.741 1.00 33 ATOM 129 CG ASP 1476 -15.930 6.480 25.163 1.00 43 ATOM 130 OD1 ASP 1476 -15.930 6.480 25.163 1.00 43 ATOM 131 OD2 ASP 1476 -15.438 5.706 24.322 1.00 44 ATOM 131 OD2 ASP 1476 -17.098 6.349 25.568 1.00 44 ATOM 132 C ASP 1476 -13.023 6.232 25.724 1.00 36 ATOM 133 O ASP 1476 -13.023 6.232 25.724 1.00 36 ATOM 134 N ARG 1477 -12.564 5.475 24.732 1.00 36 ATOM 136 CA ARG 1477 -12.564 5.475 24.732 1.00 36 ATOM 137 CB ARG 1477 -12.269 3.212 23.852 1.00 36 ATOM 138 CG ARG 1477 -12.269 3.212 23.852 1.00 36 ATOM 139 CD ARG 1477 -14.314 2.342 24.875 1.00 36 ATOM 140 NE ARG 1477 -14.314 2.342 24.875 1.00 36 ATOM 140 NE ARG 1477 -14.498 3.342 25.918 1.00 36 ATOM 143 NH1 ARG 1477 -14.822 3.055 27.174 1.00 36 ATOM 143 NH1 ARG 1477 -14.822 3.055 27.174 1.00 36 ATOM 146 NH2 ARG 1477 -14.950 4.025 28.062 1.00 36 ATOM 149 C ARG 1477 -14.950 4.025 28.062 1.00 36 ATOM 150 O ARG 1477 -9.777 3.281 25.445 1.00 36 ATOM 151 N LEU 1478 -9.923 5.466 24.984 1.00 36 ATOM 151 N LEU 1478 -8.493 5.663 25.076 1.00 36 ATOM 155 CG LEU 1478 -8.493 5.663 25.076 1.00 36 ATOM 156 CD1 LEU 1478 -8.493 5.663 25.076 1.00 36 ATOM 157 CD2 LEU 1478 -6.581 6.137 23.284 1.00 36 ATOM 157 CD2 LEU 1478 -6.581 6.137 23.284 1.00 36 ATOM 158 C LEU 1478 -8.493 5.663 25.076 1.00 36 ATOM 157 CD2 LEU 1478 -8.581 6.555 26.295 1.00 36 ATOM 159 O LEU 1478 -8.581 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.581 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.581 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.581 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.581 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.581 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.581 6.505 26.295 1.00 36 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 160 N VAL 1479 -7.558 5.879 29.742 1.00 36 ATOM 160 N VAL 1479 -7.558 5.879 29.742 1.00 36 ATOM 160 N VAL 1479 -7.558 5.879 29.742 1.00 36 ATOM 160 N VAL 1479 -7.558 5.	CA ASP 1476 -13.632 7.581 25.335 1.00 37.24 CB ASP 1476 -15.112 7.629 25.741 1.00 39.66 CG ASP 1476 -15.930 6.480 25.163 1.00 42.38 OD1 ASP 1476 -15.438 5.706 24.322 1.00 47.52 OD2 ASP 1476 -17.098 6.349 25.568 1.00 48.06 C ASP 1476 -13.023 6.232 25.724 1.00 36.93 O ASP 1476 -13.034 5.856 26.898 1.00 40.09 N ARG 1477 -12.564 5.475 24.732 1.00 34.34 CA ARG 1477 -11.961 4.171 24.993 1.00 32.47 CB ARG 1477 -12.269 3.212 23.852 1.00 31.59 CG ARG 1477 -13.716 2.939 23.640 1.00 29.66 CD ARG 1477 -14.314 2.342 24.875 1.00 30.65 NE ARG 1477 -14.498 3.342 25.918 1.00 31.37 CZ ARG 1477 -14.498 3.342 25.918 1.00 31.37 CZ ARG 1477 -14.822 3.055 27.174 1.00 32.81 NH1 ARG 1477 -14.822 3.055 27.174 1.00 32.81 NH1 ARG 1477 -14.950 4.025 28.062 1.00 31.74 C ARG 1477 -9.777 3.281 25.445 1.00 33.55 N LEU 1478 -9.923 5.466 24.984 1.00 33.55 N LEU 1478 -9.923 5.466 24.984 1.00 34.43 CA LEU 1478 -8.493 5.663 25.076 1.00 34.98 CG LEU 1478 -6.280 6.350 23.790 1.00 34.98 CG LEU 1478 -6.280 4.650 23.161 1.00 28.80 C LEU 1478 -6.280 4.650 23.161 1.00 28.80 C LEU 1478 -6.428 6.839 21.940 1.00 28.80
ATOM 128 CB ASP 1476 -15.112 7.629 25.741 1.00 33 ATOM 129 CG ASP 1476 -15.930 6.480 25.163 1.00 42 ATOM 130 OD1 ASP 1476 -15.438 5.706 24.322 1.00 42 ATOM 131 OD2 ASP 1476 -17.098 6.349 25.568 1.00 42 ATOM 132 C ASP 1476 -13.023 6.232 25.724 1.00 36 ATOM 133 O ASP 1476 -13.034 5.856 26.898 1.00 46 ATOM 134 N ARG 1477 -12.564 5.475 24.732 1.00 36 ATOM 136 CA ARG 1477 -11.961 4.171 24.993 1.00 36 ATOM 137 CB ARG 1477 -12.269 3.212 23.852 1.00 36 ATOM 138 CG ARG 1477 -13.716 2.939 23.640 1.00 26 ATOM 139 CD ARG 1477 -14.314 2.342 24.875 1.00 36 ATOM 140 NE ARG 1477 -14.498 3.342 25.918 1.00 36 ATOM 142 CZ ARG 1477 -14.498 3.342 25.918 1.00 36 ATOM 143 NH1 ARG 1477 -14.822 3.055 27.174 1.00 36 ATOM 146 NH2 ARG 1477 -14.950 4.025 28.062 1.00 36 ATOM 149 C ARG 1477 -10.452 4.266 25.153 1.00 36 ATOM 151 N LEU 1478 -9.927 3.2466 24.984 1.00 36 ATOM 153 CA LEU 1478 -8.493 5.663 25.076 1.00 36 ATOM 155 CG LEU 1478 -8.493 5.663 23.790 1.00 36 ATOM 156 CD1 LEU 1478 -6.581 6.137 23.284 1.00 36 ATOM 157 CD2 LEU 1478 -6.581 6.137 23.284 1.00 36 ATOM 158 C LEU 1478 -6.581 6.137 23.284 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 150 O N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 150 CA VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -7.558 5.879 28.491 1.00 36	CB ASP 1476 -15.112 7.629 25.741 1.00 39.66 CG ASP 1476 -15.930 6.480 25.163 1.00 42.38 OD1 ASP 1476 -15.438 5.706 24.322 1.00 47.52 OD2 ASP 1476 -17.098 6.349 25.568 1.00 48.06 C ASP 1476 -13.023 6.232 25.724 1.00 36.93 O ASP 1476 -13.034 5.856 26.898 1.00 40.09 N ARG 1477 -12.564 5.475 24.732 1.00 34.34 CA ARG 1477 -11.961 4.171 24.993 1.00 32.47 CB ARG 1477 -12.269 3.212 23.852 1.00 31.59 CG ARG 1477 -13.716 2.939 23.640 1.00 29.66 CD ARG
ATOM 129 CG ASP 1476 -15.930 6.480 25.163 1.00 42 ATOM 130 OD1 ASP 1476 -15.438 5.706 24.322 1.00 47 ATOM 131 OD2 ASP 1476 -17.098 6.349 25.568 1.00 42 ATOM 132 C ASP 1476 -13.023 6.232 25.724 1.00 36 ATOM 133 O ASP 1476 -13.034 5.856 26.898 1.00 36 ATOM 134 N ARG 1477 -12.564 5.475 24.732 1.00 36 ATOM 136 CA ARG 1477 -11.961 4.171 24.993 1.00 36 ATOM 137 CB ARG 1477 -12.269 3.212 23.852 1.00 36 ATOM 138 CG ARG 1477 -13.716 2.939 23.640 1.00 26 ATOM 139 CD ARG 1477 -14.314 2.342 24.875 1.00 36 ATOM 140 NE ARG 1477 -14.498 3.342 25.918 1.00 36 ATOM 140 NE ARG 1477 -14.498 3.342 25.918 1.00 36 ATOM 143 NH1 ARG 1477 -14.498 3.342 25.918 1.00 36 ATOM 146 NH2 ARG 1477 -14.822 3.055 27.174 1.00 36 ATOM 149 C ARG 1477 -14.950 4.025 28.062 1.00 36 ATOM 150 O ARG 1477 -9.777 3.281 25.445 1.00 36 ATOM 151 N LEU 1478 -9.9777 3.281 25.445 1.00 36 ATOM 153 CA LEU 1478 -8.493 5.663 25.076 1.00 36 ATOM 156 CD1 LEU 1478 -8.493 5.663 25.076 1.00 36 ATOM 157 CD2 LEU 1478 -8.628 4.650 23.161 1.00 36 ATOM 158 C LEU 1478 -6.581 6.137 23.284 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 27.293 1.00 36 ATOM 150 O N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 160 N VAL 1479 -7.556 6.599 28.491 1.00 36 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 163 CB VAL 1479 -7.558 5.878 27.293 1.00 36	CG ASP 1476 -15.930 6.480 25.163 1.00 42.38 OD1 ASP 1476 -15.438 5.706 24.322 1.00 47.52 OD2 ASP 1476 -17.098 6.349 25.568 1.00 48.06 C ASP 1476 -13.023 6.232 25.724 1.00 36.93 O ASP 1476 -13.034 5.856 26.898 1.00 40.09 N ARG 1477 -12.564 5.475 24.732 1.00 34.34 CA ARG 1477 -11.961 4.171 24.993 1.00 32.47 CB ARG 1477 -12.269 3.212 23.852 1.00 31.59 CG ARG 1477 -13.716 2.939 23.640 1.00 29.66 CD ARG 1477 -14.314 2.342 24.875 1.00 30.65 NE ARG
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ATOM 136 CA ARG 1477 -11.961 4.171 24.993 1.00 32 ATOM 137 CB ARG 1477 -12.269 3.212 23.852 1.00 32 ATOM 138 CG ARG 1477 -13.716 2.939 23.640 1.00 29 ATOM 139 CD ARG 1477 -14.314 2.342 24.875 1.00 30 ATOM 140 NE ARG 1477 -14.498 3.342 25.918 1.00 30 ATOM 142 CZ ARG 1477 -14.822 3.055 27.174 1.00 30 ATOM 143 NH1 ARG 1477 -15.002 1.794 27.549 1.00 30 ATOM 146 NH2 ARG 1477 -14.950 4.025 28.062 1.00 30 ATOM 149 C ARG 1477 -10.452 4.266 25.153 1.00 30 ATOM 150 O ARG 1477 -9.777 3.281 25.445 1.00 30 ATOM 151 N LEU 1478 -9.923 5.466 24.984 1.00 30 ATOM 153 CA LEU 1478 -8.493 5.663 25.076 1.00 30 ATOM 154 CB LEU 1478 -8.493 5.663 25.076 1.00 30 ATOM 155 CG LEU 1478 -6.581 6.137 23.284 1.00 30 ATOM 156 CD1 LEU 1478 -6.581 6.137 23.284 1.00 30 ATOM 157 CD2 LEU 1478 -6.280 4.650 23.161 1.00 20 ATOM 158 C LEU 1478 -8.158 6.505 26.295 1.00 30 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 30 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 30 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 30 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 30 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 30 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 30 ATOM 163 CB VAL 1479 -7.569 5.707 29.742 1.00 30 ATOM 163 CB VAL 1479 -7.569 5.707 29.742 1.00 30	CA ARG 1477 -11.961 4.171 24.993 1.00 32.47 CB ARG 1477 -12.269 3.212 23.852 1.00 31.59 CG ARG 1477 -13.716 2.939 23.640 1.00 29.66 CD ARG 1477 -14.314 2.342 24.875 1.00 30.65 NE ARG 1477 -14.498 3.342 25.918 1.00 31.37 CZ ARG 1477 -14.822 3.055 27.174 1.00 32.81 NH1 ARG 1477 -15.002 1.794 27.549 1.00 33.92 NH2 ARG 1477 -14.950 4.025 28.062 1.00 31.74 C ARG 1477 -10.452 4.266 25.153 1.00 33.13 O ARG 1477 -9.777 3.281 25.445 1.00 33.55 N LEU 1478 -9.923 5.466 24.984 1.00 34.43 CA LEU 1478 -8.493 5.663 25.076 1.00 34.43 CA LEU 1478 -6.581 6.350 23.790 1.00 34.98 CG LEU 1478 -6.581 6.137 23.284 1.00 31.11 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26.62 CD2 LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -8.158 6.505 26.295 1.00 36.21 O LEU 1478 -8.158 6.505 26.295 1.00 36.21
ATOM 137 CB ARG 1477 -12.269 3.212 23.852 1.00 3.212 ATOM 138 CG ARG 1477 -13.716 2.939 23.640 1.00 29.34 ATOM 139 CD ARG 1477 -14.314 2.342 24.875 1.00 30.34 ATOM 140 NE ARG 1477 -14.498 3.342 25.918 1.00 30.34 ATOM 142 CZ ARG 1477 -14.822 3.055 27.174 1.00 30.34 ATOM 143 NH1 ARG 1477 -15.002 1.794 27.549 1.00 30.34 ATOM 146 NH2 ARG 1477 -14.950 4.025 28.062 1.00 30.34 ATOM 149 C ARG 1477 -10.452 4.266 25.153 1.00 30.34 ATOM 150 O ARG 1477 -9.777 3.281 25.445 1.00 30.34 ATOM 151 N LEU 1478 -9.923 5.466 24.984 1.00 30.34 ATOM 153 CA LEU 1478 -8.493 5.663 25.076 1.00 30.34 ATOM 154 CB LEU 1478 -8.493 5.663 25.076 1.00 30.34 ATOM 155 CG LEU 1478 -8.493 5.663 25.076 1.00 30.34 ATOM 156 CD1 LEU 1478 -6.581 6.137 23.284 1.00 30.34 ATOM 157 CD2 LEU 1478 -6.581 6.137 23.284 1.00 30.34 ATOM 157 CD2 LEU 1478 -6.280 4.650 23.161 1.00 20.34 ATOM 158 C LEU 1478 -8.158 6.505 26.295 1.00 30.34 ATOM 159 O LEU 1478 -8.158 6.505 26.295 1.00 30.34 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 30.34 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 30.34 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 30.34 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 30.34 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 30.34 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 30.34 ATOM 163 CB VAL 1479 -7.558 5.878 27.293 1.00 30.34 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 30.34 ATOM 163 CB VAL 1479 -7.569 5.707 29.742 1.00 30.34 ATOM 163 CB VAL 1479 -7.569 5.707 29.742 1.00 30.34 ATOM 163 CB VAL 1479 -7.569 5.707 29.742 1.00 30.34 ATOM 163 CB VAL 1479 -7.569 5.707 29.742 1.00 30.34 ATOM 163 CB VAL 1479 -7.569 5.707 29.742 1.00 30.34 ATOM 163 CB VAL 1479 -7.569 5.707 29.742 1.00 30.34 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 30.34 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 30.34 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 30.34 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 30.34 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 30.34 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 30.34 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 30.34 ATOM 163 CB VA	CB ARG 1477 -12.269 3.212 23.852 1.00 31.59 CG ARG 1477 -13.716 2.939 23.640 1.00 29.66 CD ARG 1477 -14.314 2.342 24.875 1.00 30.65 NE ARG 1477 -14.498 3.342 25.918 1.00 31.37 CZ ARG 1477 -14.822 3.055 27.174 1.00 32.81 NH1 ARG 1477 -15.002 1.794 27.549 1.00 33.92 NH2 ARG 1477 -14.950 4.025 28.062 1.00 31.74 C ARG 1477 -10.452 4.266 25.153 1.00 33.13 O ARG 1477 -9.777 3.281 25.445 1.00 33.55 N LEU 1478 -9.923 5.466 24.984 1.00 34.43 CB LEU
ATOM 138 CG ARG 1477 -13.716 2.939 23.640 1.00 29 ATOM 139 CD ARG 1477 -14.314 2.342 24.875 1.00 36 ATOM 140 NE ARG 1477 -14.498 3.342 25.918 1.00 36 ATOM 142 CZ ARG 1477 -14.822 3.055 27.174 1.00 36 ATOM 143 NH1 ARG 1477 -15.002 1.794 27.549 1.00 36 ATOM 146 NH2 ARG 1477 -14.950 4.025 28.062 1.00 36 ATOM 149 C ARG 1477 -10.452 4.266 25.153 1.00 36 ATOM 150 O ARG 1477 -9.777 3.281 25.445 1.00 36 ATOM 151 N LEU 1478 -9.923 5.466 24.984 1.00 36 ATOM 153 CA LEU 1478 -8.493 5.663 25.076 1.00 36 ATOM 154 CB LEU 1478 -8.008 6.350 23.790 1.00 36 ATOM 155 CG LEU 1478 -6.581 6.137 23.284 1.00 36 ATOM 156 CD1 LEU 1478 -6.581 6.137 23.284 1.00 36 ATOM 157 CD2 LEU 1478 -6.280 4.650 23.161 1.00 26 ATOM 158 C LEU 1478 -6.428 6.839 21.940 1.00 26 ATOM 159 O LEU 1478 -8.158 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 160 CA VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 163 CB VAL 1479 -7.156 6.599 28.491 1.00 36	CG ARG 1477 -13.716 2.939 23.640 1.00 29.66 CD ARG 1477 -14.314 2.342 24.875 1.00 30.65 NE ARG 1477 -14.498 3.342 25.918 1.00 31.37 CZ ARG 1477 -14.822 3.055 27.174 1.00 32.81 NH1 ARG 1477 -15.002 1.794 27.549 1.00 33.92 NH2 ARG 1477 -14.950 4.025 28.062 1.00 31.74 C ARG 1477 -10.452 4.266 25.153 1.00 33.13 O ARG 1477 -9.777 3.281 25.445 1.00 33.55 N LEU 1478 -9.923 5.466 24.984 1.00 34.43 CA LEU 1478 -8.493 5.663 25.076 1.00 35.68 CB LEU 1478 -8.493 5.663 25.076 1.00 35.68 CB LEU 1478 -6.581 6.137 23.284 1.00 34.98 CG LEU 1478 -6.581 6.137 23.284 1.00 31.11 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26.62 CD2 LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -8.158 6.505 26.295 1.00 36.21 O LEU 1478 -8.158 6.505 26.295 1.00 36.21
ATOM 139 CD ARG 1477 -14.314 2.342 24.875 1.00 30 ATOM 140 NE ARG 1477 -14.498 3.342 25.918 1.00 30 ATOM 142 CZ ARG 1477 -14.822 3.055 27.174 1.00 30 ATOM 143 NH1 ARG 1477 -15.002 1.794 27.549 1.00 30 ATOM 146 NH2 ARG 1477 -14.950 4.025 28.062 1.00 30 ATOM 149 C ARG 1477 -10.452 4.266 25.153 1.00 30 ATOM 150 O ARG 1477 -9.777 3.281 25.445 1.00 30 ATOM 151 N LEU 1478 -9.923 5.466 24.984 1.00 30 ATOM 153 CA LEU 1478 -8.493 5.663 25.076 1.00 30 ATOM 154 CB LEU 1478 -8.493 5.663 25.076 1.00 30 ATOM 155 CG LEU 1478 -6.581 6.137 23.284 1.00 30 ATOM 156 CD1 LEU 1478 -6.581 6.137 23.284 1.00 30 ATOM 157 CD2 LEU 1478 -6.280 4.650 23.161 1.00 20 ATOM 158 C LEU 1478 -8.428 6.839 21.940 1.00 20 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 30 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 30 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 30 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 30 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 30 ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 30 ATOM 163 CB VAL 1479 -7.156 6.599 28.491 1.00 30 ATOM 163 CB VAL 1479 -7.156 6.599 28.491 1.00 30 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 30	CD ARG 1477 -14.314 2.342 24.875 1.00 30.65 NE ARG 1477 -14.498 3.342 25.918 1.00 31.37 CZ ARG 1477 -14.822 3.055 27.174 1.00 32.81 NH1 ARG 1477 -15.002 1.794 27.549 1.00 33.92 NH2 ARG 1477 -14.950 4.025 28.062 1.00 31.74 C ARG 1477 -10.452 4.266 25.153 1.00 33.13 O ARG 1477 -9.777 3.281 25.445 1.00 33.55 N LEU 1478 -9.923 5.466 24.984 1.00 34.43 CA LEU 1478 -8.493 5.663 25.076 1.00 35.68 CB LEU 1478 -8.493 5.663 25.076 1.00 35.68 CB LEU 1478 -6.581 6.137 23.284 1.00 31.11 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26.62 CD2 LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -8.158 6.505 26.295 1.00 36.21 O LEU 1478 -8.158 6.505 26.295 1.00 39.67
ATOM 139 CD ARG 1477 -14.314 2.342 24.875 1.00 30 ATOM 140 NE ARG 1477 -14.498 3.342 25.918 1.00 30 ATOM 142 CZ ARG 1477 -14.822 3.055 27.174 1.00 30 ATOM 143 NH1 ARG 1477 -15.002 1.794 27.549 1.00 30 ATOM 146 NH2 ARG 1477 -14.950 4.025 28.062 1.00 30 ATOM 149 C ARG 1477 -10.452 4.266 25.153 1.00 30 ATOM 150 O ARG 1477 -9.777 3.281 25.445 1.00 30 ATOM 151 N LEU 1478 -9.923 5.466 24.984 1.00 30 ATOM 153 CA LEU 1478 -8.493 5.663 25.076 1.00 30 ATOM 154 CB LEU 1478 -8.493 5.663 25.076 1.00 30 ATOM 155 CG LEU 1478 -6.581 6.137 23.284 1.00 30 ATOM 156 CD1 LEU 1478 -6.581 6.137 23.284 1.00 30 ATOM 157 CD2 LEU 1478 -6.280 4.650 23.161 1.00 20 ATOM 158 C LEU 1478 -6.428 6.839 21.940 1.00 20 ATOM 159 O LEU 1478 -8.158 6.505 26.295 1.00 30 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 30 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 30 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 30 ATOM 162 CA VAL 1479 -7.558 5.878 27.293 1.00 30 ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 30 ATOM 163 CB VAL 1479 -7.156 6.599 28.491 1.00 30 ATOM 163 CB VAL 1479 -7.156 6.599 28.491 1.00 30 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 30	CD ARG 1477 -14.314 2.342 24.875 1.00 30.65 NE ARG 1477 -14.498 3.342 25.918 1.00 31.37 CZ ARG 1477 -14.822 3.055 27.174 1.00 32.81 NH1 ARG 1477 -15.002 1.794 27.549 1.00 33.92 NH2 ARG 1477 -14.950 4.025 28.062 1.00 31.74 C ARG 1477 -10.452 4.266 25.153 1.00 33.13 O ARG 1477 -9.777 3.281 25.445 1.00 33.55 N LEU 1478 -9.923 5.466 24.984 1.00 34.43 CA LEU 1478 -8.493 5.663 25.076 1.00 35.68 CB LEU 1478 -8.493 5.663 25.076 1.00 35.68 CB LEU 1478 -6.581 6.137 23.284 1.00 31.11 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26.62 CD2 LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -8.158 6.505 26.295 1.00 36.21 O LEU 1478 -8.501 7.688 26.361 1.00 39.67
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ATOM 143 NH1 ARG 1477 -15.002 1.794 27.549 1.00 32 ATOM 146 NH2 ARG 1477 -14.950 4.025 28.062 1.00 32 ATOM 149 C ARG 1477 -10.452 4.266 25.153 1.00 32 ATOM 150 O ARG 1477 -9.777 3.281 25.445 1.00 32 ATOM 151 N LEU 1478 -9.923 5.466 24.984 1.00 32 ATOM 153 CA LEU 1478 -8.493 5.663 25.076 1.00 32 ATOM 154 CB LEU 1478 -8.008 6.350 23.790 1.00 32 ATOM 155 CG LEU 1478 -6.581 6.137 23.284 1.00 32 ATOM 156 CD1 LEU 1478 -6.280 4.650 23.161 1.00 32 ATOM 157 CD2 LEU 1478 -6.428 6.839 21.940 1.00 26 ATOM 158 C LEU 1478 -8.158 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 32 ATOM 159 CA LEU 1478 -8.501 7.688 26.361 1.00 32 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 32 ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 32 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 36	NH1 ARG 1477 -15.002 1.794 27.549 1.00 33.92 NH2 ARG 1477 -14.950 4.025 28.062 1.00 31.74 C ARG 1477 -10.452 4.266 25.153 1.00 33.13 O ARG 1477 -9.777 3.281 25.445 1.00 33.55 N LEU 1478 -9.923 5.466 24.984 1.00 34.43 CA LEU 1478 -8.493 5.663 25.076 1.00 35.68 CB LEU 1478 -8.008 6.350 23.790 1.00 34.98 CG LEU 1478 -6.581 6.137 23.284 1.00 31.11 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26.62 CD2 LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -8.158 6.505 26.295 1.00 36.21 O LEU 1478 -8.501 7.688 26.361 1.00 39.67
ATOM 146 NH2 ARG 1477 -14.950 4.025 28.062 1.00 33 ATOM 149 C ARG 1477 -10.452 4.266 25.153 1.00 33 ATOM 150 O ARG 1477 -9.777 3.281 25.445 1.00 33 ATOM 151 N LEU 1478 -9.923 5.466 24.984 1.00 34 ATOM 153 CA LEU 1478 -8.493 5.663 25.076 1.00 33 ATOM 154 CB LEU 1478 -8.008 6.350 23.790 1.00 34 ATOM 155 CG LEU 1478 -6.581 6.137 23.284 1.00 33 ATOM 156 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26 ATOM 157 CD2 LEU 1478 -6.428 6.839 21.940 1.00 26 ATOM 158 C LEU 1478 -8.158 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 33 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 36 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 36	NH2 ARG 1477 -14.950 4.025 28.062 1.00 31.74 C ARG 1477 -10.452 4.266 25.153 1.00 33.13 O ARG 1477 -9.777 3.281 25.445 1.00 33.55 N LEU 1478 -9.923 5.466 24.984 1.00 34.43 CA LEU 1478 -8.493 5.663 25.076 1.00 35.68 CB LEU 1478 -8.008 6.350 23.790 1.00 34.98 CG LEU 1478 -6.581 6.137 23.284 1.00 31.11 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26.62 CD2 LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -8.158 6.505 26.295 1.00 36.21 O LEU 1478 -8.501 7.688 26.361 1.00 39.67
ATOM 149 C ARG 1477 -10.452 4.266 25.153 1.00 33 ATOM 150 O ARG 1477 -9.777 3.281 25.445 1.00 33 ATOM 151 N LEU 1478 -9.923 5.466 24.984 1.00 34 ATOM 153 CA LEU 1478 -8.493 5.663 25.076 1.00 33 ATOM 154 CB LEU 1478 -8.008 6.350 23.790 1.00 34 ATOM 155 CG LEU 1478 -6.581 6.137 23.284 1.00 33 ATOM 156 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26 ATOM 157 CD2 LEU 1478 -6.428 6.839 21.940 1.00 26 ATOM 158 C LEU 1478 -8.158 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 33 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 36 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 36	C ARG 1477 -10.452 4.266 25.153 1.00 33.13 O ARG 1477 -9.777 3.281 25.445 1.00 33.55 N LEU 1478 -9.923 5.466 24.984 1.00 34.43 CA LEU 1478 -8.493 5.663 25.076 1.00 35.68 CB LEU 1478 -8.008 6.350 23.790 1.00 34.98 CG LEU 1478 -6.581 6.137 23.284 1.00 31.11 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26.62 CD2 LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -8.158 6.505 26.295 1.00 36.21 O LEU 1478 -8.501 7.688 26.361 1.00 39.67
ATOM 149 C ARG 1477 -10.452 4.266 25.153 1.00 33 ATOM 150 O ARG 1477 -9.777 3.281 25.445 1.00 33 ATOM 151 N LEU 1478 -9.923 5.466 24.984 1.00 34 ATOM 153 CA LEU 1478 -8.493 5.663 25.076 1.00 33 ATOM 154 CB LEU 1478 -8.008 6.350 23.790 1.00 34 ATOM 155 CG LEU 1478 -6.581 6.137 23.284 1.00 33 ATOM 156 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26 ATOM 157 CD2 LEU 1478 -6.428 6.839 21.940 1.00 26 ATOM 158 C LEU 1478 -8.158 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 33 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 36 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 36	C ARG 1477 -10.452 4.266 25.153 1.00 33.13 O ARG 1477 -9.777 3.281 25.445 1.00 33.55 N LEU 1478 -9.923 5.466 24.984 1.00 34.43 CA LEU 1478 -8.493 5.663 25.076 1.00 35.68 CB LEU 1478 -8.008 6.350 23.790 1.00 34.98 CG LEU 1478 -6.581 6.137 23.284 1.00 31.11 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26.62 CD2 LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -8.158 6.505 26.295 1.00 36.21 O LEU 1478 -8.501 7.688 26.361 1.00 39.67
ATOM 150 O ARG 1477 -9.777 3.281 25.445 1.00 33 ATOM 151 N LEU 1478 -9.923 5.466 24.984 1.00 34 ATOM 153 CA LEU 1478 -8.493 5.663 25.076 1.00 33 ATOM 154 CB LEU 1478 -8.008 6.350 23.790 1.00 34 ATOM 155 CG LEU 1478 -6.581 6.137 23.284 1.00 33 ATOM 156 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26 ATOM 157 CD2 LEU 1478 -6.428 6.839 21.940 1.00 26 ATOM 158 C LEU 1478 -8.158 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 33 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 36 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 36	O ARG 1477 -9.777 3.281 25.445 1.00 33.55 N LEU 1478 -9.923 5.466 24.984 1.00 34.43 CA LEU 1478 -8.493 5.663 25.076 1.00 35.68 CB LEU 1478 -8.008 6.350 23.790 1.00 34.98 CG LEU 1478 -6.581 6.137 23.284 1.00 31.11 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26.62 CD2 LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -8.158 6.505 26.295 1.00 36.21 O LEU 1478 -8.501 7.688 26.361 1.00 39.67
ATOM 151 N LEU 1478 -9.923 5.466 24.984 1.00 34 ATOM 153 CA LEU 1478 -8.493 5.663 25.076 1.00 34 ATOM 154 CB LEU 1478 -8.008 6.350 23.790 1.00 34 ATOM 155 CG LEU 1478 -6.581 6.137 23.284 1.00 33 ATOM 156 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26 ATOM 157 CD2 LEU 1478 -6.428 6.839 21.940 1.00 26 ATOM 158 C LEU 1478 -8.158 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 33 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 33 ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 33 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 36	N LEU 1478 -9.923 5.466 24.984 1.00 34.43 CA LEU 1478 -8.493 5.663 25.076 1.00 35.68 CB LEU 1478 -8.008 6.350 23.790 1.00 34.98 CG LEU 1478 -6.581 6.137 23.284 1.00 31.11 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26.62 CD2 LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -8.158 6.505 26.295 1.00 36.21 O LEU 1478 -8.501 7.688 26.361 1.00 39.67
ATOM 153 CA LEU 1478 -8.493 5.663 25.076 1.00 39 ATOM 154 CB LEU 1478 -8.008 6.350 23.790 1.00 39 ATOM 155 CG LEU 1478 -6.581 6.137 23.284 1.00 39 ATOM 156 CD1 LEU 1478 -6.280 4.650 23.161 1.00 20 ATOM 157 CD2 LEU 1478 -6.428 6.839 21.940 1.00 20 ATOM 158 C LEU 1478 -8.158 6.505 26.295 1.00 30 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 30 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 30 ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 30 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 30	CA LEU 1478 -8.493 5.663 25.076 1.00 35.68 CB LEU 1478 -8.008 6.350 23.790 1.00 34.98 CG LEU 1478 -6.581 6.137 23.284 1.00 31.11 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26.62 CD2 LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -8.158 6.505 26.295 1.00 36.21 O LEU 1478 -8.501 7.688 26.361 1.00 39.67
ATOM 154 CB LEU 1478 -8.008 6.350 23.790 1.00 34 ATOM 155 CG LEU 1478 -6.581 6.137 23.284 1.00 33 ATOM 156 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26 ATOM 157 CD2 LEU 1478 -6.428 6.839 21.940 1.00 26 ATOM 158 C LEU 1478 -8.158 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 33 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 33 ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 33 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 36	CB LEU 1478 -8.008 6.350 23.790 1.00 34.98 CG LEU 1478 -6.581 6.137 23.284 1.00 31.11 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26.62 CD2 LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -8.158 6.505 26.295 1.00 36.21 O LEU 1478 -8.501 7.688 26.361 1.00 39.67
ATOM 155 CG LEU 1478 -6.581 6.137 23.284 1.00 33 ATOM 156 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26 ATOM 157 CD2 LEU 1478 -6.428 6.839 21.940 1.00 26 ATOM 158 C LEU 1478 -8.158 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 35 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 35 ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 35 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 36	CG LEU 1478 -6.581 6.137 23.284 1.00 31.11 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26.62 CD2 LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -8.158 6.505 26.295 1.00 36.21 O LEU 1478 -8.501 7.688 26.361 1.00 39.67
ATOM 156 CD1 LEU 1478 -6.280 4.650 23.161 1.00 26 ATOM 157 CD2 LEU 1478 -6.428 6.839 21.940 1.00 26 ATOM 158 C LEU 1478 -8.158 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 36 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 36	CD1 LEU 1478 -6.280 4.650 23.161 1.00 26.62 CD2 LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -8.158 6.505 26.295 1.00 36.21 O LEU 1478 -8.501 7.688 26.361 1.00 39.67
ATOM 157 CD2 LEU 1478 -6.428 6.839 21.940 1.00 26 ATOM 158 C LEU 1478 -8.158 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 38 ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 38 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 36	CD2 LEU 1478 -6.428 6.839 21.940 1.00 28.80 C LEU 1478 -8.158 6.505 26.295 1.00 36.21 O LEU 1478 -8.501 7.688 26.361 1.00 39.67
ATOM 158 C LEU 1478 -8.158 6.505 26.295 1.00 36 ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 36 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 36 ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 36 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 36	C LEU 1478 -8.158 6.505 26.295 1.00 36.21 O LEU 1478 -8.501 7.688 26.361 1.00 39.67
ATOM 159 O LEU 1478 -8.501 7.688 26.361 1.00 39 ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 39 ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 39 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 39	O LEU 1478 -8.501 7.688 26.361 1.00 39.67
ATOM 160 N VAL 1479 -7.558 5.878 27.293 1.00 39 ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 39 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 39	
ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 39 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 39	
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	- CGI VAL 1479 -7.017 6.527 30.983 1.00 37.23
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39
ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36.86
ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36 ATOM 175 C LEU 1480 -3.274 8.970 28.783 1.00 46	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.961 11.579 24.879 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36.86 C LEU 1480 -3.274 8.970 28.783 1.00 46.37
ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36 ATOM 175 C LEU 1480 -3.274 8.970 28.783 1.00 46 ATOM 176 O LEU 1480 -3.659 9.445 29.850 1.00 48	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36.86 C LEU 1480 -3.274 8.970 28.783 1.00 46.37 O LEU 1480 -3.659 9.445 29.850 1.00 48.86
ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36 ATOM 175 C LEU 1480 -3.274 8.970 28.783 1.00 46 ATOM 176 O LEU 1480 -3.659 9.445 29.850 1.00 46 ATOM 177 N GLY 1481 -2.033 8.537 28.594 1.00 46	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36.86 C LEU 1480 -3.274 8.970 28.783 1.00 46.37 O LEU 1480 -3.659 9.445 29.850 1.00 47.13 N
ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36 ATOM 175 C LEU 1480 -3.274 8.970 28.783 1.00 46 ATOM 176 O LEU 1480 -3.659 9.445 29.850 1.00 46 ATOM 177 N GLY 1481 -2.033 8.537 28.594 1.00 46 ATOM 179 CA GLY 1481 -1.081 8.573 29.678 1.00 48	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36.86 C LEU 1480 -3.274 8.970 28.783 1.00 46.37 O LEU 1480 -3.659 9.445 29.850 1.00 48.86 N GLY 1481 -2.033 8.537 28.594 1.00 47.13 CA GLY 1481 -1.081 8.573 29.678 1.00 48.19
ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36 ATOM 175 C LEU 1480 -3.274 8.970 28.783 1.00 46 ATOM 176 O LEU 1480 -3.659 9.445 29.850 1.00 46 ATOM 177 N GLY 1481 -2.033 8.537 28.594 1.00 46 ATOM 179 CA GLY 1481 -1.081 8.573 29.678 1.00 46 ATOM 180 C GLY 1481 0.163 9.388 29.425 1.00 56	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36.86 C LEU 1480 -3.274 8.970 28.783 1.00 46.37 O LEU 1480 -3.659 9.445 29.850 1.00 48.86 N GLY 1481 -2.033 8.537 28.594 1.00 47.13 CA GLY 1481 -1.081 8.573 29.678 1.00 48.19 C GLY 1481 0.163 9.388 29.425 1.00 50.27
ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36 ATOM 175 C LEU 1480 -3.274 8.970 28.783 1.00 46 ATOM 176 O LEU 1480 -3.659 9.445 29.850 1.00 46 ATOM 177 N GLY 1481 -2.033 8.537 28.594 1.00 46 ATOM 179 CA GLY 1481 -1.081 8.573 29.678 1.00 46 ATOM 180 C GLY 1481 0.163 9.388 29.425 1.00 56 ATOM 181 O GLY 1481 0.152 10.367 28.675 1.00 56	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36.86 C LEU 1480 -3.274 8.970 28.783 1.00 46.37 O LEU 1480 -3.659 9.445 29.850 1.00 48.86 N GLY 1481 -2.033 8.537 28.594 1.00 47.13 CA GLY 1481 -1.081 8.573 29.678 1.00 48.19 C GLY 1481 0.163 9.388 29.425 1.00 50.27 O GLY 1481 0.152 10.367 28.675 1.00 51.19
ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36 ATOM 175 C LEU 1480 -3.274 8.970 28.783 1.00 46 ATOM 176 O LEU 1480 -3.659 9.445 29.850 1.00 46 ATOM 177 N GLY 1481 -2.033 8.537 28.594 1.00 46 ATOM 179 CA GLY 1481 -1.081 8.573 29.678 1.00 46 ATOM 180 C GLY 1481 0.163 9.388 29.425 1.00 56 ATOM 181 O GLY 1481 0.152 10.367 28.675 1.00 56 ATOM 182 N LYS 1482 1.240 8.965 30.078 1.00 56	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.969 10.179 25.460 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36.86 C LEU 1480 -3.659 9.445 29.850 1.00 46.37 O LEU 1
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ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36 ATOM 175 C LEU 1480 -3.274 8.970 28.783 1.00 46 ATOM 176 O LEU 1480 -3.659 9.445 29.850 1.00 46 ATOM 177 N GLY 1481 -2.033 8.537 28.594 1.00 46 ATOM 179 CA GLY 1481 -1.081 8.573 29.678 1.00 46 ATOM 180 C GLY 1481 0.163 9.388 29.425 1.00 56 ATOM 181 O GLY 1481 0.152 10.367 28.675 1.00 56 ATOM 182 N LYS 1482 1.240 8.965 30.078 1.00 56 ATOM 184 CA LYS 1482 2.543 9.606 30.007 1.00 56 ATOM 185 CB LYS 1482 3.509 8.866 30.933 1.00 56	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.969 10.179 25.460 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.879 1.00 39.39 CD2 LEU 1480 -3.274 8.970 28.783 1.00 46.37 O LEU 1481 -2.033 8.537 28.594 1.00 47.13 CA
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ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36 ATOM 175 C LEU 1480 -3.274 8.970 28.783 1.00 46 ATOM 176 O LEU 1480 -3.659 9.445 29.850 1.00 46 ATOM 177 N GLY 1481 -2.033 8.537 28.594 1.00 46 ATOM 179 CA GLY 1481 -1.081 8.573 29.678 1.00 46 ATOM 180 C GLY 1481 0.163 9.388 29.425 1.00 56 ATOM 181 O GLY 1481 0.152 10.367 28.675 1.00 56 ATOM 182 N LYS 1482 1.240 8.965 30.078 1.00 56 ATOM 184 CA LYS 1482 2.543 9.606 30.007 1.00 56 ATOM 185 CB LYS 1482 3.509 8.866 30.933 1.00 56 ATOM 186 CG LYS 1482 4.971 9.026 30.567 1.00 56 ATOM 187 CD LYS 1482 5.810 7.874 31.087 1.00 56	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.961 11.579 24.879 1.00 39.39 CD LEU 1480 -3.274 8.970 28.783 1.00 46.37 O LEU
ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 36	
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ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 39 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 39	
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ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 39 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 39	N VAL 14/9 -/.000 0.0/0 2/.290 1.00 00.42
ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 39 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 39	N VAL 14/9 -/.558 5.8/8 2/.293 1.00 35.42
ATOM 162 CA VAL 1479 -7.156 6.599 28.491 1.00 39 ATOM 163 CB VAL 1479 -7.269 5.707 29.742 1.00 39	
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ATOM 164 CG1 VAL 1479 -7.017 6.527 30.983 1.00 3	CB VAL 1479 -7.269 5.707 29.742 1.00 36.29
ATOM 164 CG1 VAL 1479 -7.017 6.527 30.983 1.00 3	
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	CGI VAL 1479 -7.017 6.527 30.983 1.00 37.23
ATOM 166 C VAL 1479 -5.704 7.046 28.244 1.00 39	
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41
ATOM 167 O VAL 1479 -4.764 6.246 28.319 1.00 3	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41
ATOM 167 O VAL 1479 -4.764 6.246 28.319 1.00 33	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68
ATOM 168 N LEU 1480 -5.538 8.315 27.885 1.00 38	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68
ATOM 168 N LEU 1480 -5.538 8.315 27.885 1.00 38	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68
ATOM 168 N LEU 1480 -5.538 8.315 27.885 1.00 3	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45
ATOM 170 CA LEU 1480 -4.213 8.860 27.584 1.00 43	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15
ATOM 171 CB LEU 1480 -4.332 10.205 26.857 1.00 39	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61
ATOM 172 CG LEU 1480 -4.969 10.179 25.460 1.00 30	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61
ATOM 172 CG LEU 1480 -4.969 10.179 25.460 1.00 3	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14
ATOM 173 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39
ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36.86
ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36 ATOM 175 C LEU 1480 -3.274 8.970 28.783 1.00 46	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.961 11.579 24.879 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36.86 C LEU 1480 -3.274 8.970 28.783 1.00 46.37
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ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36 ATOM 175 C LEU 1480 -3.274 8.970 28.783 1.00 46 ATOM 176 O LEU 1480 -3.659 9.445 29.850 1.00 48	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36.86 C LEU 1480 -3.274 8.970 28.783 1.00 46.37 O LEU 1480 -3.659 9.445 29.850 1.00 48.86
ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36 ATOM 175 C LEU 1480 -3.274 8.970 28.783 1.00 46 ATOM 176 O LEU 1480 -3.659 9.445 29.850 1.00 46 ATOM 177 N GLY 1481 -2.033 8.537 28.594 1.00 46	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36.86 C LEU 1480 -3.274 8.970 28.783 1.00 46.37 O LEU 1480 -3.659 9.445 29.850 1.00 47.13 N
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ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36 ATOM 175 C LEU 1480 -3.274 8.970 28.783 1.00 46 ATOM 176 O LEU 1480 -3.659 9.445 29.850 1.00 46 ATOM 177 N GLY 1481 -2.033 8.537 28.594 1.00 46	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.961 11.579 24.879 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36.86 C LEU 1480 -3.274 8.970 28.783 1.00 46.37 O LEU 1480 -3.659 9.445 29.850 1.00 47.13 N
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	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39
	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39
ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36.86
ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36.86
ATOM 174 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36	CG2 VAL 1479 -8.650 5.059 29.812 1.00 34.41 C VAL 1479 -5.704 7.046 28.244 1.00 35.68 O VAL 1479 -4.764 6.246 28.319 1.00 33.45 N LEU 1480 -5.538 8.315 27.885 1.00 38.15 CA LEU 1480 -4.213 8.860 27.584 1.00 42.61 CB LEU 1480 -4.332 10.205 26.857 1.00 39.14 CG LEU 1480 -4.969 10.179 25.460 1.00 38.44 CD1 LEU 1480 -4.901 11.579 24.879 1.00 39.39 CD2 LEU 1480 -4.263 9.194 24.533 1.00 36.86



	7.000						206				
	ATOM		NZ	LYS	1400						
	ATOM	193	C	LYS	1482	٠.,	251	5.433	30 000		
	ATOM		0		1482	3.	145	9.676	30.986		49.92
	ATOM	195	N	LYS	1482		L15	8.700	28.609	1.00	52.31
	ATOM	196		PRO	1483	3.7		0.700	27.851	1.00	52.30
	ATOM	197	CD	PRO	1483	3.6		10.838	28.250	1.00	53.47
	ATOM		CA	PRO	1483	4.3	_	.2.105	28.997	1.00	
	ATOM	198	CB	PRO	1483	4 7		1.021	26.937	1.00	54.19
		199	CG	PRO	1483	4.7		2.480	26.976		54.10
	ATOM	200	C	PRO	1483	3.7		3.118	27.895	1.00	54.25
	ATOM	201	0	PRO		5.5	35 1	0.096	26.827	1.00	55.30
	ATOM	202	N	LEU	1483	6.34	13 10	0.017	20.02/	1.00	54.72
	MOTA	204	CA		1484	5.61	_	9.351	27.751	1.00	53.48
	ATOM	205	CB	LEU	1484	6.73	_		25.731	1.00	57.05
	ATOM	206			1484	6.30	_ ~	3.447	25.503	1.00	59.26
	ATOM		CG	LEU	1484	5.39		.241	24.669	1.00	59.26
	3	207	CD1	LEU	1484		-	.216	O = -		59.35
	7 mos.	208	CD2		1484	4.97			~		60.87
	_	209	C	_	1484	6.08	1 5		a -	1.00	57.14
		210	0			7.847	79.	_	24 770	1.00	59.79
	ATOM :	211	N		1484	8.980	9.		`	1.00	61.30
A		213	~~	_	485	7.494	10		4.701	1.00 (52.17
A	ma	214	~	GLY 1	485	8.456	- •		4.220	L.00 e	3.75
	m		_		485	8.081		173 2	3.507	00 6	6.33
	ma			GLY 1	485	6.918		412 2		_	
		`		GLN 1	491		11.	653 ₂	7 7 7 7		7.79
		18	CA (191	4.615	13.	762 ₁ :	0 20-	_	9.61
			CB G		191	4.353	13.	353 19		_	8.26
		20 (~~		191	3.476	14.3				7.98
		21 (-			3.134	14.0		_	.00 6:	1.80
AT	'OM 22		_		91	2.019	14.9			.00 70	31
AT	OM 22	. ~	_	_	91	1.355	15.6		.482 1.		. 91
AT				LN 14		1.820	14 0		.748 1.		.85
ATO		_ ` `	٠.	LN 14	91	3.709	14.8	_	.788 1.		.30
ATO			٠.	N 14	91	2.701	11.9		.881 1.		.50
ATO		^	• • •	L 149	92	4.305	11.66	59 19	.222 1.		.67
ATC			• • •			7.305	11.12	25 20.	729 1.	_	. 91
			ya Va		•	3.825	9.76	3 20.	000		. 04
ATO			l VA	L 149		4.861	8.70	5 20	F00		93
ATO.		CG				1.378	7.32	- •	050	~~.	65
ATO			VA		_ ~	5.119	8.76		_	10 39.	71
ATO						.584	9.66		_	0 40.	98
ATOM			VAI			.451	10.029	-	⁴⁹⁰ 1.0	0 43.	4.3
ATOM	1 238	CA	VAI		3 2	.400	9.212		289 1.0	0 43.	43
ATOM		~-	VAL		2	.107			388 1.00	41.	
ATOM	240	CB	VAL			.052	9.080		304 1.00		77
ATOM		CG1				410	10.133	24.7	82 1.00		
ATOM		CG2	VAL	1493		. 410	11.508	24.2	87 1.00		
		C	VAL	1493	- •	329	9.755	24.3	39 1.00		
ATOM		0	VAL	1493		589	7.693	24.6	- •	_	
ATOM	244	N	LEU		0.	948	7.058	23.7	- •		
ATOM	246	CA		1494	1.	949	7.187	25.70	-	38.8	3
ATOM	247	CB	LEU	1494	1.	468	5.880	25.79		36.24	1
ATOM	248		LEU	1494	2.2	252		26.20	05 1.00	35.92	-)
ATOM	249	CG	LEU	1494	1.8	386	5.383	27.42	9 1.00	35.41	
ATOM		CD1	LEU	1494	1.9		4.009	28.00	4 1.00	20.41	
ATOM	250	CD2	LEU	1494	2.5	. ~ -	2.931	26.92	4 1.00	36.21	
	251	C	LEU	1494	2.8		3.670	29.14	_	33.60	
ATOM	252	0	LEU	1494	-0.0	10	6.095	26.56	- •	36.03	
ATOM	253	N	ALA		-0.4	25	7.215	26.88	- 0	35.27	
				1495	-0.8	ي 07	5.043	26 45		34.35	
SSSD/55	145, v01					•	25	26.468	1.00	34.93	

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ATOM	255	CA	ALA	1495	-2.220	5.145	26.768	1.00	34.44
MOTA	256	CB	ALA	1495	-2.955	5.794	25.616	1.00	35.29
MOTA	257	С	ALA	1495	-2.781	3.770	27.018	1.00	34.59
MOTA	258	0	ALA	1495	-2.128	2.766	26.748	1.00	35.52
MOTA	259	N	GLU	1496	-3.996	3.723	27.536	1.00	36.64
MOTA	261	CA	GLU	1496	-4.652	2.462	27.806	1.00	37.57
MOTA	262	CB	GLU	1496	-5.000	2.354	29.287	1.00	38.97
MOTA	263	CG	GLU	1496	-3.769	2.304	30.185	1.00	41.79
MOTA	264	CD	${ t GLU}$	1496	-4.110	2.475	31.645	1.00	43.65
MOTA	265	OE1	\mathtt{GLU}	1496	-4.408	3.617	32.036	1.00	42.97
MOTA	266	OE2	GLU	1496	-4.086	1.475	32.398	1.00	46.65
ATOM	267	С	GLU	1496	-5.896	2.404	26.943	1.00	38.50
MOTA	268	0	GLU	1496	-6.660	3.371	26.867	1.00	40.28
ATOM	269	N	ALA	1497	-6.051	1.301	26.223	1.00	37.34
ATOM	271	CA	ALA	1497	-7.194	1.131	25.352	1.00	37.42
MOTA	272	CB	ALA	1497	-6.743	0.625	23.985	1.00	35.92
MOTA	273	C	ALA	1497	-8.146	0.148	26.000	1.00	36.77
ATOM	274	0	ALA	1497	-7.759	-0.977	26.323	1.00	35.74
MOTA	275	N	ILE	1498	-9.354	0.616	26.291	1.00	37.03
ATOM	277	CA	ILE	1498	-10.378	-0.224	26.896	1.00	36.80
ATOM	278	CB	ILE	1498	-11.372	0.612	27.728	1.00	34.53
ATOM	279	CG2	ILE	1498	-12.373	-0.290	28.425	1.00	34.59
ATOM	280	CG1	ILE	1498	-10.640	1.438	28.778	1.00	31.97
ATOM ·	281	CD1	ILE	1498	-11.552	2.344	29.541	1.00	31.12
ATOM	282	С	ILE	1498	-11.126	-0.807	25.709	1.00	38.72
ATOM	283	0	ILE	1498	-11.647	-0.066	24.879	1.00	37.74
ATOM	284	N	GLY	1499	-11.137	-2.126	25.590	1.00	40.98
MOTA	286	CA	GLY	1499	-11.839	-2.728	24.482	1.00	44.64
MOTA	287	C	GLY	1499	-10.931	-3.115	23.332	1.00	48.45
MOTA	288	0	GLY	1499	10.260	-4.147	23.401	1.00	51.92
ATOM	289	N	LEU	1500	-10.877	-2.269	22.303	1.00	47.87
ATOM	291	CA	LEU	1500	-10.076	-2.530	21.102	1.00	46.80
MOTA	292	CB	LEU	1500	-8.594	-2.770	21.434	1.00	45.37
ATOM	293	CG	LEU	1500	-7.543	-1.661	21.293	1.00	44.84
ATOM	294	CD1	LEU	1500	·-6.174	-2.290	21.450	1.00	43.33
MOTA	295	CD2	LEU	1500	-7.623	-0.959	19.948	1.00	40.43
MOTA	296	С	LEU	1500	-10.631	-3.737	20.349	1.00	45.63
MOTA	297	0	LEU	1500	-10.797	-4.823	20.915	1.00	44.42
MOTA	298	N	PRO	1505	-13.569	-5.910	25.549	1.00	52.13
MOTA	299	CD	PRO	1505	-14.316	-7.170	25.398	1.00	54.09
ATOM	300	CA	PRO	1505	-14.451	-4.828	25.999	1.00	50.46
ATOM	301	CB	PRO	1505	-15.841	-5.455	25.891	1.00	49.86
ATOM	302	CG	PRO	1505	-15.586	-6.898	26.193	1.00	52.17
MOTA	303	С	PRO	1505	-14.136	-4.370	27.422	1.00	47.75
ATOM	304	0	PRO	1505	-14.148	-3.180	27.710	1.00	47.93
MOTA	305	N	ASN	1506	-13.778	-5.313	28.285	1.00	46.20
ATOM	307	CA	ASN	1506	-13.458	-4.986	29.666	1.00	49.52
ATOM	308	CB	ASN	1506	-14.310	-5.829	30.612	1.00	52.42
ATOM	309	CG	ASN	1506	-15.788	-5.489	30.526	1.00	54.50
ATOM	310	OD1	ASN	1506	-16.179	-4.331	30.680	1.00	57.16
ATOM	311	ND2	ASN	1506	-16.610	-6.489	30.244	1.00	56.82
ATOM	314	C	ASN	1506	-11.973	-5.124	30.003	1.00	50.65
ATOM	315	0	ASN	1506	-11.583	-5.174	31.178	1.00	50.65
ATOM	316	N	ARG	1507	-11.142	-5.145	28.968	1.00	50.90

								~00					
	Į	MOTA	318	CA	ARG	1505							
	P	MOTA	319	CB	ARG	1507	,0		.276	29.	127	1.00	40.55
	,	MOTA	320	CG	ARG	1507			.483	28.		1.00	
	A	MOTA	321	CD	ARG	1507			. 833	28.9		1.00	55.81
	A	TOM	322		ARG	1507	0.40		149	30.0		1.00	61.63
			324	CZ		1507		0 -9.	490	30.5			66.01
	A		325		ARG	1507	-8.02	4 -9.	944	31.6		1.00	72.55
			328		ARG	1507	-7.19		169	32.3		1.00	77.32
			31	_	ARG	1507	-8.33	5 -11.		32.1		1.00	78.41
		-	32	_	ARG	1507	-9.015	-4.		28.5		1.00	79.30
					ARG	1507	~9.452	-3.		27.5		1.00	45.60
					JAL	1508	-7.977	-3.				1.00	42.08
					/AL	1508	-7.216			29.29		1.00	42.86
				·	'AL	1508	-6.903			28.85		1.00	40.75
				~	AL	1508	-8.184			30.01		1.00	38.75
	AT					1508	-5.919	-2.0		30.70		1.00	43.29
	AT		39 (•	AL	1508	-5.929	-2.9		31.01		1.00	37.56
	AT(_ `				1508	-5.369			28.24		1.00	39.14
	ATO		_	-	HR	1509	-5.517	-3.9		28.70		00	39.16
	ATO				HR :	1509	-4.298	-2.3		27.15		00	37.26
			_	B T		1509	-4.571	-2.7		6.48	6 1	.00	36.52
	ATC					1509	-5.423	-3.1		5.01	9 1		37.83
	ATC			G2 TI	IR 1	1509	-3.267	-4.3		5.01			43.88
	ATO			TH		.509	-3.434	-3.54		4.310) 1		34.51
	ATO		_	TH		509	-3.927	-1.49		6.473			35.82
	ATO			LY		510	-2.175	-0.40		6.174	1.		34.37
	ATO			A LY	_	510	-1.291	-1.62		6.880	1.		35.96
	ATO			3 LY		510	-0.032	-0.47		5.843	1.		86.13
	ATO			LY		510	-0.277	-0.69		7.680			7.77
	ATON			LY		510	1.023	-0.85		9.162			4.58
	ATOM			LY		510	0.947	-0.65		9.948			1.33
	ATOM			LYS		510	-0.149	-1.28		.342	1.		8.15
	ATOM		C	LYS		510	-0.149	-0.72		.187	1.		4.94
	ATOM		0	LYS		10	-0.929	-0.359		.373	1.		4.59
	ATOM		N	VAL			-0.574	-1.345		.734	1.0	_	1.43
	ATOM		CA	VAL			-1.092	0.846		.835	1.0		2.95
	ATOM		CB	VAL			-0.810	1.121		.441	1.0		2.29
	ATOM	367	CG1				-2.129	1.213		.621	1.0		2.95
	ATOM	368	CG2		15:		-2.879	-0.109		. 686	1.0	- -	. 79
	ATOM	369	С	VAL	15:		-3.026	2.354	23.	148	1.0		.84
	ATOM	370	0	VAL	151		-0.058	2.446		353	1.0		.65
	ATOM	371	N	ALA	151		0.021	3.185	24.	344	1.0		.62
	ATOM	373	CA	ALA	151		0.521	2.721		186	1.0		.24
•	ATOM	374	CB	ALA	151		1.244	3.969	21.	954	1.0		.18
	MOTA	375	C	ALA	151		2.599	3.700	21.	316	1.00	_	
	MOTA	376	0	ALA	151		0.373	4.783	21.	015	1.00		.62
	ATOM	377	N	VAL			0.151	4.264	20.0	040	1.00		
	ATOM	379	CA	VAL	151		0.204	6.054	21.3		1.00		
	ATOM	380	CB	VAL	151		0.630	6.914	20.5		1.00		
	ATOM	381	CG1		151	-	1.731	7.591	21.3		1.00		
	ATOM	382	CG2	VAL	1513	-	2.607	8.444	20.4	_	1.00		
	ATOM	383	C	VAL	1513		2.567	6.549	22.0		-	••.	
	ATOM	384	0	VAL	1513	-	203	8.008	19.8		1.00	•	45
	ATOM	385	N	VAL	1513		.924	8.750	20.5		1.00	36.	
	ATOM	387	CA	LYS	1514	-	.105	8.093	18.5		1.00	35.	
		,	CA	LYS	1514	0	.818	9.104	17.74		1.00	38.5	
	SSSD/551	145 v01								- U	.00	40.1	12
	5 ,												

ATOM	388	СВ	LYS	1514	1.339	8.513	16.439	1.00	40.93
MOTA	389	CG	LYS	1514	2.452	7.488	16.632	1.00	42.52
ATOM	390	CD	LYS	1514	2.861	6.803	15.338	1.00	46.25
MOTA	391	CE	LYS	1514	3.268	7.796	14.261	1.00	49.76
MOTA	392	NZ	LYS	1514	4.304	8.771	14.705	1.00	52.14
MOTA	396	C	LYS	1514	-0.166	10.215	17.458	1.00	40.69
MOTA	397	0	LYS	1514	-1.313	9.953	17.110	1.00	41.69
MOTA	398	N	MET	1515	0.277	11.454	17.613	1.00	43.28
ATOM	400	CA	MET	1515	-0.569	12.610	17.379	1.00	46.21
MOTA	401	CB	MET	1515	-1.363	12.936	18.644	1.00	46.96
MOTA	402	CG	MET	1515	-0.488	13.293	19.837	1.00	
MOTA	403	SD	MET	1515	-1.413	13.464	21.358	1.00	49.77
MOTA	404	CE	MET	1515	-1.593	11.761	21.814	1.00	47.84
MOTA	405	C	MET	1515	0.299	13.805	17.000	1.00	49.90
MOTA	406	0	MET	1515	1.519	13.788	17.194	1.00	49.83
MOTA	407	N	LEU	1516	-0.339	14.822	16.430	1.00	54.45
MOTA	409	CA	LEU	1516	0.335	16.053	16.023	1.00	57.57
MOTA	410	CB	LEU	1516	-0.483	16.762	14.944	1.00	54.10
ATOM	411	CG	LEU	1516	-0.800	16.007	13.664	1.00	50.71
ATOM	412	CD1	LEU	1516	-1.830	16.800	12.901	1.00	51.20
ATOM	413	CD2	LEU	1516	0.467	15.809		1.00	50.08
ATOM	414	C	LEU	1516	0.487	17.010	17.202	1.00	61.88
ATOM	415	N O	LEU	1516 1517	-0.170	16.852 18.018	18.235 17.021	1.00	63.30 66.83
ATOM ATOM	416 418	CA	LYS LYS	1517	1.335 1.568	19.036	18.037	1.00	71.46
ATOM	419	CB	LYS	1517	2.985	19.593	17.911	1.00	76.28
ATOM	420	CG	LYS	1517	4.084	18.626	18.349	1.00	82.19
ATOM	421	CD	LYS	1517	5.450	19.085	17.846	1.00	86.93
ATOM	422	CE	LYS	1517	6.579	18.228	18.411	1.00	90.46
ATOM	423	NZ	LYS	1517	7.896	18.513	17.763	1.00	92.51
ATOM	427	С	LYS	1517	0.549	20.156	17.837	1.00	72.44
ATOM	428	0	LYS	1517	-0.142	20.198	16.819	1.00	72.12
ATOM	429	N	SER	1518	0.474	21.075	18.793	1.00	73.90
ATOM	431	CA	SER	1518	-0.470	22.185	18.697	1.00	74.96
MOTA	432	CB	SER	1518	-0.498	22.980	20.002	1.00	74.72
ATOM	433	С	SER	1518	-0.133	23.100	17.525	1.00	76.16
MOTA	434	0	SER	1518	-1.029	23.667	16.897	1.00	76.56
MOTA	435	N	ASP	1519	1.158	23.245	17.232	1.00	77.24
MOTA	437	CA	ASP	1519	1.601	24.094	16.125	1.00	78.51
MOTA	438	CB	ASP	1519	2.849	24.888	16.535	1.00	79.70
MOTA	439	C	ASP	1519	1.887	23.264	14.865	1.00	78.29
ATOM	440	0	ASP	1519		23.580	14.088	1.00	78.52
ATOM	441	N	ALA	1520		22.192	14.682	1.00	76.90
ATOM	443	CA	ALA	1520		21.313	13.529	1.00	74.09
ATOM	444	CB	ALA	1520	0.737	19.930	13.840	1.00	74.20
ATOM	445	C	ALA	1520	0.580	21.895	12.318	1.00	71.82
ATOM	446	0	ALA	1520	-0.573	22.311	12.4.00	1.00	71.78
ATOM	447	N	THR	1521	1.291	21.951	11.202	1.00	69.97
ATOM	449	CA	THR	1521	0.734	22.480	9.970	1.00	68.86
ATOM	450	CB	THR	1521	1.848	22.911	9.026	1.00	68.87
ATOM	451 452	OG1	THR	1521	2.621	21.762	8.651	1.00	70.03
ATOM	453	CG2	THR	1521	2.756	23.912	9.715 9.292	1.00 1.00	71.55
ATOM ATOM	454 455	C O	THR THR	1521 1521	-0.081 0.111	21.389 20.204	9.292	1.00	67.89 69.03
MION	-z > 2	J	MILL	1341	0.111	20.204	دەد.ر		09.03





							2:	LO					
1	MOTA	456	N	GLU	7.500								
		458	CA	GLU	1522 1522	• • •			783	8.38	32 1	.00	66 50
7	MOTA	159	CB	GLU	1522			20.		7.65		.00	66.59
24	YOM 4	160	C	GLU	1522			21.		6.69	`	.00	65.71
A	TOM 4	61	0	GLU	1522			19.		6.90	_	.00	65.61 64.32
A	TOM 4	62		LYS	1523			18.		6.54		.00	
A	TOM 4	64		LYS	1523	0.3		20.2	205	6.67		.00	66.29
A	TOM 4	65		LYS		1.3		19.3	326	6.01		.00	59.93
		66		LYS	1523 1523	2.6		20.0		5.74		00	57.38
		67	~	LYS	1523	3.8		19.1	.62	5.370	_	00	60.47
		68	~	LYS		3.5		18.2	88	4.160		00	62.75
ΑT	COM 4	_		YS	1523	4.75		17.5	96	3.652		00	63.95
AT	COM 4			YS	1523 1523	4.42		16.7	21	2.494	_ •		65.88
ΑT	OM 4	_	_	YS	1523	1.56		18.1	73 (5.974			70.37
AT	'OM 47		_			1.54		17.0		5.581			54.80
AT	OM 47				1524	1.78		18.52		3.239			54.44
AT	OM 47				1524 1524	2.03		17.54	19 9	.295			51.67
AT	OM 47	_			1524 1524	2.29		18.27	71 10	.622	1.0		49.43
AT	OM 48				1524	3.59		19.08		.613	1.0		51.06
ATO	OM 48	1 0			L524	3.64		20.13	6 11	.283	1.0		54.03 56.32
ATO		2 C			1524	4.580		18.65	8 9	. 956	1.0		56.32 56.02
ATO		3 0			.524	0.847		16.59	6 9	.413	1.0	_	47.73
ATC		ı n			.525	1.017		15.38	7 9	.580	1.0		±7.73 £5.85
ATO		C			525	-0.354		L7.15		.300	1.0		17.62
ATO		' C1			525 525	-1.585		6.38	.و ٥	354	1.0		5.95
ATO		C			525	-2.801		7.30	79.	271	1.00		3.61
ATO:		CI			525	-4.193		6.665	59.	234	1.00		4.56
ATO		CI			525	-4.364		5.543	10.	268	1.00		6.02
ATO		C	LE		525	-5.215		7.740		468	1.00	_	3.80
ATO		0	LE		525	-1.605		5.372		210	1.00		5.67
ATON		N	SER		526	-1.921		4.204		416	1.00	_	6.78
ATOM		CA	SER		26	-1.245 -1.211		5.822		014	1.00		5.44
ATOM		CB	SER		26	-0.903		1.945		351	1.00		5.33
ATOM		OG	SER		26	-2.012	7.5	744	4.	84	1.00		3.48
ATOM		C ·	SER		26	-0.192		5.546	4.2		1.00		.28
ATOM		0	SER			-0.480		.821	5.9		1.00		.84
ATOM		N	ASP	15		0.994		.669	5.6		1.00		.24
ATOM	503	CA	ASP	15		2.024		.144	6.4		1.00		. 88
ATOM	504	CB	ASP	15:	27	3.376	13	.128	6.6		1.00		. 70
ATOM ATOM	505	CG	ASP	152	27	3.934	1.0	.767	6.9		1.00		.62
ATOM	506	OD1		152	27	3.399	14	.555	5.7		1.00		.01
ATOM	507	OD2	ASP	152	7	4.916	16	.434	4.6		L.00	35.	
ATOM	508	С	ASP	152		1.652	10	. 295	5.9		1.00	40.	
ATOM	509	0	ASP	152		1.951		053	7.65		.00	38.	
	510	N	LEU	152	8	0.973		872	7.46		.00	37.	68
ATOM ATOM	512	CA	LEU	152	8	0.532		460	8.72		.00	38.	
	513	CB	LEU	152		0.026		513	9.74		.00	38.	
ATOM	514	CG	LEU	152		0.505		258	10.98		.00	37.	
ATOM	515	CD1	LEU	152		0.499	11.		12.15		.00	39.	
ATOM ATOM	516	CD2	LEU	1528		0.825	10.		12.53		.00	35.	
	517	С	LEU	1528		0.568	12.		13.33		.00	35.2	
ATOM	518	0	LEU	1528		0.607	10.6		9.15		.00	38.	
ATOM	519	N	ILE	1529	•	1.450	7.4	100	9.41	-	00	37.2	
ATOM	521	CA	ILE	1529	_	2.531	11.2	41U	8.359			36.7	
SSSDIE	145 -				-		10.4	12	7.718	3 1.		35.9	
SSSD/55	145. v01					•							



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				2 496	11.419	6.931	1.00	35.67
ATOM 522	CB	ILE	1529	-3.486 -4.492	10.619	6.119	1.00	34.04 33.81
ATOM 523		ILE	1529	-4.452 -4.259	12.295	7.916	1.00	33.51
ATOM 524		ILE	1529	-5.177	13.288	7.276	1.00	37.49
ATOM 52		IF	1529	-1.912	9.447	6.786	1.00	37.11
ATOM 52	_	ILE	1529	-2.274	8.269	6.829	1.00	38.20
ATOM 52	_	ILE	1529	-0.926	9.893	6.003	1.00	38.20
ATOM 52		SER	1530	-0.323	9.036	5.050	1.00	43.32
ATOM 53	~ ~	SER	1530	0.911	9.822	4.370	1.00	52.31
ATOM 53		SER	1530	0.424	10.970	3.687	1.00	
ATOM 53	~~	SER	1530	0.424	7.808	5.719	1.00	34.40
ATOM 53		SER	1530	0.382	6.691	5.219	1.00	31.51 32.08
7140	35 0	SER	1530	1.048	8.028	6.851	1.00	
11.	36 N	GLU	1531	1.690	6.952	7.594	1.00	_
ALC:	38 CA	GLU		2.506	7.515	8.759	1.00	
A10	39 CB	GLU		3.094	6.428	9.657		
	40 CG	GLU		3.034	6.962	10.839	1.00	00
111011	41 CD	GLU				11.552		
ALC.		1 GLU		4.473 3.883		11.062	2 1.00	
F11 0	543 OF	2 GL		0.698		8.094		
	544 C	GL/	յ 1531	0.890	. 71	8.10		
	545 0	GL		-0.464	_	9 8.53		
7110	546 N	ME		-1.52		6 9.01	5 1.0	
7110	548 C.	A ME		~ ~ ~ ~		6 9.59		
	549 C	B ME				3 10.02		· -
ATOM	550 C	G ME		- 17			7 1.0	
ATOM		D ME		- 10	-	9.45		
ATOM		E MI				38 7.84		
ATOM	553	•	ET 1532)1 7.9		
MOTA	554	•	ET 1532			19 6.7		
MOTA			LU 153			74 5.5		
MOTA	557		LU 153		_	25 4.4		
MOTA			LU 153			77 4.7	-	
MOTA	559		LU 153			54 5.0	-	00
ATOM	560		LU 153			30 4.1		
ATOM	561		LU 153	_	-	.04 6.3		
MOTA	562	U	3LU 153		-	38 5. ¹		00
ATOM	563	•	GLU 15		232 2.	541 4.	-	•
MOTA	564	•	GLU 15		590 4.			
MOTA	565		MET 15	· 0 !	515 3.		. —	
ATOM		CA	MET 15	_	826 3.	02 -		
MOTA		CB	111111		038 3.			
MOTA		CG		_	479 3.			
ATOM		SD			349 4	607 2		- ·
ATOM		CE		•		.896 5		
OTA		С			689 0			
OTA		0				.100 6		
ATO		И			.336 0	.986 7		
ATO		CA			.252 1	.503 9	.294	
ATO		CB		330	.509 2	.216	.810	
OTA OTA		CG		. • -	.520 2	.433 11	617	06
ATC		SD		_		1.173 11	L.723	
ATC		CE).052 ·	7.521	
OTA		С				1.175	7.589	1.00 32.03
ATC	_	0	MET	1535 - (j. 10-x			
AI	J — —							

						2	212				
ATOM	583	N	TVO								
ATOM	585	CA	LYS	1536		. 974	0	. 638	7 140	_	
ATOM	586		LYS	1536	-3.	170			7.142	1.00	31.04
ATOM	587	CB	LYS	1536	-4.	334			5.767	1.00	31.15
ATOM		CG	LYS	1536	-4.	864			.415	1.00	31.21
	588	CD	LYS	1536	-5	973		625 7	.552	1.00	27.76
ATOM	589	CE	LYS	1536					.103	1.00	21.44
MOTA	590	NZ	LYS	1536	-6.	434		401 8	.248	1.00	24.69
MOTA	594	С	LYS	1536	-7.		4.	241 7	.868	1.00	
ATOM	595	0	LYS		-2.8	887	-1.		.561	1.00	25.84
ATOM	596		MET	1536	-3.2	238	-2.		.560		30.71
ATOM	598			1537	-2.3	309	-0.4			1.00	34.73
ATOM	599		MET	1537.	-1.9	967	-1.3			1.00	31.18
-			MET	1537	-1.3	70	-0.2			1.00	31.53
			MET	1537	-2.3	77	0.7			1.00	35.11
			/IET	1537	-3.6		0.7		654	1.00	42.40
·			IET	1537	-3.0		-0.0		685	1.00	50.10
·		C M		1537	-0.9	26	0.2		^ - -	1.00	50.20
) <u>w</u>		1537			-2.2	76 3.		L.00	30.86
	505 r	v i		1538	-1.2		-3.4	25 3.		. 00	
	07 C		_	538	0.11		-1.9	50 4.;			30.07
ATOM 6					1.17		-2.92	23 4.5			30.92
ATOM 6				538	2.35		-2.25				28.12
	`			538	3.31	.0	-3.30)3 5.8			28.71
3				538	3.12	6	-1.34				29.72
	12 C			538	4.37	5	-0.74	-		.00	30.79
		II		538	0.71		-4.17	-		.00	32.46
ATOM 6:		II		538	1.17		-5.27			.00 2	26.33
	_	GL	Y 1	539	-0.188		4 00	_		.00 2	4.20
		A GL	Y 15	539	-0.651		-4.02				7.41
	_	GL	Y 15	539	0.240		-5.19		97 1.		7.83
ATOM 61	_	GL		39	1 700		-5.533	8.17		_	9.10
ATOM 61	9 N	LY	-	40	1.308		-4.937	8.36			
ATOM 62	1 CA			40	-0.157		-6.561	8.91			0.33
ATOM 62	2 CB				0.539		-6.976	10.12			9.46
ATOM 62		LYS			-0.470	-	7.520		_		9.27
ATOM 62					-1.438	-	6.483				7.01
ATOM 62		LYS			-2.496	-	7.103	12.53			9.58
ATOM 626		LYS			-3.548		6.069		_		.41
ATOM 630		LYS			-2.994	_	4.996	12.95			.14
ATOM 631	_	LYS		10	1.679	_	7.962	13.82			.92
ATOM 632	_	LYS	154	0	1.745	-	8.794	10.020			.17
3		HIS	154	1	2.565			9.111			.20
3.55	CA	HIS	154	1	3.690		7.856	11.006	1.0		. 96
	CB	\mathtt{HIS}	154	1	4.787		3.761	11.144	1.0		.30
ATOM 636	CG	HIS	154				3.506	10.120	1.00		
ATOM 637	CD2	HIS	154		5.849	- 5	.555	10.125	1.00		
ATOM 638	NDl	HIS	154		5.886		.789	9.555	1.00		
ATOM 640	CEl	HIS			7.052	- 9	.413	10.791	1.00	•	
ATOM 641	NE2	HIS	1541		7.775	-10	.509	10.633		- •	
ATOM 643	C		154]		7.097	-11	.355	9.889	1.00		
ATOM 644		HIS	1541		1.245	8	.640		1.00		
ATOM 645	O N7	HIS	1541	. 4	.290		.549	12.565	1.00		64
	N ~-	LYS	1542	4	.650	~ 0	. 791	13.132	1.00	30.	
	CA	LYS	1542		.200	- 9	. / AT	13.108	1.00	29.4	
*	CB	LYS	1542	_	.683		893	14.457	1.00	28.	
ATOM 649	CG	LYS	1542	_		-11.	326	14.714	1.00	30.1	
ATOM 650	CD	LYS	1542		.232	-11.	572	16.112	1.00		
ATOM 651	CE	LYS			. 277	-11.	046	17.155	1.00	32.6	
			1542	5	.659	-11.		18.551	1.00	42.9	
SSSD/55145. v0	1								00	48.1	3
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MOTA	652	NZ	LYS	1542	4.726	-10.930	19.564	1.00	54.87
MOTA	656	C	LYS	1542	6.351	-8.928	14.705	1.00	26.54
MOTA	657	0	LYS	1542	6.440	-8.321	15.773	1.00	26.19
MOTA	658	N	ASN	1543	7.193	-8.733	13.697	1.00	24.36
MOTA	660	CA	ASN	1543	8.357	-7.874	13.852	1.00	24.08
MOTA	661	CB	ASN	1543	9.601	-8.596	13.359	1.00	22.69
ATOM	662	CG	ASN	1543	9.781	-9.950	14.029	1.00	22.81
ATOM	663	OD1	ASN	1543	9.664	-10.996	13.388	1.00	23.62
MOTA	664	ND2	ASN	1543	10.028	-9.938	15.324	1.00	24.94
ATOM	667	С	ASN	1543	8.318	-6.429	13.377	1.00	23.48
MOTA	668	0	ASN	1543	9.351	-5.861	13.059	1.00	22.94
MOTA	669	N	ILE	1544	7.130	-5.821	13.380	1.00	24.15
ATOM	671	CA	ILE	1544	6.976	-4.407	13.012	1.00	24.60
MOTA	672	CB	ILE	1544	6.516	-4.191	11.531	1.00	24.90
MOTA	673	CG2	ILE	1544	7.495	-4.852	10.571	1.00	21.57
ATOM	674	CG1	ILE	1544	5.081	-4.688	11.316	1.00	26.66
ATOM	675	CD1	ILE	1544	4.481	-4.321	9.945	1.00	23.98
MOTA	676	С	ILE	1544	5.954	-3.785	13.955	1.00	24.78
ATOM	677	0	ILE	1544	5.160	-4.503	14.558	1.00	27.87
MOTA	678	N	ILE	1545	6.035	-2.474	14.159	1.00	26.39
MOTA	680	CA	ILE	1545	5.089	-1.779	15.025	1.00	26.79
MOTA	681	CB	ILE	1545	5.588	-0.345	15.384	1.00	28.85
ATOM	682	CG2	ILE	1545	4.512	0.449	16.103	1.00	23.60
ATOM	683	CG1	ILE	1545	6.833	-0.423	16.269	1.00	27.20
ATOM	684	CD1	ILE	1545	6.565	-0.990	17.639	1.00	27.12
MOTA	685	С	ILE	1545	3.792	-1.708	14.224	1.00	26.99
ATOM	686	0	ILE	1545	3.720	-1.023	13.197	1.00	27.61
MOTA	687	N	ASN	1546	2.809	-2.495	14.654	1.00	26.70
MOTA	689	CA	ASN	1546	1.514	-2.565	13.983	1.00	26.53
ATOM	690	CB	ASN	1546	0.871	-3.953	14.169	1.00	26.23
ATOM	691	CG	ASN	1546	1.695	-5.072	13.551	1.00	24.96
ATOM	692	OD1	ASN	1546	1.773	-5.206	12.330	1.00	28.08
ATOM	693	ND2	ASN	1546	2.319	-5.872	14.387	1.00	22.38
ATOM	696	С	ASN	1546	0.521	-1.497	14.418	1.00	26.89
ATOM	697	0	ASN	1546	0.610	-0.952	15.523	1.00	27.40
ATOM	698	N	LEU	1547	-0.349	-1.138	13.481	1.00	27.77
ATOM	700	CA	LEU	1547	-1.416	-0.175	13.701	1.00	28.28
MOTA	701	CB	LEU	1547	-1.958	0.313	12.361	1.00	27.04
MOTA	702	CG	LEU	1547	-3.199	1.194	12.408	1.00	25.74
MOTA	703	CD1	LEU	1547	-2.836	2.575	12.950	1.00	27.66
MOTA	704	CD2	LEU	1547	-3.799	1.289	11.014	1.00	23.38
MOTA	705	С	LEU	1547	-2.498	-0.972	14.435	1.00	29.80
ATOM	706	0	LEU	1547	-2.766	-2.135	14.105	1.00	28.63
ATOM	707	N	LEU	1548	-3.088	-0.351	15.448	1.00	29.91
ATOM	709	CA	LEU	1548	-4.114	-0.997	16.256	1.00	28.46
ATOM	710	CB	LEU	1548	-3.735	-0.956	17.749	1.00	26.76
ATOM	711	CG	LEU	1548	-2.460	-1.701	18.162	1.00	22.44
ATOM	712	CD1	LEU	1548	-2.277	-1.554	19.653	1.00	21.91
ATOM	713	CD2	LEU	1548	-2.551	-3.179	17.778	1.00	20.79
ATOM	714	C	LEU	1548	-5.480	-0.365	16.058	1.00	27.31
ATOM	715	Ö	LEU	1548	-6.489	-1.043	16.193	1.00	28.25
ATOM	716	N	GLY	1549	-5.506	0.925	15.732	1.00	24.02
MOTA	718	CA	GLY	1549	-6.774	1.598	15.553	1.00	24.57
ATOM	719	C	GLY	1549	-6.548	3.077	15.395	1.00	25.19
		-							

	3.000						~ 1 1				
	ATOM	720	0	GLY	1549	-					
	ATOM	721	N	ALA	1550	-5.4	_	.488	15.231	1.00	20 75
	ATOM	723	CA	ALA	1550	-7.6		.875	15.427		
	ATOM	724	CB	ALA	1550	-7.4	87 5	.319	15.282	1.00	24.66
	ATOM	725	С	ALA		-7.2		.680	13.824	1.00	24.17
	ATOM	726	0	ALA	1550	-8.6		.103	15.765		24.29
	ATOM	727	N	CYS	1550	-9.8	10 5	.590	15.780	1.00	23.95
1	ATOM	729	CA	CYS	1551	-8.4	44 7	.336	16.199	1.00	24.95
i	-	730.	CB		1551	-9.48	32 g	_		1.00	25.03
		731	SG	CYS	1551	-9.22			16.639	1.00	28.21
		732	C	CYS	1551	-9.37			18.055	1.00	26.76
		733		CYS	1551	-9.35			19.317	1.00	34.39
		34	0	CYS	1551	-8.48			15.656	1.00	29.98
			N	THR	1552	-10.19	_		15.800	1.00	32.14
	~~			THR	1552	-10.13			14.625	1.00	31.09
			CB		1552	-10.05			L3.595	1.00	32.91
	TIO		OG1		1552	-11 05		781 1	2.189	1.00	32.60
		40			1552	-11.27	• •	97 1	1.890	1.00	
			_			-8.928		768 1	2.144	1.00	32.12
A	COM 74	12 (_			-11.282	2 11.4		3.591		32.74
AT	OM 74	. ~			.552	-11.171	12.5		3.057	1.00	35.26
ΑΊ	OM 74	_		_	.553	-12.397	11.0				35.10
AT	'OM 74	_	-		553	-13.585	11.8				39.01
AT	OM 74	~		-	553 .	-14.832	10.9			1.00	41.97
AT			_		553 .	-14.915	10.2			1.00	41.17
AT		_		LN 1	553 -	14.900	11.2			1.00 ;	39.06
ATO		_			553	15.785	12.04		.496		11.84
ATO			E2 G	LN 19		13.876			.359]		1.92
ATO		. •	G1	N 15	553 ~	13.727	11.09		.652 1		2.33
ATO		_	GI			13.358	12.77		.372 1	.00 4	5.35
			AS	P 15	54	14.225	12.42		.489 1	.00 4	7.02
ATO			A AS			14.479	13.98		.090 1		8.60
ATO			As				15.01	6 16			0.64
ATO			AS			15.832	14.76	б 16.		_	
ATO		OD				L7.003	14.95	5 15.		_	1.52
ATO	M 761	OD			-	18.072	15.40	9 16.			.54
ATO		С	AS		_	.6.860	14.663	14.			.04
ATON		0	ASI			3.395	15.173	17.			.09
ATON	764	N	GL)		_	3.611	14.879	18.	_		.89
MOTA	766	CA			_	2.232	15.643	16.		00 51	.48
ATOM		C	GLY			1.131	15.834	17.6		00 48	.40
ATOM		0	GLY		-	9.798	15.626	16.9			.16
ATOM		N	GLY	-05	-	9.737	15.581	10.3			.64
ATOM			PRO		6 -8	3.708	15.525	15.7		00 45	. 22
ATOM	. •	CD	PRO		6 -e	3.672	15.683	17.7	702 1.(00 44.	68
ATOM		CA	PRO	1556		.359		19.1	64 1.0		
ATOM	772	CB	PRO	1556		.484	15.326	17.1		0 42.	
	773	CG	PRO	1556	-	.354	15.549	18.4	11 1.0	0 43.	
ATOM	774	C	PRO	1556		.164	16.347	19.3	45 1.0		
ATOM	775	0	PRO	1556	-	.164	13.912	16.6	65 1.0		
ATOM	776	N	LEU	1557	•	.636	12.953	17.28			
ATOM	778	CA	LEU		_	.451	13.788	15.54			/5
MOTA	779	CB	LEU	1557		.169	12.490	14.95			33
ATOM	780	CG		1557		496	12.669	13.58		•	54
ATOM	781	CD1	LEU	1557	-5.	009	11.404				
ATOM	782	CD2	LEU	1557	-6.		10.436	12.87			9
ATOM	783		LEU	1557	-4.	_	11.775	12.62		27.8	
	, 03	С	LEU	1557			11.732	11.57	_	25.4	
SSSD/55	145 ~:				•	- - .	/32	15.89	4 1.00	35.4	
222D/33	145. VO1										_

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MOTA	784	0	LEU	1557	-4.210	12.264	16.316	1.00	36.12
MOTA	785	N	TYR	1558	-5.664	10.539	16.292	1.00	32.49
MOTA	787	CA	TYR	1558	-4.861	9.697	17.157	1.00	31.87
MOTA	788	CB	TYR	1558	-5.590	9.348	18.470	1.00	33.93
MOTA	789	CG	TYR	1558	-5.695	10.476	19.471	1.00	35.34
MOTA	790	CD1	TYR	1558	-6.566	10.394	20.565	1.00	37.12
MOTA	791	CE1	TYR	1558	-6.683	11.456	21.479	1.00	36.44
MOTA	792	CD2	TYR	1558	-4.945	11.636	19.317	1.00	37.27
MOTA	793	CE2	TYR	1558	-5.054	12.690	20.213	1.00	39.62
MOTA	794	CZ	TYR	1558	-5.921	12.598	21.289	1.00	40.05
MOTA	795	OH	TYR	1558	-6.008	13.668	22.155	1.00	44.98
MOTA	797	С	TYR	1558	-4.600	8.419	16.387	1.00	31.58
ATOM	798	0	TYR	1558	-5.532	7.750	15.936	1.00	30.22
ATOM	799	N	VAL	1559	-3.331	8.129	16.153	1.00	33.43
ATOM	801	CA	VAL	1559	-2.947	6.907	15.463	1.00	31.42
ATOM	802	CB	VAL	1559	-1.849	7.160	14.419	1.00	32.31
ATOM	803	CG1	VAL	1559	-1.516	5.851	13.675	1.00	26.79
ATOM	804	CG2	VAL	1559	-2.308	8.265	13.453	1.00	30.63
ATOM	805	C	VAL	1559	-2.438	5.979	16.556	1.00	28.67
ATOM	806	o	VAL	1559	-1.393	6.223	17.155	1.00	30.08
ATOM	807	N	ILE	1560	-3.230	4.960	16.852	1.00	25.80
ATOM	809	CA	ILE	1560	-2.915	3.998	17.894	1.00	25.33
ATOM	810	CB	ILE	1560	-4.219	3.443	18.506	1.00	22.34
ATOM	811	CG2	ILE	1560	-3.931	2.695	19.784	1.00	20.34
ATOM	812	CG1	ILE	1560	-5.172	4.603	18.809	1.00	21.34
ATOM	813	CD1	ILE	1560	-6.583	4.190	19.093	1.00	20.68
ATOM	814	CDI	ILE	1560	-2.073	2.857	17.341	1.00	27.16
ATOM	815	0	ILE	1560	-2.520	2.116	16.455	1.00	29.67
ATOM	816	N	VAL		-0.858	2.714	17.860	1.00	27.69
ATOM	818	CA	VAL	1561	0.060	1.667	17.411	1.00	28.27
ATOM	819	CB	VAL	1561	1.311	2.269	16.696	1.00	27.34
ATOM	820	CG1	VAL	1561	0.892	3.019	15.445	1.00	21.76
ATOM	821	CG2	VAL	1561	2.074	3.201	17.639	1.00	26.00
ATOM	822	C	VAL	1561	0.509	0.809	18.588	1.00	28.70
MOTA	823	0	VAL	1561	0.221	1.139	19.746	1.00	30.52
MOTA	824	N	GLU	1562	1.166	-0.311	18.286	1.00	28.64
ATOM	826	CA	GLU	1562	1.658	-1.220	19.318	1.00	27.77
	827	CB	GLU	1562		-2.465	18.693	1.00	24.57
ATOM					2.278	-3.452	18.208		24.76
MOTA	828 829	CG CD	GLU GLU	1562 1562	1.251 1.864	-3.452	17.501	1.00	24.76
ATOM ATOM	830	OE1	GLU	1562	1.272	-5.739	17.580	1.00	28.27
ATOM	831	OE2	GLU	1562	2.920	-4.487	16.849	1.00	29.25
ATOM	832	C	GLU	1562	2.674	-0.538	20.217	1.00	28.79
ATOM	833	0	GLU	1562	3.453	0.292	19.760	1.00	29.38
ATOM	834	N	TYR	1563	2.627	-0.871	21.503	1.00	30.84
ATOM	836	CA	TYR	1563	3.534	-0.304	22.493	1.00	31.43
MOTA	837	CB	TYR	1563	2.782	-0.088	23.799	1.00	32.10
MOTA	838	CG	TYR	1563	3.632	0.376	24.952	1.00	33.93
MOTA	839	CD1	TYR	1563	4.366	1.552	24.873	1.00	34.85
MOTA	840	CE1	TYR	1563	5.140	1.992	25.947	1.00	37.53
ATOM	841	CD2	TYR	1563	3.683	-0.356	26.136	1.00	34.81
MOTA	842	CE2	TYR	1563	4.452	0.072	27.211	1.00	34.01
MOTA	843	CZ	TYR	1563	5.173	1.245	27.113	1.00	35.79
MOTA	844	OH	TYR	1563	5.920	1.677	28.184	1.00	39.10



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A	TOM	846	C	TYR 1	563								
A	MOT.	847	_		563	4.76		.166	22.7	31	1.00	31.3	3 0
		348			564	4.67	-	385	22.9		1.00	30.7	
A	TOM 8	350			564	5.93	-	525	22.7		1.00	32.2	
A	TOM 8	351			564	7.19		212	22.9		1.00	35.9	
A'	TOM 8	52			564	8.17		866	21.8		1.00	36.4	
A.	rom 8	53	_	_	564	7.71	- •	719	24.3		00	36.5	
A	rom 8	54			565	8.332		349	24.40		.00	39.1	
		56			665	7.424			25.35		.00	34.6	
		57			65	7.801			26.70		.00	34.9	
					65	7.124	_		27.75	0 1	.00	32.1	
	'OM 86	50 (c s		65	7.606			27.69	6 1	.00	32.92	
	OM 86	-) s		65	9.288 9.674	_		26.99	6 1	.00	35.56	
	OM 86	_	l L	YS 15		10.127			27.88	6 1	.00	38.69	
AT			A L	YS 15		11.557			26.24		.00	33.70	
AT	_	-	B L	YS 15		12.137	-1.6		26.52	61.	00	31.40	
ATO			G L	YS 15		11.555	-3.0		26.53		00	30.56	
ATO		_	D L'			11.997	-3.8		27.664		00	32.32	
ATO	_	_				11.632	-5.3		27.599		00	36.47	
ATC			Z LY			12.104	-6.0		28.872			36.97	
ATO			LY	S 156	6	12.380	-7.43		28.804		00	41.62	
ATO		_	LY	S 156	6	13.616	-0.66 -0.69		25.683			32.18	
ATO		,	GL	Y 156	7	11.686	0.83		25.715			32.57	
ATO:					7	12.345	1.22		24.973			33.39	
ATO			GL.		7	13.074	0.71		24.156			32.13	
ATO		-	GL.		7	12.912	-0.43		22.928	1.0		31.70	
ATO			ASI			13.883	1.58		22.530 22.331	1.0		33.30	
ATON						14.632	1.23		1.139	1.0		31.08	
ATOM		CB CG	ASI			15.066	2.47		0.365	1.0	_	1.00	
ATOM		OD:	ASN	,		16.127	3.27		1.074	1.0		1.30	
ATOM		ND:				17.130	2.733		1.508	1.0 1.0		0.47	
ATOM		C C	2 ASN ASN			15.934	4.580		1.144	1.0	_	2.19	
ATOM		Ö	ASN			15.802	0.295		1.393	1.00		2.13	
ATOM	891	N	LEU	0		16.357	0.256	2:	2.483	1.00	_	0.62	
ATOM	893	CA	LEU			16.193	-0.428	20	0.354	1.00		2.91 0.92	
ATOM	894	CB	LEU			17.269	-1.403	20	0.417	1.00		L.22	
ATOM	895	CG	LEU	1569		17.418	-2.083	19	054	1.00		9.57	
ATOM	896	CD1	LEU	1569		18.415	-3.231	18	.893	1.00		9.22	
ATOM	897	CD2	LEU	1569		8.284	-4.261	20	.024	1.00		30	
ATOM	898	C	LEU	1569		.8.184 .8.609	~3.863	17	.523	1.00		.99	
ATOM	899	0	LEU	1569		9.328	-0.838		.878	1.00		.44	
ATOM	900	N	ARG	1570		8.954	-1.499		.618	1.00		.12	
ATOM	902	CA	ARG	1570		0.218	0.370		.432	1.00		. 24	
ATOM	903	CB	ARG	1570		0.348	0.983		.834	1.00		.01	
ATOM	904	CG	ARG	1570		1.586	2.394		.256	1.00	32		
ATOM	905	CD	ARG	1570		1.672	3.129		. 758	1.00	38.		
ATOM	906	NE	ARG	1570	20	0.428	4.538		221	1.00	41.		
ATOM	908	CZ	ARG	1570		9.975	5.278			1.00	49.		
ATOM	909	NHl	ARG	1570		.659	5.721			1.00	52.		
ATOM	912	NH2	ARG	1570		8.824	5.510			1.00	51.		
ATOM	915	C	ARG	1570		.308	6.377	21.		1.00	53.		
ATOM ATOM	916	0	ARG	1570		.184	1.023 0.391	22.		1.00	33.		
T OM	917	N	GLU	1571		.359	1.730	22.		.00	33.		
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MOTA	919	CA	GLU	1571	19.284	1.861	24.432	1.00	34.87
ATOM	920	CB	GLU	1571	18.052	2.688	24.794	1.00	35.83
MOTA	921	CG	GLU	1571	18.158	4.145	24.354	1.00	41.61
MOTA	922	CD	GLU	1571	16.814	4.870	24.318	1.00	47.33
MOTA	923	OE1	GLU	1571	15.759	4.199	24.362	1.00	50.68
MOTA	924	OE2	GLU	1571	16.812	6.120	24.218	1.00	48.07
MOTA	925	C	GLU	1571	19.223	0.487	25.098	1.00	34.39
MOTA	926	0	GLU	1571	19.968	0.202	26.041	1.00	34.04
MOTA	927	N	TYR	1572	18.363	-0.376	24.572	1.00	33.49
MOTA	929	CA	TYR	1572	18.204	-1.728	25.083	1.00	30.45
MOTA	930	CB	TYR	1572	17.210	-2.495	24.202	1.00	28.13
MOTA	931	CG	TYR	1572	17.074	-3.971	24.487	1.00	25.80
MOTA	932	CD1	TYR	1572	16.105	-4.443	25.371	1.00	28.92
MOTA	933	CE1	TYR	1572	15.954	-5.804	25.618	1.00	30.03
MOTA	934	CD2	TYR	1572	17.899	-4.899	23.863	1.00	24.61
MOTA	935	CE2	TYR	1572	17.760	-6.260	24.102	1.00	26.05
MOTA	936	CZ	TYR	1572	16.790	-6.705	24.982	1.00	29.23
ATOM	937	OH	TYR	1572	16.651	-8.052	25.227	1.00	33.74
ATOM	939	C	TYR	1572	19.549	-2.447	25.113	1.00	31.30
ATOM	940	0	TYR	1572	19.880	-3.126	26.090	1.00	32.43
ATOM	941	N	LEU	1573	20.334	-2.266	24.058	1.00	29.68
MOTA	943	CA	LEU	1573	21.625	-2.923	23.972	1.00	30.04
ATOM	944	CB	LEU	1573	22.145	-2.909	22.529	1.00	26.13
MOTA	945	CG	LEU	1573	21.532	-3.870	21.490	1.00	25.24
MOTA	946	CD1	LEU	1573	22.097	-3.563	20.113	1.00	19.70
MOTA	947	CD2	LEU	1573	21.807	-5.317	21.839	1.00	22.05
MOTA	948	C	LEU	1573	22.645	-2.308	24.927	1.00	34.47
MOTA	949	0	LEU	1573	23.354	-3.031	25.644	1.00	34.95
MOTA	950	N	GLN	1574	22.691	-0.980	24.978	1.00	35.47
MOTA	952	CA	GLN	1574	23.639	-0.293	25.850	1.00	37.09
MOTA	953	CB	GLN	1574	23.601	1.206	25.579	1.00	36.70
MOTA	954	CG	GLN	1574	24.033	1.559	24.171	1.00	39.77
MOTA	955	CD	GLN	1574	23.960	3.045	23.884	1.00	41.51
MOTA	956	OE1	GLN	1574	23.592	3.837	24.751	1.00	42.57
ATOM	957	NE2	GLN	1574	24.288	3.431	22.652	1.00	41.34
MOTA	960	С	GLN	1574	23.400	-0.588	27.332	1.00	37.85
MOTA	961	0	GLN	1574	24.343	-0.801	28.090	1.00	38.87
MOTA	962	N	ALA	1575	22.131	-0.667	27.720	1.00	39.01
MOTA	964	CA	ALA	1575	21.740	-0.944	29.098	1.00	37.00
MOTA	965	CB	ALA	1575	20.261	-0.678	29.273	1.00	35.71
MOTA	966	C	ALA	1575	22.061	-2.359	29.559	1.00	39.14
MOTA	967	0	ALA	1575	21.839	-2.692	30.719	1.00	43.81
MOTA	968	N	ARG	1576	22.563	-3.201	28.665	1.00	38.39
MOTA	970	CA	ARG	1576	22.897	-4.568	29.032	1.00	37.71
ATOM	971	CB	ARG	1576	21.994	-5.544	28.290	1.00	38.26
ATOM	972	CG	ARG	1576	20.555	-5.383	28.700	1.00	38.00
MOTA	973	CD	ARG	1576	19.653	-6.282	27.920	1.00	34.74
ATOM	974	NE	ARG	1576	18.279	-6.190	28.388	1.00	32.88
MOTA	976	CZ	ARG	1576	17.572	-5.066	28.442	1.00	34.02
MOTA	977	NH1	ARG	1576	18.114	-3.913	28.068	1.00	35.57
MOTA	980	NH2	ARG	1576	16.298	-5.102	28.800	1.00	36.71
MOTA	983	С	ARG	1576	24.365	-4.927	28.828	1.00	39.59
MOTA	984	0	ARG	1576	24.735	-6.113	28.788	1.00	39.83
MOTA	985	N	ARG	1577	25.200	-3.900	28.687	1.00	38.82



						210			
		87	CA A	RG 157	77 26.6	21			
				RG 157	-0.0				39.07
			CG A	RG 157				_	
			CD A	RG 157					
				RG 157	7 27.7		-0.12		33.06
				RG 157	7 28.1				38.87
	'OM 99			RG 157	7 28.6				39.76
AT	OM 99	_		RG 157				_	40.68
AT	_	00 0		RG 157				_	43.26
AT		01 0		RG 157					41.58
ATO		02 N			3 28.29				42.48
ATO		_	D PF			.0 -5.81		_	43.07
ATO						9 -5.62			43.36
ATO						6 -6.59		_	42.69
ATC						2 -6.10			42.22
ATO			PR	0		6 -4.35			43.64
ATO		-	PR	•		0 -3.31			43.37
ATO			PR			6 -4.380	_	• • •	42.50
ATO					29.27		34.174		45.24
ATO					30.099	9 -3.187			44.69
ATO					29.979	-3.567		1.00	46.27
ATO		_			28.894	-4.615		1.00	45.78
ATO		_	PRC PRC		31.548	-2.869		1.00	46.15 48.38
ATON		_	GLU		32.410		33.478	1.00	50.64
ATON			GLU		19.022		32.495	1.00	65.98
ATOM			GLU		20.442		32.492		64.80
ATOM	1 102		GLU		20.796		33.740		67.30
ATOM			GLU		21.351		32.371		63.80
ATOM	1022		GLU		22.545		32.089		65.21
ATOM	1024		GLU	1593	20.789	-7.458	32.607		61.44
ATOM			GLU	1593	21.560	-8.691	32.495		50.82
MOTA	1026	C	GLU	1593	20.681	-9.899	32.807		51.47
ATOM	1027	0	GLU	1593	22.144	-8.803	31.089		59.12
ATOM	1028	N	GLN	1594	21.468	-8.525	30.097		9.49
MOTA	1030	CA	GLN	1594	23.408 24.103	-9.201	31.017		57.33
ATOM	1031	CB	GLN	1594	25.523	-9.334	29.744		5.30
ATOM	1032	CG	GLN	1594	26.438	-9.880	29.957		4.87
ATOM	1033	CD	GLN	1594	27.704	-8.959	30.757	1.00 5	3.34
ATOM	1034	OE1	GLN	1594	28.256	-9.660 -10.536	31.248	1.00 5	5.27
MOTA	1035	NE2	GLN	1594	28.166	-10.536 -9.275	30.572	1.00 5	6.47
ATOM	1038	C ,	GLN	1594	23.336	-10.229	32.434	1.00 5	1.46
ATOM	1039	0	${ t GLN}$	1594	22.648	-10.229	28.781		2.29
ATOM	1040	N	LEU	1595	23.447	-9.913	29.190	1.00 5	2.56
ATOM	1042	CA	LEU	1595	22.783	-10.676	27.499		9.40
ATOM	1043	CB	LEU	1595	22.452	-9.760	A		5.00
ATOM	1044	CG	LEU	1595	21.390	-8.711	A		2.94
ATOM	1045	CD1	LEU	1595	21.495	-7.484			3.90
ATOM	1046	CD2	LEU	1595	20.005	-9.347			.46
MOTA	1047	C	LEU	1595	23.741	-11.762			. 86
ATOM	1048	0	LEU	1595	24.950				. 96
ATOM	1049	N	SER	1596	23.217				.24
ATOM	1051	CA		1596	24.076		a = -		.29
ATOM	1052	CB	SER	1596	23.388		~		.40
CC0 = !						/4	25.484]	00 41	.83

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MOTA	1053	OG	SER	1596	22.218	-15.483	24.697	1.00	44.25	
ATOM	1055	C	SER	1596	24.392	-13.817	23.800	1.00	42.64	
ATOM	1056	0	SER	1596	23.857	-12.900	23.171	1.00	43.14	
ATOM	1057	N	SER	1597	25.277	-14.645	23.255	1.00	42.59	
ATOM	1059	CA	SER	1597	25.629	-14.553	21.850	1.00	42.91	
ATOM	1060	CB	SER	1597	26.739	-15.547	21.516	1.00	45.26	
ATOM	1061	OG	SER	1597	27.812	-15.436	22.431	1.00	56.41	
ATOM	1063	С	SER	1597	24.380	-14.909	21.048	1.00	42.35	
ATOM	1064	0	SER	1597	24.113	-14.322	20.003	1.00	43.71	
ATOM	1065	N	LYS	1598	23.621	-15.881	21.544	1.00	40.61	
ATOM	1067	CA	LYS	1598	22.405	-16.298	20.867	1.00	38.61	
ATOM	1068	CB	LYS	1598	21.848	-17.575	21.483	1.00	36.33	
ATOM	1069	CG	LYS	1598	21.135	-18.439	20.468	1.00	40.09	
ATOM	1.070	CD	LYS	1598	20.213	-19.434	21.118	1.00	43.39	
ATOM	1071	CE	LYS	1598	19.766	-20.494	20.122	1.00	48.25	
ATOM	1072	NZ	LYS	1598	20.930	-21.290	19.623	1.00	50.46	
ATOM	1076	C	LYS	1598		-15.194	20.895	1.00	38.17	
ATOM	1077	Ō	LYS	1598	20.579	-15.053	19.945	1.00	41.27	
ATOM	1078	N	ASP	1599	21.321	-14.408	21.969	1.00	35.90	
ATOM	1080	CA	ASP	1599	20.366	-13.307	22.099	1.00	34.08	
ATOM	1081	CB	ASP	159.9	20.450	-12.661	23.477	1.00	37.83	
ATOM	1082	CG	ASP	1599	19.822	-13.505	24.562	1.00	39.93	
ATOM	1083	OD1	ASP	1599	20.089	-13.217	25.742	1.00	45.85	
ATOM	1084	OD2	ASP	1599	19.060	-14.444	24.240	1.00	41.06	
ATOM	1084	C	ASP	1599	20.634	-12.243	21.061	1.00	32.37	•
ATOM	1086	0	ASP	1599	19.704	-11.701	20.466	1.00	32.58	
ATOM	1087	Ŋ	LEU	1600	21.915	-11.701	20.400	1.00	30.45	
ATOM	1087	CA	LEU	1600	22.355	-10.948	19.902	1.00	29.59	
ATOM	1089	CB	LEU	1600	23.841	-10.546	20.097	1.00	28.59	
ATOM	1090	CG	LEU	1600	24.238	-10.054	21.449	1.00	24.59	
MOTA	1091	CD1	LEU	1600	25.747	-9.869	21.522	1.00	18.40	
	1092	CD1	LEU	1600		-8.745	21.626	1.00	21.71	
ATOM	1093	CD2	LEU		23.529	-11.393	18.458	1.00	28.54	
ATOM		0	LEU	1600	22.073	-10.613	17.648	1.00	25.59	
ATOM	1095	N		1600 1601	21.578		18.134	1.00	29.13	
ATOM	1096		VAL		22.377	-12.645				
ATOM	1098	CA	VAL	1601	22.111	-13.154	16.793	1.00	29.74	
MOTA	1099	CB	VAL	1601	22.780	-14.513	16.551	1.00	29.63	
MOTA	1100	CG1	VAL	1601	22.615	-14.922	15.105	1.00	29.30	
ATOM	1101	CG2	VAL	1601	24.259	-14.422	16.873	1.00	28.52	
ATOM	1102	C	VAL	1601	20.591	-13.247	16.564	1.00	29.98	
ATOM	1103	0	VAL	1601	20.106	-13.040	15.452	1.00	29.73	
MOTA	1104	N	SER	1602	19.855	-13.493	17.645	1.00	30.97	
MOTA	1106	CA	SER	1602	18.399	-13.576	17.607	1.00	29.64	
MOTA	1107	CB	SER	1602	17.894	-14.141	18.925	1.00	30.45	
ATOM	1108	OG	SER	1602	16.483	-14.158	18.962	1.00	39.63	
ATOM	1110	С	SER	1602	17.784	-12.192	17.343	1.00	29.30	
MOTA	1111	0	SER	1602	16.772	-12.071	16.641	1.00	28.74	
MOTA	1112	N	CYS	1603	18.385	-11.157	17.925	1.00	27.68	
MOTA	1114	CA	CYS	1603	17.931	-9.783	17.717	1.00	27.32	
MOTA	1115	CB	CYS	1603	18.791	-8.790	18.516	1.00	25.40	
ATOM	1116	SG	CYS	1603	18.472	-7.039	18.177	0.50	20.76	PRT1
ATOM	1117	C	CYS	1603	18.057	-9.468	16.225	1.00	28.34	
MOTA	1118	0	CYS	1603	17.134	-8.926	15.629	1.00	29.70	
ATOM	1119	N	ALA	1604	19.192	-9.837	15.627	1.00	29.36	

AT	•		CA A	LA 160	4 19.43	38 -9.60	01 24 22		
AT			B A	LA 160					
AT	_	123 C	: A	LA 160			_	-	
AT		.24 0	A	LA 160					
ATO		.25 N	T	YR 160					
ATO		.27 C	A T	YR 160					
ATO		28 C	B T	YR 160					28.26
ATC		29 C	G T	YR 160					28.74
ATC		30 CI	D1 T		-0.01				31.12
ATC		31 CI	El Ty						32.53
ATO	M 11:	32 CI	D2 TY				_	_	30.84
ATO		33 CE	E2 TY						31.21
ATO	M 113	34 C2	TY						29.69
ATO:		35 OH						_	30.82
ATO	M 113	37 C	TY		55				33.77
ATO	M 113	8 0	TY						27.33
OTA	M 113	9 N	GL		-0.232		_		27.94
ATO	M 114	1 CA		•	15.323				27.93
ATON		2 CB			14.008				27.20
ATON	1 114	3 CG	GLI	•	13.686			1.00	26.40
MOTA	1 114	4 CD	GLi		13.301 13.114			1.00	28.12
MOTA	1 114	5 OE:		•		-11.215		1.00	30.41
ATOM		6 NE2			12.188	-10.489		1.00	34.34
ATOM	1149	9 C	GLN		14.008	-11.701		1.00	31.44
ATOM	1150	0 0	GLN		13.906	-9.397		1.00	29.67
ATOM		L N	VAL		12.884	-9.148	12.622	1.00	30.74
ATOM	1153	CA	VAL		14.970	-8.602	13.281	1.00	29.59
ATOM	1154	CB	VAL		14.996	-7.377	12.501	1.00	27.00
ATOM	1155				16.235	-6.544	12.842	1.00	27.20
ATOM	1156	CG2			16.382	-5.397	11.859	1.00	28.11
MOTA	1157		VAL	1607	16.113	-5.996	14.266	1.00	24.79
ATOM	1158	0	VAL	1607	14.966	-7.725	11.014	1.00	28.02
ATOM	1159	N	ALA	1608	14.229	-7.108	10.241		28.28
ATOM	1161	CA	ALA	1608	15.736	-8.741	10.626		27.56
ATOM	1162	CB	ALA	1608	15.787	-9.206	9.236		27.36
ATOM	1163	С	ALA	1608	16.801	-10.339	9.095		26.25
ATOM	1164	0	ALA	1608	14.402	-9.674	8.779		28.58
ATOM	1165	N	ARG	1609	14.013	-9.446	7.624		29.11
MOTA	1167	CA	ARG	1609	13.660 12.306	-10.326	9.680		28.88
ATOM	1168	CB	ARG	1609	11.797	-10.797	9.376		27.17
ATOM	1169	CG	ARG	1609	12.458	-11.731	10.464		9.68
ATOM	1170	CD	ARG	1609		-13.062	10.439	1.00 3	1.65
ATOM	1171	NE	ARG	1609	11.612	-14.049	11.177		8.21
ATOM	1173	CZ	ARG	1609	10.856	-14.897	10.269		1.10
ATOM	1174	NHl	ARG	1609	10.048	-15.872	10.667		1.97
MOTA	1177	NH2	ARG	1609	9.886	-16.125		1.00 4	0.69
ATOM	1180	С	ARG	1609	9.411	-16.609	9.770	_	3.57
ATOM	1181	Ö	ARG	1609	11.312	-9.654	9.183		5.38
MOTA	1182	N	GLY	1610	10.480	-9.693	8.260	_	5.75
ATOM	1184	CA	GLY	1610	11.365	-8.661	10.070	_	4.03
ATOM	1185	C	GLY	1610	10.480	-7.517			L.74
ATOM	1186	0	GLY		10.734	-6.864			3.32
ATOM	1187	N	MET	1610	9.805	-6.540			3.39
	1189	CA	MET	1611	12.016	-6.714			.48
	-		***** 1	1611	12.453	-6.125			5.13
SSD/551	45 v01								

1.00 19.46 7.035 -5.860 13.949 1611 MET ATOM CB 1190 22.46 1.00 7.910 -4.671 14.339 MET 1611 CG MOTA 1191 25.27 1.00 7.536 -3.123 13.457 1611 SD MET 1192 ATOM 22.25 1.00 5.876 -2.801 13.900 1611 CE MET 1193 MOTA 24.87 1.00 5.811 -7.005 12.100 1611 MET 1194 С MOTA 24.09 1.00 -6.497 4.755 11.699 1611 MET MOTA 1195 0 25.48 5.975 1.00 -8.321 12.230 1612 1196 N GLU MOTA 25.42 1.00 4.890 -9.232 11.894 1198 CA GLU 1612 ATOM 23.41 5.288 1.00 -10.691 12.155 1612 CB GLU 1199 ATOM 25.14 1.00 4.232 -11.679 11.664 1612 CG GLU 1200 ATOM 28.60 4.599 1.00 -13.141 11.872 1612 1201 CD GLU MOTA 1.00 30.10 5.777 11.637 -13.514 OE1 GLU 1612 1202 MOTA 1.00 29.53 3.694 -13.928 12.244 GLU 1612 OE2 1203 MOTA 26.92 1.00 -9.021 4.521 10.418 GLU 1612 1204 С MOTA 29.61 1.00 3.343 -8.928 10.065 GLU 1612 1205 0 MOTA 27.88 1.00 5.542 -8.884 9.576 TYR 1613 1206 N MOTA 23.82 1.00 5.337 -8.675 8.154 1613 CA TYR 1208 MOTA 1.00 24.17 6.667 -8.769 1613 7.415 TYR 1209 CB MOTA 1.00 23.73 -8.492 6.545 5.941 1613 TYR1210 CG MOTA 1.00 22.17 6.096 -9.483 5.064 1613 TYR 1211 CD1 MOTA 1.00 21.08 5.965 -9.235 3.698 1613 TYR CE1 MOTA 1212 1.00 23.16 6.865 -7.237 5.419 1613 TYR 1213 CD2 MOTA 1.00 26.38 6.736 -6.976 4.054 1613 TYR 1214 CE2 MOTA 23.16 1.00 6.287 -7.981 3.200 1613 TYR 1215 CZMOTA 1.00 25.50 -7.725 6.149 1.855 TYR 1613 OH 1216 MOTA 4.670 1,00 23.17 -7.327 7.885 1613 TYR C MOTA 1218 24.21 1.00 3.689 -7.246 TYR 7.147 1613 MOTA 1219 0 1.00 23.04 5.206 -6.266 1614 8.481 LEU N MOTA 1220 21.81 -4.920 4,652 1.00 8.316 1614 LEU 1222 CA MOTA 19.94 5.484 1.00 9.107 -3.906 LEU 1614 CB MOTA 1223 1.00 21.94 6.902 -3.616 8.609 1614 LEU CG MOTA 1224 14.28 1.00 7.654 -2.719 9.580 1614 LEU 1225 CD1 MOTA 17.45 1.00 6.814 -2.977 7.227 1614 LEU CD2 1226 MOTA 23.74 3.182 1.00 -4.858 8.764 1614 LEU C 1227 MOTA 1.00 25.26 2.367 -4.150 8.169 LEU 1614 1228 0 MOTA 1.00 25.00 2.862 -5.587 9.831 ALA 1615 N MOTA 1229 1.00 23.04 -5.644 1.502 10.357 ALA 1615 1231 CA MOTA 20.02 1.00 -6.360 1.483 11.710 ALA 1615 CB 1232 MOTA 23.15 1.00 0.605 -6.357 9.351 ALA 1615 C 1233 MOTA 1.00 25.25 -5.891 -0.503 9.076 ALA 1615 MOTA 1234 0 1.00 23.64 1.104 -7.441 8.754 SER 1616 1235 N MOTA 23.60 1.00 -8.199 0.337 7.758 1616 1237 CA SER MOTA 22.46 1.107 1.00 -9.453 7.346 SER 1616 1238 CB MOTA 1.00 26.66 2.224 -9.131 6.531 SER 1616 1239 OG MOTA 1.00 25.45 0.025 -7.369 6.505 SER 1616 1241 C MOTA 1.00 26.67 -0.967 -7.607 5.813 SER 1616 1242 0 MOTA 1.00 25.47 0.916 -6.436 6.193 LYS 1617 1243 N MOTA 1.00 25.04 0.781 -5.551 5.051 LYS 1617 CA 1245 MOTA 26.30 1.00 2.163 -5.183 4.513 LYS 1617 CB 1246 MOTA 28.58 1.00 2.851 -6.318 3.778 LYS 1617 CG 1247 MOTA 1.00 33.00 2.169 -6.530 2.438 CD LYS 1617 1248 MOTA 38.57 2.764 1.00 ~7.676 1.652 LYS 1617 CE 1249 MOTA 45.15 1.00 2.300 -8.987 2.167 1617 LYS NZ1250 MOTA 26.34 1.00 0.002 -4.293 5.417 LYS 1617 C 1254 MOTA

ATOM	1255	0	LYS	1617	4.649	-3.336	-0.034	1.00	26.77
ATOM	1256	N	LYS	1618	6.592	-4.319	-0.632		27.17
ATOM	1258	CA	LYS	1618	7.084	-3.197	-1.447		28.20
MOTA	1259	CB	LYS	1618	6.053	-2.819	-2.528	1.00	28.42
ATOM		CG	LYS	1618	5.971	-3.749	-3.730	1.00	
ATOM	1261	CD	LYS	1618	5.573	-5.163	-3.364	1.00	30.45
ATOM	1262	CE	LYS	1618	5.636	-6.087	-4.570	1.00	32.50
ATOM	1263	NZ	LYS	1618	4.621	-5.729	-5.600	1.00	34.89
ATOM	1267	C	LYS	1618	7.466	-1.951	-0.643	1.00	28.78
ATOM	1268	0	LYS	1618	7.556	-0.848	-1.199	1.00	28.78
ATOM	1269	N	CYS	1619	7.753	-2.130	0.646	1.00	
MOTA	1271	CA	CYS	1619	8.111	-1.022	1.522	1.00	29.26
ATOM	1272	CB	CYS	1619	7.391	-1.173	2.873	1.00	28.32
ATOM	1273	SG	CYS	1619	7.754	0.105	4.136	1.00	26.33
MOTA	1274	C	CYS	1619	9.622	-0.841	1.728	1.00	27.82
ATOM	1275	0	CYS	1619	10.336	-1.786	2.072	1.00	29.15
ATOM	1276	N	ILE	1620	10.096	0.378	1.457	1.00	29.55
ATOM	1278	CA	ILE	1620	11.502	0.761	1.625		29.39
ATOM	1279	CB.	ILE	1620	12.030	1.543	0.381	1.00	27.44
ATOM	1280	CG2	ILE	1620	13.521	1.806	0.506	1.00	25.37
MOTA	1281	CG1	ILE	1620	11.767	0.764	-0.913	1.00	19.80
ATOM	1282	CD1	ILE	1620	12.100	1.557	-2.164	1.00	25.40
ATOM	1283	C	ILE	1620	11.553	1.686	2.855	1.00	27.51
ATOM	1284	0	ILE	1620	11.011	2.792	2.833	1.00	26.56
ATOM	1285	N	HIS	1621	12.193	1.210	3.916	1.00	26.68
ATOM	1287	CA	HIS	1621	12.297	1.967	5.162	1.00	26.31
MOTA	1288	CB	HIS	1621	13.081	1.174	6.210	1.00	25.00
ATOM	1289	CG	HIS	1621	12.848	1.633	7.618	1.00	23.08
MOTA	1290	CD2	HIS	1621	12.224	1.027	8.656	1.00 1.00	23.21
MOTA	1291	ND1	HIS	1621	13.260	2.862	8.088	1.00	22.69
ATOM	1293	CE1	HIS	1621	12.909	2.993	9.356	1.00	25.34
ATOM	1294	NE2	HIS	1621	12.273	1.891	9.719	1.00	24.18
ATOM	1296	C	HIS	1621	12.963	3.316	4.976	1.00	25.86
MOTA	1297	0	HIS	1621	12.408	4.328	5.349	1.00	25.09 28.21
MOTA	1298	N	ARG	1622.	14.162	3.315	4.402	1.00	26.21
ATOM	1300	CA	ARG	16 2 2	14.976	4.520	4.183	1.00	26.50
MOTA	1301	CB	ARG	1622	14.180	5.670	3.558	1.00	
MOTA	1302	CG	ARG	1622	13.673	5.326	2.202	1.00	23.52
ATOM	1303	CD	ARG	1622	12.995	6.494	1.551	1.00	23.81
MOTA	1304	NE	ARG	1622	12.677	6.170	0.180	1.00	28.42 32.52
MOTA	1306	CZ	ARG	1622	11.623	5.455	-0.197	1.00	
MOTA	1307	NH1	ARG	1622	10.774	4.994	0.711	1.00	32.34
MOTA	1310	NH2	ARG	1622	11.460	5.138	-1.489	1.00	30.07
ATOM	1313	С	ARG	1622	15.740	4.993	5.423	1.00	28.30
MOTA	1314	0	ARG	1622	16.698	5.757	5.313	1.00	26.31
MOTA	1315	N	ASP	1623	15.379	4.495	6.596		26.19
MOTA	1317	CA	ASP	1623	16.114	4.879	7.788	1.00	27.41
ATOM	1318	CB	ASP	1623	15.562	6.155			29.94
ATOM	1319	CG	ASP	1623	16.481	6.689	8.430	1.00	34.83
MOTA	1320	OD1	ASP	1623	15.971	7.265	9.533 10.514	1.00	38.84
MOTA	1321	OD2	ASP	1623	17.721	6.514	9.423	1.00	44.51
MOTA	1322	C	ASP	1623	16.203	3.763	9.423 8.812	1.00	37.59
MOTA	1323	0	ASP	1623	15.845	3.763		1.00	28.71
ATOM	1324	N	LEU	1624	16.735	2.633	9.990 8.357	1.00	26.21
					_0.,55	4.033	0.35/	1.00	26.82

MOTA	1326	CA	LEU	1624	16.905	1.469	9.216	1.00	25.91
MOTA	1327	CB	LEU	1624	17.025	0.209	8.367	1.00	23.35
MOTA	1328	CG	LEU	1624	17.089	-1.107	9.127	1.00	21.09
ATOM	1329	CD1	LEU	1624	15.824	-1.303	10.009	1.00	14.44
MOTA	1330	CD2	LEU	1624	17.282	-2.215	8.101	1.00	18.30
ATOM	1331	C	LEU	1624	18.136	1.640	10.105	1.00	24.93
MOTA	1332	0	LEU	1624	19.235	1.897	9.611	1.00	25.58
MOTA	1333	N	ALA	1625	17.912	1.557	11.416	1.00	26.30
MOTA	1335	CA	ALA	1625	18.945	1.702	12.445	1.00	23.59
ATOM	1336	CB	ALA	1625	19.271	3.174	12.654	1.00	15.82
ATOM	1337	C	ALA	1625	18.351	1.116	13.732	1.00	23.64
ATOM	1338	0	ALA	1625	17.135	0.928	13.825	1.00	26.66
MOTA	1339	N	ALA	1626	19.197	0.815	14.712	1.00	21.59
MOTA	1341	CA	ALA	1626	18.708	0.266	15.974	1.00	21.66
MOTA	1342	CB	ALA	1626	19.860	-0.179	16.838	1.00	22.97
MOTA	1343	C	ALA	1.626	17.835	1.272	16.731	1.00	24.98
ATOM	1.344	0	ALA	1626	17.072	0.891	17.620	1.00	26.84
MOTA	1345	N	ARG	1627	17.978	2.558	16.409	1.00	24.55
ATOM	1347	CA	ARG	1627	17.178	3.598	17.042	1.00	25.29
ATOM	1348	CB	ARG	1627	17.699	4.983	16.673	1.00	26.66
MOTA	1349	CG	ARG	1627	17.675	5.276	15.179	1.00	30.56
MOTA	1350	CD	ARG	1627	18.033	6.715	14.902	1.00	34.97
ATOM	1351	NE	ARG	1627	18.177	6.980	13.470	1.00	40.03
MOTA	1353	CZ	ARG	1627	19.322	6.864	12.809	1.00	40.62
ATOM	1354	NH1	ARG	1627	20.421	6.485	13.441	1.00	46.52
MOTA	1357	NH2	ARG	1627	19.377	7.159	11.523	1.00	43.25
ATOM	1360	C	ARG	1627	15.739				



ATOM	1394	CG1	VAL	1631	12.995	-5.469	23.243	1.00	23.92
MOTA	1395	CG2	VAL	1631	14.197	-3.714	21.895	1.00	24.26
ATOM	1396	С	VAL	1631	10.450	-3.773	22.885	1.00	32.64
ATOM	1397	0	VAL	1631	10.198	-2.821	23.643	1.00	33.01
ATOM	1398	N	THR	1632	9.697	-4.863	22.827	1.00	34.45
MOTA	1400	CA	THR	1632	8.516	-5.035	23.660	1.00	34.29
MOTA	1401	CB	THR	1632	7.466	-5.941	22.962	1.00	34.62
ATOM	1402	OG1	THR	1632	7.965	-7.288	22.881	1.00	34.40
ATOM	1404	CG2	THR	1632	7.154	-5.414	21.551	1.00	31.61
ATOM	1405	C	THR	1632	8.896	-5.678	24.989	1.00	35.41
ATOM	1406	0	THR	1632	10.002	-6.189	25.146	1.00	34.79
ATOM	1407	N	GLU	1633	7.939	-5.706	25.913	1.00	36.86
ATOM	1409	CA	GLU	1633	8.156	-6.298	27.224	1.00	37.27
ATOM	1410	CB	GLU	1633	6.893	-6.182	28.079	1.00	37.66
ATOM	1411	CG	GLU	1633	7.031	-6.718	29.514	1.00	44.43
ATOM	1412	CD	GLU	1633	8.048	-5.959	30.378	1.00	46.68
ATOM	1413	OE1	GLU	1633	8.104	-4.708	30.300	1.00	49.88
ATOM	1414	OE2	GLU	1633	8.783	-6.612	31.156	1.00	48.53
	1415	C	GLU	1633	8.561	-7.753	27.088	1.00	37.15
ATOM	1415	0	GLU	1633	9.227	-8.292	27.954	1.00	38.60
ATOM	1417	N	ASP	1634	8.167	-8.384	25.990	1.00	38.41
MOTA	1417	CA	ASP	1634	8.505	-9.787	25.770	1.00	38.86
ATOM	1419	CB	ASP	1634	7.381	-10.499	25.013	1.00	44.27
ATOM		CG	ASP	1634	6.022	-10.349	25.690	1.00	50.18
MOTA	1421	OD1	ASP	1634	5.726	-11.141	26.617	1.00	52.07
MOTA	1422	OD1	ASP	1634	5.253	-9.439	25.295	1.00	50.17
MOTA	1423	C C	ASP	1634	9.804	-9.947	25.007	1.00	36.23
ATOM	1424		ASP	1634	10.141	-11.049	24.608	1.00	35.82
ATOM	1425	O			10.528	-8.851	24.799	1.00	36.51
ATOM	1426	N	ASN	1635 1635	11.795	-8.864	24.052	1.00	37.41
ATOM	1428	CA	asn asn	1635	12.801	-9.842	24.678	1.00	38.49
ATOM	1429	CB		1635	13.343	-9.359	26.003	1.00	37.71
ATOM	1430	CG	ASN	1635	13.499	-8.156	26.227	1.00	38.09
ATOM	1431	OD1	asn asn	1635	13.433	-10.300	26.874	1.00	39.63
ATOM	1432	ND2			11.655	-9.162	22.552	1.00	36.37
ATOM	1435	C	ASN	1635	12.522	-9.811	21.944	1.00	36.41
MOTA	1436	0	ASN	1635 1636	10.547	-8.721	21.966	1.00	33.79
ATOM	1437	N	VAL	1636	10.315	-8.910	20.543	1.00	30.59
ATOM	1439	CA	VAL		8.820	-9.139	20.218	1.00	28.83
ATOM	1440	CB	VAL	1636		-9.182	18.712	1.00	26.13
MOTA	1441	CG1	VAL	1636	8.615 8.339	-10.431	20.838	1.00	25.67
MOTA	1442	CG2	VAL	1636	10.782	-7.630	19.863	1.00	30.18
MOTA	1443	C	VAL	1636		-6.527	20.301	1.00	27.86
MOTA	1444	0	VAL	1636	10.436	-7.792	18.832	1.00	30.93
ATOM	1445	N	MET	1637	11.609	-6.679	18.060	1.00	28.34
MOTA	1447	CA	MET	1637	12.140		17.330	1.00	30.84
MOTA	1448	CB	MET	1637	13.397	-7.138		1.00	30.73
MOTA	1449	CG	MET	1637	14.480	-7.693 6.490	18.254 19.477	1.00	32.20
MOTA	1450	SD	MET	1637	15.050	-6.490			28.71
MOTA	1451	CE	MET	1637	15.074	-7.500	20.938	1.00	
MOTA	1452	C	MET	1637	11.082	-6.264	17.051	1.00	27.29
MOTA	1453	0	MET	1637	10.587	-7.099	16.297	1.00	27.32
MOTA	1454	N	LYS	1638	10.733	-4.983	17.045	1.00	27.19
MOTA	1456	CA	LYS	1638	9.716	-4.450	16.143	1.00	26.38
MOTA	1457	CB	LYS	1638	8.437	-4.120	16.912	1.00	27.09

	223	
	- 2	51 17.407 1.00 29.71
-AF8 CG LYS 1638	7.702 -5.3	10 100 1.00 31.40
ATOM 1458 CG TVC 1638	6.386 -5.0	1,00 27.05
ATOM 1459 CD 112	5.485 -6.2	1.00 20.00
ATOM 1460 CB -170 1638	4.888 -6.5	100 26.56
ATOM 1461 NZ 1638	10 196 -3.2	208 13.20 1.00 27.40
NEOM 1465 C LYS 1030	10 514 -2.	194 10.00 1.00 24.31
ATOM 1466 O LYS 1630	10 211 -3.2	2/1 1 2 2 00 24.84
ATOM 1467 N ILE 1639	10 649 -2.	147 13.265 1 00 25.81
ATOM 1469 CA ILE 1633	10 924 -2.	588 11.830 1.00 24.18
1470 CB ILE 1833	11 248 -1.	395 10.952 1 00 25.01
A10 CG2 ILE 1639	12.094 -3.	566 11.826 1.00
7472 CG1 ILE 1639	12.075 -4.	499 10.675 1.00
1473 CD1 ILE 1635	9.641 -0	999 13.348 1.00
ATOM 1475 C ILE 1639	8.435 -1	186 13.1/0 1.00
ATOM 1472 O ILE 1639	0	183 13.635 1.00
ATOM 1475 N ALA 1640	10.10	392 13.744 1.00
ATOM 1470 CA ALA 1640	J. J. +	094 15.070 1.00
ATOM 1470 011 777 1640	9.000	348 12.576 1.00 28.33
ATOM 14/9 02 272 1640	J	11.871 1.00 28.30
ATOM 1480 0 ATA 1640	10.00	12.354 1.00 29.74
ATOM 1481 0 1641	0.07-	1 272 11.325 1.00 32.13
ATOM 1482 N 700 1641	0.,0-	- 272 11.688 1.00 34.31
ATOM 1484 CA 150 1641	9.075	1.00 30.32
ATOM 1485 CB ASE 1641	9.507	2 250 1.00 42.10
ATOM 1486 CG ACT 1641	10.299	- 274 13.483 1.00 41.03
ATOM 1487 ODI AGE 1641	8.420	2 267 1 00 32.00
ATOM 1488 OD2 AS2 - 1641	8.882	3.840 2021 1.00 32.65
ATTOM 1489 C ASI	0 220	4.617
270M 1490 O ASP 101		2.634 200 1.00 30.06
2 MOM 1491 N FIID	- 2 473	2.119 0.24.46
-mov 1493 CA FILL		0.606 3.254 1.00 23.26
ATOM 1494 CB PHE 164		0.176 8.834 1.00 19.66
NTOM 1495 CG PHE 104	- 700	0.075 8.123
NUM 1496 CDI PHE 10	- 066	-0.134 10.203 1 00 20.97
ATTOM 1497 CD2 PHE 10-		-0.331 8.734 1 00 26.61
AMON 1498 CE1 PHE 10	- 705	-0.540 10.830 24.82
1499 CE2 PHE 10		-0.639 10.003 20
ATOM	12	2 830 7.225 1.00
PHE 10		2 922 6.029 1.00
ATON O PHE IN	- 497	3 372 7.741 1.00
GLY I		4.059 6.876 1.00
ATOM 1505 CA GLY 16	5.462	5 560 6.913 1.00 324
ATOM 1300 C GLY 1	5.629	6 310 6.415 1.00
ATOM 1500 GLY 1	643 4.795	5 997 7.486 1.00
ATOM 1507 TELL 1	644 6.739	7 406 7.630 1.00 41.93
ATOM 1500 F. TELL 1	644 7.052	8.439 1.00 37.41
ATOM 1510 CA	644 8.332	9.369 1.00 38.30
ATOM 1511 CB LEU 1	644 8.377	100 40.45
ATOM 1512 CG 22-	1644 7.384	2 229 1.00 41.94
ATOM 1513 CDI III	1644 9.775	6 296 1.00 47.33
ATOM 1514 CD2 1150	1644 7.189	5 341 1.00 50.55
ATOM 1515 C LEU	1644 7.787	7.648 5.347 1.00 52.59
лиом 1516 O	1645 6.637	9.356 5.55 1.00 56.88
ACOM 1517 N ALA	1645 6.686	10.194 5.033 1.00 58.01
ACOM 1519 CA ALA		10.999 4.942 1 00 58.95
AMON 1520 CB ALA	- 000	. 42E 5.L/O = -
ATOM 1521 C ALA	1645 7.880	
AION 222		

											- 1,000,7/12
							226				
	ATOM	1522	. 0								
	ATOM	1523	-	ALA	1645	8.	064	77 770			
	ATOM	1525	٠.	ARG	1646		_	11.770	6.224	1.00	59.37
	ATOM			ARG	1646			11.211	4.133	1.00	60.26
	ATOM	1526	_	ARG	1646		_	12.088	4.165	1.00	
		1527	C	ARG	1646	10.		ll.444	4.976	1.00	63.04
	ATOM	1528	0	ARG	1646	10.	_	2.461	2.782		64.92
	MOTA	1529	N	ASP	1647	10.	361 <u>1</u>	1.641	1.864	1.00	63.84
	MOTA	1531	CA	ASP		10.8	³⁰¹ 1	3.714	2.633	1.00	63.55
	MOTA	1532	СВ	ASP	1647	11.3	332 1	4.190		1.00	65.18
A	MOT	1533	CG		1647	10.9	89 1	5.670	1.361	1.00	67.26
A	m	1534	OD1	700	1647	11.1		_	1.150	1.00	68.92
A		1535	OD2		1647	12.1			-0.304	1.00	70.88
		1536			1647	10.2			-0.943	1.00	70.33
			C	ASP :	1647	12.8		825 .	0.808	1.00	71.39
		1537	0	ASP :	L647	13.54		.005			60 40
		L538	N	ILE]	648	10.04		.711	2 7 4 0	_	68.40
		540	CA		648	13.34		.055		_	68.66
		541	CB		648	14.77			A 555		68.48
		542	CG2	 -	648	15.09	1 11		-	١.٥٥ (59.00
	OM 1	543	000			14.23	1 10	-		.00	56.28
AT					648	14.86	9 11.			.00 6	55.14
AT		_	~		548	15.27	4 10.			.00 6	3.01
ATO			`	_,	548	15.542				.00 6	0.11
ATO		547 N	-		48	16.628	14.		.046 1	.00 7	1.12
ATO			•-	IIS 16	49	14.923			.525 1	.00 7	2.41
ATO					49	15.546	-		.883 1		3.09
ATO				IS 16	49	14.921			.469 1.		1.66
ATO		~-		IS 16		15.178		191 -2			
ATO		_	D2 H	IS 16	49	16.214		157 - 3.			5.00
ATO			D1 H	IS 164		16.314	14.4	!25 -4.			.03
			E1 H			14.245	14.7	39 -4.			.85
ATOM		96 M	E2 H)		-	14.765	13.8		C 0 .		.49
ATOM		8 C	ні		_	6.005	13.6	23 -5.			. 94
ATOM		9 0	HI		_	5.466	17.1	08 -0.		-,	.22
ATOM		0 N	HI			5.567	18.2		_		. 04
ATOM						5.265	16.86	-			49
ATOM	156					5.181	17.91		743 1.0	0 76.	11
ATOM	1564			-05	0 1:	3.723	18.32			0 77.	63
ATOM	1565		HIS) 13	3.206	19.35		95 1.0	0 81.	10
ATOM	1566	_) 13	3.662	20.55			0 86.	06
ATOM	1568) 12	2.099	20.59	2 0.7	30 1.0		
ATOM	1569			1650	11	.893	19.14	_	39 1.00		
ATOM			HIS	1650	_	.823	20.21		11 1.00		
ATOM	1571	C	HIS	1650		.824	21.10	3 -0.2	38 1.00		
	1572	0	HIS	1650		. 624	17.482	2 3.04	1.00		
ATOM	1573	N	ILE	1651	12	.651	18.133	4.09			
ATOM	1575	CA	ILE	1651		. 573	16.385	3.02	_	_	2
ATOM	1576	CB	ILE		17.	241	15.864	4.21	-		
ATOM	1577	CG2	ILE	1651	17.	788	14.433			77.0	2
ATOM	1578	CG1		1651	18.	647	13.963			78.24	4
ATOM	1579		ILE	1651	16.	633	13 450	5.15		77.92	
	1580	CD1	ILE	1651	17.	094	13.458	3.75	0 1.00	80.90)
	1581	C	ILE	1651	18.		12.032	3.483	3 1.00	82.41	•
		0	ILE	1651	19.		16.748	4.620	1.00	76 7	
3 5 6 6 6	1582	N	ASP	1652			17.078	3.803	1.00	76.15	
3000	1584	CA	ASP	1652	18.4		17.150	5.882		76.52	
7 0000	1585	CB	ASP	1652	19.5	527	17.957	6.384		75.13	
ATOM 1	1586	CG	ASP		19.0)68 <u>:</u>	18.781	7.592	_	73.91	
				1652	20.2	16]	19.499	8 200	. •	76.30	
SSSD/5514	45. v01							8.286	1.00	79.91	
											•

MOTA	1587	OD1	ASP	1652	21.247	19.786	7.636	1.00	82.38
MOTA	1588	OD2	ASP	1652	20.081	19.780	9.497	1.00	81.51
MOTA	1589	C	ASP	1652	20.637	16.984	6.783	1.00	72.31
MOTA	1590	0	ASP	1652	20.599	16.403	7.866	1.00	71.41
MOTA	1591	N	TYR	1653	21.610	16.805	5.894	1.00	71.44
ATOM	1593	CA	TYR	1653	22.736	15.900	6.143	1.00	70.07
ATOM	1594	CB	TYR	1653	23.655	15.849	4.921	1.00	66.96
ATOM	1595	CG	TYR	1653	23.153	14.932	3.834	1.00	66.43
ATOM	1596	CD1	TYR	1653	23.881	14.757	2.657	1.00	66.60
MOTA	1597	CE1	TYR	1653	23.434	13.898	1.653	1.00	68.33
MOTA	1598	CD2	TYR	1653	21.960	14.224	3.981	1.00	66.58
ATOM	1599	CE2	TYR	1653	21.500	13.363	2.990	1.00	68.84
MOTA	1600	CZ	TYR	1653	22.241	13.205	1.823	1.00	69.34
MOTA	1601	ОН	TYR	1653	21.781	12.360	0.833	1.00	69.88
MOTA	1603	C	TYR	1653	23.557	16.227	7.391	1.00	70.80
MOTA	1604	0	TYR	1653	24.197	15.351	7.975	1.00	70.62
MOTA	1605	N	TYR	1654	23.531	17.488	7.802	1.00	70.76
ATOM	1607	CA	TÝR	1654	24.280	17.902	8.972	1.00	70.97
ATOM	1608	CB	TYR	1654	24.795	19.328	8.783	1.00	69.27
MOTA	1609	CG	TYR	1654	25.935	19.401	7.787	1.00	69.68
MOTA	1610	CD1	TYR	1654	25.696 ·	19.352	6.415	1.00	69.51
MOTA	1611	CE1	TYR	1654	26.750	19.380	5.498	1.00	70.15
ATOM	1612	CD2	TYR	1654	27.256	19.482	8.221	1.00	69.92
ATOM	1613	CE2	TYR	1654	28.314	19.513	7.316	1.00	70.26
MOTA	1614	CZ	TYR	1654	28.057	19.462	5.958	1.00	70.22
MOTA	1615	OH	TYR	1654	29.111	19.492	5.069	1.00	69.67
MOTA	1617	С	TYR	1654	23.503	17.763	10.272	1.00	72.19
MOTA	1618	0	TYR	1654	24.035	18.043	11.344	1.00	73.21
MOTA	1619	N	LYS	1655	22.269	17.275	10.183	1.00	73.05
MOTA	1621	CA	LYS	1655	21.424	17.108	11.363	1.00	74.81
ATOM	1622	CB	LYS	1655	19.955	17.124	10.953	1.00	75.63
MOTA	1623	CG	LYS	1655	18.978	17.239	12.102	1.00	79.16
ATOM	1624	CD	LYS	1655	17.581	17.513	11.576	1.00	84.09
ATOM	1625	CE	LYS	1655	16.517	17.244	12.634	1.00	87.56
MOTA	1626	NZ	LYS	1655	15.139	17.478	12.097	1.00	89.36
ATOM	1630	C	LYS	1655	21.738	15.834	12.156	1.00	75.72
MOTA	1631	0	LYS	1655	21.900	14.751	11.586	1.00	77.14
MOTA	1632	N	LYS	1656	21.815	15.977	13.477	1.00	75.08
MOTA	1634	CA	LYS	1656	22.106	14.857	14.363	1.00	73.36
MOTA	1635	CB	LYS	1656	23.062	15.296	15.477	1.00	72.88
ATOM	1636	CG	LYS	1656	24.475	15.599	15.007	1.00	72.87
ATOM	1637	CD	LYS	1656	25.346	16.048	16.167	1.00	74.66
ATOM	1638	CE	LYS	1656	26.830	15.945	15.828	1.00	74.84
ATOM	1639	NZ	LYS	1656	27.701	16.322	16.981	1.00	73.74
ATOM	1643	С	LYS	1656	20.827	14.311	14.982	1.00	72.45
ATOM	1644	0	LYS	1656	19.795	14.991	15.007	1.00	72.74
MOTA	1645	N	THR	1657	20.900	13.075	15.469	1.00	71.26
ATOM	1647	CA	THR	1657	19.763	12.426	16.107	1.00	70.05
MOTA	1648	CB	THR	1657	19.969	10.886	16.206	1.00	68.30
MOTA	1649	OG1	THR	1657	21.084	10.598	17.060	1.00	69.34
MOTA	1651	CG2	THR	1657	20.244	10.292	14.839	1.00	66.16
MOTA	1652	С	THR	1657	19.707	13.019	17.504	1.00	70.37
MOTA	1653	0	THR	1657	20.608	13.761	17.892	1.00	71.47
ATOM	1654	N	THR	1658	18.669	12.691	18.263	1.00	70.80

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	ATOM	1656	CA	THR	1650						
	ATOM	1657	СВ	THR	1658	-0.5		3.205	19.626	1 0-	
	ATOM	1658	C	THR	1658	- /	34 1		20.325	1.00	71.54
	ATOM	1659	ō		1658		44 1:	_	0.325	1.00	71.20
	ATOM	1660	N	THR	1658	20.4		_	0.394	1.00	70.91
	ATOM	1662		ASN	1659	20.3	_		1.063	1.00	71.25
	ATOM		CA	ASN	1659	21.5			0.199	1.00	68.87
		1663	CB	ASN	1659	21.6	_	.157 2	0.871	1.00	65.52
	3	1664	CG	ASN	1659	22.00		.635 2	0.796	1.00	
		1665	OD1	ASN	1659	22.41		.032 2	1.916	1.00	67.39
	ATOM	1666	ND2		1659	22.26	1 9	.410 23		1.00	69.42
		1669	C	_	1659	23.27	8 8			7 A-	71.70
P	MOTA	1670	0			22.83	0 11			_	68.93
· A	TOM 1	671			1659	23.91	7 11		800	1.00	62.51
A				~	1660	22.70			. 733	1.00	61.47
			~		660	23.85			.348		59.76
	mas.			GLY 1	.660	24.55			.750		57.70
				GLY 1	660	25.659	-	593 17			6.98
			N A		661	23.055		979 17			57.55
	TOM 1	678 (CA Z		661	23.909		573 17.	_		
		579 (~		661	24.504	10.				5.34
AT	COM 16	580 C		~~		24.255	9.		_		2.28
ΑŢ	OM 16	81 6			561	24.811			a	.00 5	0.68
AT	'OM 16				661	24.542				.00 4	9.61
AT					61	24.942	6.5			.00 5	2.30
AT					61	24.731	5.3			.00 5	3.64
AT				RG 16	61	24.124					5.32
ATO			H2 AI	RG 16	61	25.145	4.5				.04
ATO			AI	≀G 16		24.015	4.7	~ ~	965 1.		.48
		-	AF	RG 16		22.015	11.2				.89
ATO			LE			22.916	11.8	12 14.4			
ATC		95 C#	LE			24.839	11.0	³⁰ 13.5			.43
ATO		6 CE				24.503	11.48	31 12.1			.78
ATO		7 CG				25.762	12.02	0 11.4			.05
ATO:	M 169					26.351	13.30				.15
ATO						27.780	13.51				.60
ATO						25.484	14.49				14
ATON		_	LE		2 ;	23.867	10.34		-	0 42.	
ATON		. •	LEU		2 2	24.548			70 1.0	0 41.	81
ATOM	_		PRC	166	3 2	22.546	9.40			0 40.	46
ATOM			PRO		3 2	1.659	10.42			0 40.	40
ATOM			PRO	1663	3 2	1.794	11.519		1 1.0		-
			PRO				9.423	10.35	1 1.00		
ATOM	00	CG	PRO	1663		0.433	10.095	10.15			L /
MOTA	_, _,	C	PRO	1663	~	0.282	10.901	11.41	1.00		
MOTA	1708	0	PRO			2.445	9.059	9.012			
ATOM	1709	N	VAL	1663		2.265	7.949				
ATOM	1711	CA		1664		3.200	9.989			33.0	1
ATOM	1712		VAL	1664	23	3.889	9.722				6
ATOM	1713	CB	VAL	1664				7.160			1
ATOM		CG1	VAL	1664			10.916	6.659		33.1	3
ATOM	1714	CG2	VAL	1664	25		11.929	5.968	1.00	33.4	4
	1715	C	VAL	1664	2.2	.321	11.554	7.792	1.00		
ATOM	1716	0	VAL	1664	24	.812	8.511	7.266	1.00	33.68	
ATOM	1717	N	LYS		25	.157	7.903	6.257		30.58	
ATOM	1719	CA	LYS	1665		.211	8.171	8.489	1.00	29.20	
ATOM	1720	CB		1665	26	.102	7.044		1.00	28.02	
ATOM	1721	CG	LYS	1665	26.	749	7.153	8.726	1.00	24.95	
ATOM	1722		LYS	1665	27.	811		10.098	1.00	24.39	
	-144	CD	LYS	1665	28	189	8.231	10.140	1.00	28.36	
SSSD/55	145 ~				•		8.628	11.548	1.00	29.24	
2000/33	145. V()1									4 - 1	•



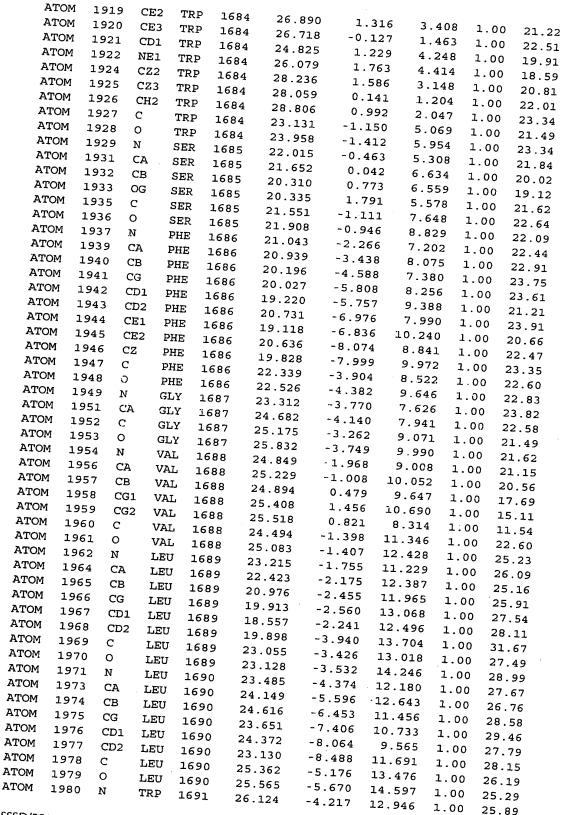
			0 1	00 31.15
	3665	29.269 9.6	190 == 1	00 35.47
ATOM 1723 CE	1665	29.639 10.1	.94 12	00 25.16
ATOM 1724 NZ		25.440 5.6	592	1.00 24.34
ATOM 1728 C		26.096 4.0	5/1	1.00 25.16
ATOM 1729 O	LYS 1665 TRP 1666	24.138 ⁵ ·	698	1.00 26.61
ATOM 1730 N		23.414 ⁴ ·	401	1.00 28.17
ATOM 1732 CF	1666	22 157 4.	412	1.00 30.26
ATOM 1733 CH	1666	22.428 3.	931 201	1.00 26.92
ATOM 1734 CO	1666	22.930 4.	714 11.426	1.00 26.34
ATOM 1735 C	D2 TRP 1666	23 063 3.	837 12.537	1.00 24.69
ATOM 1736 C	E2 TRP 1666	23.286 6	.057 11.598	1.00 26.44
ATOM 1737 C	E3 TRP 1666	22 276 2	.656 10.800	1.00 25.65
ATOM 1738 C	D1 TRP 1666	22.659 2	.592 12.118	
ATOM 1739 N	NE1 TRP 1666	23.535 4	.264 13.779	1.00 24.97 1.00 22.23
ATOM 1741 C	ZZ2 TRP 1666	23.758 6	.484 12.837	
ATOM 1742 (CZ3 TRP 1666	23 877 5	.587 13.908	
ATOM 1743 (CH2 TRP 1666	23.048 ⁴	.345 6.572	
ATOM 1744	C TRP 1666	22 573	3.301 6.116	
	O TRP 1666	23 355	5.390 5.811	1.00 26.70 1.00 25.21
ATOM 1746	N MET 1667	23.022	5.444 4.398	1.00 28.81
	CA MET 1667	22.828	6.893 3.963	1.00 35.42
ATOM 1749	CB MET 1667	21.704	7.630 4.637	1.00 42.64
ATOM 1750	CG MET 1667		9.283 3.924	1.00 41.32
ATOM 1751	SD MET 1667	050	8.858 2.369	1.00 25.03
ATOM 1752	CE	001	4.807 3.417	
ATOM 1753	166	102	5.047 3.446	. 06 70
ATOM 1754	O	120	4.034 2.501	00
ATOM 1755	14		3.398 1.441	
ATOM 1757	166	~ ~ ~ ~ ~ ~	2.509 0.601	40
ATOM 1758	77.7 166	- 4 720	4.528 0.575	
ATOM 1759	777 166	-4 044	5.521 0.32	0"
ATOM 1760	770 166	072	4.374 0.06	07.00
ATOM 1761	N 0 3.66		3.214 0.17 5.418 -0.77	76
ATOM 1762	166	71		5 50 50
ATOM 1763	770 160	014		- 00 30 22
ATOM 1764	770 16	69 28.193	3.00-	3 1.00 27.08
ATOM 1765	- ppo 16	69 25.647	3.5	3 1.00 28.31
ATOM 1766	npO 16	69 25.496		2 - 22
ATOM 1767	GIII 16	70 24.993		- 0 - 02
ATOM 1768	3 N C20	70 24.110		42 1.00 27.18
ATOM 1770	- CTI 16	570 23.680	4.20	11 1.00 27.66
ATOM 1771	CIII 16	570 22.662	5 •	12 1.00 27.75
ATOM 1772	CIII 10	670 23.280		47 1.00 27.12
ATOM 177	3 CD STILL 1	670 22.488		1.00 21.64
ATOM 177	4 OEI CIII 1	670 24.526	- · - ·	89 1.00 26.88
ATOM 177	5 052 -	670 22.896	0	1.00 24.52
ATOM 177	or II 1	670 22.348	/ • • -	948 1.00 29.43
ATOM 177	77 0 -	671 22.477		392 1.00 29.29
ATOM 177	70 17 77 77 77 77 77 77 77 77 77 77 77 77	671 21.342	• • • • • • • • • • • • • • • • • • • •	217 1.00 26.98
ATOM 178	80 CA ALA	1671 20.751	3	939 1.00 31.14
ATOM 17	81 CD	1671 21.826	0	143 1.00 31.67
ATOM 17	82	1671 21.159	J. —	343 1.00 32.31
	83	1672 23.013	J. —	154 1.00 33.79
• • •	84 1	1672 23.636	9.352 0	.
ATOM 17	786 CA LEU			



							230				
		1787	СВ	LEU	1672						
		1788	CG	LEU	1672			986 1	.008	1.00	34.49
		1789	CD1	LEU	1672	-5.50		166 1	.618	1.00	
		1790	CD2	LEU	1672	24.71		840 2	.666	1.00	42.22
	OM :	1791	C	LEU	1672	26.86		665 2	.237	1.00	33.93
		1792	0	LEU	1672	24.07			.972	1.00	36.30
		L 7 93	N	PHE	1673	23.78			.949	1.00	39.09
		795	CA	PHE	1673	24.77 25.26		723 -1	. 957	1.00	34.39
AT		796	CB	PHE	1673	26.55			075	1.00	33.81
ATO			CG	PHE	1673	27.66			625	1.00	33.15
AT(_			PHE	1673	28.313			617	1.00	33.44
AT(~		PHE	1673	28.055			419	1.00	32.17
ATC ATC				PHE	1673	29.346			861	1.00	34.87
ATC		_		PHE	1673	29.090	_		484	1.00	31.98
				~	1673	29.736				1.00	36.31
ATO ATO		303	_	·	1673	24.273			732	1.00	34.55
ATO		304 C	-	HE :	1673	24.135				1.00	34.79
ATO		05 N			1674	23.584	11.7			1.00	35.74
ATO				SP ;	L674	22.650	9.58		72]	1.00	37.31
ATO				SP 1	674	22.917	9.60	_		.00	35.61
ATOM				SP 1	674	24.362	8.39			.00	37.01
ATOM				SP 1	674	25.030	8.28				41.02
ATOM			D2 A:	SP 1	674	24.828	9.34				43.07
ATOM			AS	SP 1	674	21.162	7.14				42.24
ATOM	~~~		AS	_	674	20.315	9.63				37.06
ATOM		_	AF		675	20.840	9.50				36.37
ATOM		_			575	19,445	9.74! 9.79]				37.78
ATOM		_			575	18.832	11.137			.00 3	9.41
ATOM	181 181				75	19.413	12.299			00 4	4.39
ATOM	182				75	19.516	13.551	. – •		00 5	4.30
ATOM	182		AR		75	20.060	14.664		_	00 6	3.84
ATOM	182	- -	AR		75	19.652	15.925		_		3.69
ATOM	1826				75	18.695	16.253			00 7	7.10
ATOM	1829				75	20.177	16.855				9.65
ATOM	1830		ARG		75 :	18.617	8.639	-2.66			9.31
ATOM	1831	_	ARG		75 :	17.447	8.808	-4.22			7.46
ATOM	1833		ILE		76]	19.235	7.475	-4.557 -4.351			1.57
ATOM	1834	CB	ILE		76 1	.8.545	6.313	-4.874			.37
ATOM	1835		ILE	167	_	.9.358	5.644	-5.976		_	.99
ATOM	1836	CG1	ILE	167	_	8.552	4.529	-6.602		_	.98
ATOM	1837	CD1	ILE	167	_	9.708	6.663	-7.050			.04
ATOM	1838	C	ILE	167	_	0.799	6.200	-7.962			. 92
ATOM	1839	0	ILE	167	_	8.315	5.315	-3.743	1.0		.16
ATOM	1840	N	ILE	167		9.245	4.632	-3.300	1.0		
	1842	CA	TYR TYR	167	_	7.082	5.279	-3.246	1.00	٠٠,	
3 5 5 5 5 5	1843	CB		167		5.701	4.371	-2.173	1.00		
	1844	CG	TYR	1677		771	5.074	-1.208	1.00		
* ** -	1845	CD1	TYR	1677		.457	6.136	-0.406	1.00		
	1846	CE1	TYR	1677		.598	7.432	-0.905	1.00		
3	1847	CD2	TYR	1677		.212	8.424	-0.159	1.00		
	1848	CE2	TYR TYR	1677		. 952	5.857	0.863	1.00		
7	1849	CZ		1677		.567	6.842	1.621	1.00		
·	.850	OH	TYR	1677		.688	8.125	1.110	1.00	32.6	
			TYR	1677	18		9.118	1.888	1.00	34.5	
SSSD/5514	15. v01						_		1.00	38.8	9

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ATOM	1852	C	TYR	1677	16.029	3.149	-2.743	1.00	25.47
ATOM	1853	0	TYR	1677	15.132	3.264	-3.578	1.00	26.00
ATOM	1854	N	THR	1678	16.459	1.983	-2.272	1.00	24.27
MOTA	1856	CA	THR	1678	15.942	0.701	-2.734	1.00	24.09
MOTA	1857	CB	THR	1678	16.830	0.123	-3.853	1.00	24.19
ATOM	1858	OG1	THR	1678	18.165	-0.008	-3.349	1.00	27.81
MOTA	1860	CG2	THR	1678	16.843	1.009	-5.085	1.00	24.15
ATOM	1861	С	THR	1678	15.979	-0.297	-1.577	1.00	25.02
MOTA	1862	0	THR	1678	16.379	0.036	-0.465	1.00	27.65
MOTA	1863	N	HIS	1679	15.569	-1.530	-1.844	1.00	25.04
MOTA	1865	CA	HIS	1679	15.591	-2.560	-0.818	1.00	24.35
MOTA	1866	CB	HIS	1679	14.853	-3.812	-1.298	1.00	23.78
ATOM	1867	CG	HIS	1679	13.390	-3.592	-1.536	1.00	27.24
ATOM	1868	CD2	HIS	1679	12.627	-3.758	-2.643	1.00	28.22
ATOM	1869	ND1	HIS	1679	12.532	-3.137	-0.551	1.00	30.64
ATOM	1871	CE1	HIS	1679	11.310	-3.028	-1.041	1.00	28.13
MOTA	1872	NE2	HIS	1679	11.339	-3.400	-2.307	1.00	28.52
MOTA	1874	С	HIS	1679	17.056	-2.846	-0.514	1.00	22.52
MOTA	1875	0	HIS	1679	17.419	-3.179	0.613	1.00	22.58
MOTA	1876	N	GLN	1680	17.898	-2.604	-1.516	1.00	24.34
ATOM	1878	CA	GLN	1680	19.341	-2.800	-1.406	1.00	23.52
MOTA	1879	CB	GLN	1680	19.998	-2.781	-2.782	1.00	25.36
MOTA	1880	CG	GLN	1680	19.741	-4.050	-3 577	1.00	33.28
MOTA	1881	CD	GLN	1680	19.212	-3.763	-4.949	1.00	34.68
ATOM	1882	OE1	GLN	1680	18.683	-2.686	~5.187	1.00	41.24
MOTA	1883	NE2	GLN	1680	19.357	-4.713	-5.867	1.00	32.10
MOTA	1886	С	GLN	1680	19.998	-1.767	-0.514	1.00	23.38
ATOM	1887	0	GLN	1680	20.925	-2.094	0.224	1.00	25.12
MOTA	1888	N	SER	1681	19.533	-0.521	-0.562	1.00	20.87
MOTA	1890	CA	SER	1681	20.133	0.480	0.303	1.00	20.53
MOTA	1891	CB	SER	1681	19.821	1.919	-0.151	1.00	19.58
MOTA	1892	OG	SER	1681	18.445	2.126	-0.425	1.00	20.67
MOTA	1894	C	SER	1681	19.696	0.189	1.741	1.00	22.22
MOTA	1895	0	SER	1681	20.439	0.455	2.681	1.00	23.62
ATOM	1896	N	ASP	1682	18.530	-0.436	1.900	1.00	22.44
ATOM	1898	CA	ASP	1682	18.054	-0.816	3.231	1.00	22.70
ATOM	1899	CB	ASP	1682	16.607	-1.293	3.180	1.00	24.24
ATOM	1900	CG	ASP	1682	15.603	-0.165	3.352	1.00	28.23
MOTA	1901	OD1	ASP	1682	14.410	-0.425	3.108	1.00	28.14
MOTA	1902	OD2	ASP	1682	15.976	0.960	3.757	1.00	25.23
ATOM	1903	С	ASP	1682	18.926	-1.941	3.777	1.00	23.92
MOTA	1904	0	ASP	1682	19.121	-2.057	4.990	1.00	26.24
MOTA	1905	N	VAL	1683	19.433	-2.788	2.884	1.00	23.67
MOTA	1907	CA	VAL	1683	20.300	-3.888	3.302	1.00	22.42
MOTA	1908	СВ	VAL	1683	20.562	-4.881	2.141	1.00	23.70
MOTA	1909	CG1	VAL	1683	21.724	-5.802	2.459	1.00	19.73
MOTA	1910	CG2	LAV	1683	19.292	-5.713	1.889	1.00	19.85
ATOM	1911	С	VAL	1683	21.584	-3.298	3.860	1.00	21.94
MOTA	1912	0	VAL	1683	22.030	-3.688	4.938	1.00	22.69
ATOM	1913	N	TRP	1684	22.141	-2.320	3.154	1.00	20.51
ATOM	1915	CA	TRP	1684	23.349	-1.633	3.611	1.00	20.31
ATOM	1916	CB	TRP	1684	23.659	-0.446	2.680	1.00	19.01
ATOM	1917	CG	TRP	1684	24.802	0.410	3.145	1.00	20.67
ATOM	1918	CD2	TRP	1684	26.114	0.468	2.587	1.00	22.26



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MOTA	1982	CA	TRP	1691	27.302	-3.682	13.631	1.00	27.31
MOTA	1983	CB	TRP	1691	27.979	-2.628	12.755	1.00	25.21
MOTA	1984	CG	TRP	1691	29.338	-2.170	13.257	1.00	27.00
MOTA	1985	CD2	TRP	1691	29.606	-1.060	14.134	1.00	24.28
MOTA	1986	CE2	TRP	1691	31.001	-0.988	14.297	1.00	23.03
MOTA	1987	CE3	TRP	1691	28.792	-0.118	14.778	1.00	22.80
MOTA	1988	CD1	TRP	1691	30.562	-2.712	12.944	1.00	24.10
MOTA	1989	NE1	TRP	1691	31.557	-2.010	13.567	1.00	23.41
MOTA	1991	CZ2	TRP	1691	31.617	-0.011	15.097	1.00	25.00
ATOM	1992	CZ3	TRP	1691	29.398	0.851	15.573	1.00	26.78
MOTA	1993	CH2	TRP	1691	30.802	0.900	15.719	1.00	27.78
MOTA	1994	C	TRP	1691	26.947	-3.088	15.012	1.00	28.70
MOTA	1995	O	TRP	1691	27.708	-3.245	15.974	1.00	29.56
MOTA	1996	N	GLU	1692	25.808	-2.400	15.104	1.00	29.51
MOTA	1998	CA	GLU	1692	25.349	-1.817	16.371	1.00	27.55
MOTA	1999	CB	GLU	1692	24.120	-0.935	16.171	1.00	28.35
MOTA	2000	CG	GLU	1692	24.273	0.221	15.219	1.00	24.70
ATOM	2001	CD	GLU	1692	22.982	0.989	15.100	1.00	25.44
MOTA	2002	OE1	GLU	1692	22.224	0.744	14.148	1.00	24.34
MOTA	2003	OE2	GLU	1692	22.696	1.816	15.982	1.00	27.57
ATOM	2004	С	GLU	1692	24.958	-2.918	17.352	1.00	28.74
MOTA	2005	0	GLU	1692	25.099	-2.753	18.557	1.00	28.76
MOTA	2006	N	ILE	1693	24.421	-4.023	16.844	1.00	29.23
MOTA	2008	CA	ILE	1693	24.027	-5.125	17.712	1.00	27.48
MOTA	2009	CB	ILE	1693	23.205	-6.226	16.944	1.00	28.80
ATOM	2010	CG2	ILE	1693	22.983	-7.469	17.842	1.00	22.98
ATOM	2011	CG1	ILE	1693	21.840	-5.658	16.508	1.00	27.36
MOTA	2012	CD1	ILE	1693	21.005	-6.585	15.635	1.00	24.84
MOTA	2013	C	ILE	1693	25.259	-5.750	18.357	1.00	27.27
MOTA	2014	0	ILE	1693	25.320	-5.902	19.575	1.00	28.15
MOTA	2015	N	PHE	1694	26.273	-6.043	17.552	1.00	27.83
ATOM	2017	CA	PHE	1694	27.473	-6.677	18.095	1.00	29.88
ATOM	2018	CB	PHE	1694	28.143	-7.525	17.011	1.00	28.66
MOTA	2019	CG	PHE	1694	27.223	-8.574	16.463	1.00	29.92
MOTA	2020	CD1	PHE	1694	26.628	-8.424	15.220	1.00	30.20
ATOM	2021	CD2	PHE	1694	26.809	-9.630	17.269	1.00	30.81
MOTA	2022	CE1	PHE	1694	25.625	-9.294	14.801	1.00	32.42
MOTA	2023	CE2	PHE	1694	25.805	-10.508	16.857	1.00	32.30
MOTA	2024	CZ	PHE	1694	25.210	-10.337	15.628	1.00	31.13
MOTA	2025	C	PHE	1694	28.429	-5.784	18.890	1.00	31.07
MOTA	2026	0	PHE	1694	29.376	-6.273	19.509	1.00	33.16
MOTA	2027	N	THR	1695	28.157	-4.480	18.897	1.00	29.20
MOTA	2029	CA	THR	1695	28.934	-3.532	19.670	1.00	27.38
MOTA	2030	CB	THR	1695	29.412	-2.333	18.823	1.00	24.77
MOTA	2031	OG1	THR	1695	28.287	-1.652	18.274	1.00	26.27
ATOM	2033	CG2	THR	1695	30.305	-2.800	17.706	1.00	20.18
MOTA	2034	C	THR	1695	28.053	-3.034	20.822	1.00	29.84
MOTA	2035	0	THR	1695	28.430	-2.103	21.548	1.00	32.77
MOTA	2036	N	LEU	1696	26.898	-3.687	20.988	1.00	28.52
MOTA	2038	CA	LEU	1696	25.915	-3.364	22.029	1.00	28.82
MOTA	2039	CB	LEU	1696	26.356	-3.886	23.394	1.00	32.50
ATOM	2040	CG	LEU	1696	26.658	-5.379	23.476	1.00	33.24
MOTA	2041	CD1	LEU	1696	27.205	-5.717	24.849	1.00	34.15
ATOM	2042	CD2	LEU	1696	25.398	-6.150	23.191	1.00	37.24

							234				
A'	TOM 2	043	C 1	LEU 1	.696	25.55					
A:	rom 2	044			.696	45.5	~.	888	22.13		00 26.98
Α̈́	rom 2	045	`		.697	25.57		297	23.20	7 1.0	
A	rom 2				697	25.14		317	21.00	7 1.0	
ΡŢ	OM 2				697	24.76		074	20.98	0 1.0	0 27.40
AT				-	697	25.92		962	20.61	8 1.0	
ΑT	OM 20			_	698	25.95		132	20.99	8 1.0	
AT	'OM 20			_	698	26.88		416	19.88		
AT	OM 20		_	_	698	28.03		212	19.48	2 1.0	0 29.54
AT	OM 20		_		598	27.65		301	18.49	2 1.0	
AT	OM 20		_		599	26.66	_		17.75	5 1.0	
ATO	OM 20	57 (599	28.418			18.48	1 1.0	
ATO	OM 20				99	28.168			17.57°		29.37
ATO	OM 20	59 C			99	28.438			18.319	1.00	
ATO	OM 20	61 C			99	28.575	_		17.431	1.00	
ATC	DM 20				99	29.093			16.369	1.00	
ATC	OM 206	53 N			00	30.299			16.529	1.00	
ATO		54 C				28.537			L5.153	1.00	
ATO		55 C.				27.104	—		4.794		31.22
ATO	M 206				00 .	29.381			.3.958	1.00	
ATO	M 206	7 C				28.356			2.807		
ATO	M 206	8 C	PR			27.095			3.460	1.00	29.33
ATO	M 206	9 0	PR			30.205	5.3		3.773	1.00	28.78
ATO		0 N	TY			29.737	6.46		4.110	1.00	30.04
ATO		2 C#				31.426 32.296	5.23		3.264	1.00	28.35
ATO						31.921	6.39		2.987	1.00	30.77
ATON		4 CG	TYF	170		32.060	6.98		1.615	1.00	31.67
ATOM		5 CD				30.952	6.03	_	0.454	1.00	34.61
ATOM	=		1 TYR			31.083	5.67		9.686	1.00	38.26
ATOM		7 CD	2 TYR			33.301	4.80		3.587	1.00	40.99
ATOM			2 TYR			33.449	5.52 4.66	_	.106	1.00	38.16
ATOM			TYR	170	1	32.343	4.31	-	.020	1.00	41.04
ATOM			TYR	170	1	32.531	3.47	_	.263	1.00	43.11
ATOM		_	TYR	170	1	32.305	7.532		.181	1.00	49.53
ATOM		-	TYR	170	l.	32.026	8.689		.029	1.00	31.41
ATOM			PRO	1702	2	32.635	7.230		.698 .296	1.00	33.59
ATOM ATOM			PRO	1702	2	32.998	5.938		.888	1.00	30.92
ATOM	2086		PRO	1702	?	32.656	8.283		.314	1.00	32.30
ATOM	2087		PRO	1702		33.123	7.548		.561	1.00	30.05
ATOM	2088		PRO	1702		32.676	6.174		.338	1.00	27.77
ATOM	2089 2090		PRO	1702		33.659	9.366		944	1.00	32.34
ATOM	2090	0	PRO	1702		34.769	9.055		513	1.00	31.42
ATOM	2091	N	GLY	1703		33.257	10.627		117	1.00	30.95
ATOM	2093	CA	GLY	1703	;	34.122	11.751		817		31.30
ATOM	2094	C	GLY	1703	:	34.172	12.138			1.00	29.66
ATOM	2095	0	GLY	1703	3	34.752	13.165				31.00
ATOM		N	VAL	1704		33.551	11.331				30.69
ATOM	2098 2099	CA	VAL	1704	3	33.553	11.610	12.			31.11
ATOM	2100	CB	VAL	1704	3	3.539	10.310	11.			29.88
ATOM	2100	CG1	VAL	1704	3	3.585	10.624		_		28.41
ATOM	2101	CG2	VAL	1704		4.702	9.429	11.			26.24
ATOM	2102	C	VAL	1704	3	2.396	12.508	11.6			24.10
ATOM	2103	O N	VAL	1704	3	1.224	12.146	11.3			30.80
2-2-OF1	2104	N	PRO	1705		2.718	13.705	11.1			32.50
							-		1	1.00	30.86

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MOTA	2105	CD	PRO	1705	34.039	14.350	11.077	1.00	30.59
MOTA	2106	CA	PRO	1705	31.682	14.625	10.645	1.00	31.47
MOTA	2107	CB	PRO	1705	32.400	15.971	10.680	1.00	32.75
MOTA	2108	CG	PRO	1705	33.774	15.607	10.289	1.00	32.59
MOTA	2109	C	PRO	1705	31.258	14.264	9.239	1.00	32.19
MOTA	2110	0	PRO	1705	31.974	13.536	8.549	1.00	33.91
ATOM	2111	N	VAL	1706	30.124	14.814	8.806	1.00	32.57
MOTA	2113	CA	VAL	1706	29.560	14.576	7.474	1.00	31.80
MOTA	2114	CB	VAL	1706	28.483	15.632	7.172	1.00	34.66
ATOM	2115	CG1	VAL	1706	28.022	15.538	5.738	1.00	39.06
ATOM	2116	CG2	VAL	1706	27.309	15.455	8.106	1.00	36.62
ATOM	2117	C	VAL	1706	30.578	14.560	6.320	1.00	31.58
MOTA	2118	0	VAL	1706	30682	13.585	5.570	1.00	32.35
MOTA	2119	N	GLU	1707	31.326	15.649	6.189	1.00	31.46
ATOM	2121	CA	GLU	1707	32.329	15.788	5.139	1.00	31.68
ATOM	2122	CB	GLU	1707	33.021	17.148	5.267	1.00	32.59
MOTA	2123	С	GLU	1707	33.381	14.678	5.114	1.00	32.23
ATOM	2124	0	GLU	1707	33.740	14.183	4.050	1.00	33.47
ATOM	2125	N ·	GLU	1708	33.902	14.316	6.279	1.00	32.90
ATOM	2127	CA	GLU	1708	34.909	13.268	6.352	1.00	33.86
ATOM	2128	CB	GLU	1708	35.570	13.244	7.730	1.00	38.54
ATOM	2129	CG	GLU	1708	36.190	14.575	8.165	1.00	47.63
ATOM	2130	CD	GLU	1708	37.442	14.962	7.383	1.00	58.35
ATOM	2131	OE1	GLU	1708	38.117	14.067	6.816	1.00	62.88
ATOM	2132	OE2	GLU	1708	37.770	16.176	7.355	1.00	64.79
ATOM	2133	C	GLU	1708	34.276	11.921	6.043	1.00	33.56
ATOM	2134	0	GLU	1708	34.927	11.038	5.489	1.00	34.18
ATOM	2135	N	LEU	1709	32.997	11.774	6.374	1.00	32.91
ATOM	2137	CA	LEU	1709	32.285	10.532	6.108	1.00	33.83
ATOM	2138	CB	LEU	1709	30.862	10.563	6.685	1.00	32.28
ATOM	2139	CG	LEU	1709	30.015	9.363	6.231	1.00	32.92
ATOM	2140	CD1	LEU	1709	30.541	8.071	6.853	1.00	28.37
ATOM	2141	CD2	LEU	1709	28.563	9.580	6.568	1.00	31.90
ATOM	2142	C!	LEU	1709	32.222	10.283	4.60€	1.00	34.15
ATOM	2143	0	LEU	1709	32.412	9.152	4.156	1.00	34.75
MOTA	2144	N	PHE	1710	31.918	11.332	3.844	1.00	33.83
ATOM	2146	CA	PHE	1710	31.828	11.248	2.388	1.00	32.90
ATOM	2147	СВ	PHE	1710	31.531	12.622	1.787	1.00	34.85
MOTA	2148	CG	PHE	1710	30.162	13.132	2.082	1.00	38.60
ATOM	2149	CD1	PHE	1710	29.150	12.268	2.469	1.00	43.69
MOTA	2150	CD2	PHE	1710	29.882	14.480	1.984	1.00	45.10
ATOM	2151	CE1	PHE	1710	27.873	12.742	2.764	1.00	46.23
ATOM	2152	CE2	PHE	1710	28.611	14.966	2.274	1.00	48.15
ATOM	2153	CZ	PHE	1710	27.603	14.086		1.00	46.90
MOTA	2154	C	PHE	1710	33.131	10.739	1.803	1.00	31.84
ATOM	2155	0	PHE	1710	33.134	9.931	0.877	1.00	29.97
ATOM	2156	N	LYS	1711	34.231	11.224	2.373	1.00	32.45
ATOM	2158	CA	LYS	1711	35.582	10.860	1.947	1.00	34.53
ATOM	2159	CB	LYS	1711	36.588	11.755	2.675	1.00	36.17
ATOM	2160	CG	LYS	1711	38.008	11.669	2.182	1.00	41.07
ATOM	2161	CD	LYS	1711	38.912	12.582	3.001	1.00	46.23
ATOM	2162	CE	LYS	1711	40.311	12.648	2.418	1.00	51.79
ATOM	2162	NZ	LYS	1711	41.036	11.360	2.556	1.00	57.27
ATOM	2163	C	LYS	1711	35.867	9.375	2.215	1.00	33.82
ATON	210/		ويد	* / * *	55.667	2.313	<i>د</i> ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ	1.00	33.02

							230				
		2168	0	LYS	171						
A	TOM 2	2169	N	LEU				688 1.	376	1.00	33.20
A	TOM 2	171	CA	LEU		· - · -				1.00	34.52
A	TOM 2	172	CB	LEU				177 3.		1.00	
A		173	CG				94 7.2			1.00	33.25
		174	CD1	LEU	1712	• •	46 7. <u>s</u>				30.99
				LEU	1712		⁴⁷ 7.5			.00	29.71
			CD2	LEU	1712		7.5			00	24.11
			C	LEU	1712	34.83				.00	32.21
			0	LEU	1712	35.37				.00	32.16
			N	LEU	1713	33.56				.00	32.77
			CA	LEU	1713	32.70				.00	31.72
			CB	LEU	1713	31.29				.00	33.60
		.82 (CG .	LEU	1713	30.52	_			.00	36.57
ΑT		.83 (CD1	LEU	1713					.00	37.60
AT		84 (LEU	1713	29.28				.00	35.03
AT	OM 21	85 C		LEU	1713	30.18				00	33.22
ATO	OM 21		_	EU		33.289		8 0.2		00	
ATO		_	_	YS	1713	33.318	5.20			00	35.33
ATO					1714	33.741	7.40				36.00
ATC				YS	1714	34.331	7.50			00	36.24
ATC		_		YS	1714	34.707	8.94			00	36.35
ATO			_	YS	1714	33.520			_		35.82
ATO		-	_	YS	1714	32.712			_		37.23
ATO			_	YS	1714	31.506				00	40.53
			Z L	YS	1714	30.747	,			00	44.51
ATO		•	L.	YS	1714	35.559	- · · · · ·				50.76
ATO		_	L.		1714	35.808				0.0	37.60
ATO		0 N	GI		1715	36.299		_			10.82
ATON		2 CA		_	1715				5 1.0		35.61
ATOM	4 220	3 CB			1715	37.496	5.630		3 1.0		34.65
ATON		4 CG			1715	38.517	6.188		1 0		37.83
ATOM	1 2205	5 CD		_	715	38.897	7.613	-0.036			2.28
ATOM	2206					39.634	8.342	1.061		_	5.64
ATOM					715	39.928	7.726	2.114		_	
ATOM			GL GL		715	39.918	9.544	0.853			3.09
ATOM		_			715	37.244	4.145	-0.419			7.56
ATOM			GL:		715	38.177	3.348	-0.419			2.94
ATOM			GL.	-	716	35.983	3.779	~0.213	1.00		3.31
ATOM	2212		GL:	_	716	35.634	2.391	0.004	1.00		9.12
ATOM	2214	-	GL		716	35.946	1.895	1.396	1.00		5.02
ATOM		0	GL'	_	716	36.223	0.715		1.00		9.60
	2215	N	HIS	1.	717	35.879	2.783	1.588	1.00		8.81
ATOM	2217	CA	HIS	17	717	36.158		2.379	1.00		9.97
ATOM	2218	CB	HIS	17	717	36.369	2.409	3.763	1.00		.78
ATOM	2219	CG	HIS		17	36.653	3.659	4.623	1.00		.25
ATOM	2220	CD2	HIS		17	27 022	3.360	6.067	1.00		.70
ATOM	2221	ND1	HIS			37.820	3.155	6.715	1.00		.77
MOTA	2223	CE1	HIS			35.656	3.219	7.010	1.00		.90
ATOM	2224	NE2	HIS	17		36.200	2.932	8.180	1.00		. 87
ATOM	2226	C		17		37.513	2.887	8.027	1.00		
ATOM	2227	0	HIS	17		35.035	1.577	4.375	1.00		. 93
ATOM	2228		HIS	17		33.861	1.847	4.133		29.	
ATOM		N	ARG	17	18	35.406	0.600		1.00	30.	
ATOM	2230	CA	ARG	17:		34.436	-0.258	5.201	1.00	27.	92
	2231	CB	ARG	17		34.379	-1.641	5.878	1.00	27.	30
ATOM	2232	CG	ARG	171		33.939		5.236	1.00	24.	10
ATOM	2233	CD	ARG	171		32.469	-1.655	3.789	1.00	26.	
0005					-	~.407	-1.288	3.627	1.00	26.	
SSSD/55	145. v01									- •	

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MOTA	2234	NE	ARG	1718	32.020	-1.374	2.232	1.00	24.41
MOTA	2236	CZ	ARG	1718	32.090	-0.377	1.352	1.00	25.51
MOTA	2237	NHl	ARG	1718	32.611	0.801	1.706	1.00	23.61
MOTA	2240	NH2	ARG	1718	31.553	-0.521	0.149	1.00	21.28
ATOM	2243	С	ARG	1718	34.881	-0.384	7.330	1.00	28.81
MOTA	2244	0	ARG	1718	36.080	-0.425	7.611	1.00	29.77
MOTA	2245	N	MET	1719	33.920	-0.377	8.250	1.00	30.40
MOTA	2247	CA	MET	1719	34.215	-0.485	9.673	1.00	30.62
MOTA	2248	CB	MET	1719	32.942	-0.339	10.497	1.00	28.91
MOTA	2249	CG	MET	1719	32.235	1.003	10.316	1.00	30.85
MOTA	2250	SD	MET	1719	30.829	1.237	11.432	1.00	33.27
MOTA	2251	CE	MET	1719	29.521	0.416	10.561	1.00	31.81
ATOM	2252	С	MET	1719	34.900	-1.793	10.005	1.00	31.32
MOTA	2253	0	MET	1719	34.755	-2.769	9.278	1.00	31.47
MOTA	2254	N	ASP	1720	35.651	-1.799	11.103	1.00	33.78
A'TOM	2256	CA	ASP	1720	36.387	-2.983	11.550	1.00	33.45
MOTA	2257	CB	ASP	1720	37.478	-2.580	12.546	1.00	36.99
MOTA	2258	CG	ASP	1720	38.585	-1.762	11.908	1.00	41.56
ATOM	2259	OD1	ASP	1720	38.403	-1.339	10.742	1.00	48.43
MOTA	2260	OD2	ASP	1720	39.634	-1.546	12.568	1.00	40.99
ATOM	2261	С	ASP	1720	35.473	-4.001	12.211	1.00	32.12
ATOM	2262	0	ASP	1720	34.381	-3.657	12.668	1.00	30.89
MOTA	2263	N	LYS	1721	35.944	-5.241	12.328	1.00	31.82
ATOM	2265	CA	LYS	1721	35.127	-6.270	12.953	1.00	31.71
ATOM	2266	CB	LYS	1721	35.691	-7.679	12.747	1.00	32.34
ATOM	2267	CG	LYS	1721	34.762	-8.738	13.344	1.00	34.85
ATOM	2268	CD	LYS	1721	35.111	-10.155	12.961	1.00	37.39
ATOM	2269	CE	LYS	1721		-10.674	13.765	1.00	41.42
ATOM	2270	ΝZ	LYS	1721	.36.348	-12.154	13.635	1.00	46.55
ATOM	2274	C	LYS	1721	35.007	-6.018	14.430	1.00	33.40
MOTA	2275	0	LYS	1721	36.017	-5.879	15.121	1.00	34.26
MOTA	2276	N	PRO	1722	33.768	-5.924	14.934	1.00	34.26
ATOM	2277	CD	PRO	1722	32.494	-6.002	14.203	1.00	32.16
ATOM	2278	CA	PRO	1722	33.546	-5.692	16.362	1.00	35.84
ATOM	2279	CB	PRO	1722	32.027	-5.682	16.473	1.00	35.35
ATOM	2280	CG	PRO	1722	31.575	-5.255	15.108	1.00	35.35
MOTA	2281	C	PRO	1722	34.105	-6.904	17.099	1.00	40.41
ATOM	2282	0	PRO	1722	34.010	-8.038	16.607	1.00	41.14
MOTA	2283	N	SER	1723	34.739	-6.680	18.240	1.00	43.60
ATOM	2285	CA	SER	1723	35.260	-7.808	18.999	1.00	45.51
MOTA	2286	CB	SER	1723	36.078	-7.324	20.191	1.00	45.30
MOTA	2287	OG	SER	1723	35.384	-6.300	20.879	1.00	49.62
MOTA	2289	C	SER	1723	34.031	-8.589	19.460	1.00	46.39
MOTA	2290	0	SER	1723	32.939	-8.028	19.614	1.00	45.16
MOTA	2291	N	ASN	1724	34.199	-9.891	19.631	1.00	48.53
ATOM	2293	CA	ASN	1724	33.088	-10.723	20.065	1.00	51.13
MOTA	2294	CB	ASN	1724	32.509	-10.194	21.390	1.00	56.87
ATOM	2295	CG	ASN	1724	33.595	-9.892	22.427	1.00	61.65
ATOM	2296	OD1	ASN	1724	34.503	-10.702	22.649	1.00	63.73
MOTA	2297	ND2	ASN	1724	33.526	-8.713	23.039	1.00	64.64
ATOM	2300	C	ASN	1724	32.034	-10.743	18.941	1.00	48.83
MOTA	2301	0	ASN	1724	30.846	-10.534	19.145	1.00	50.50
ATOM	2302	N	CYS	1725	32.511	-10.977	17.734	1.00	45.23
ATOM	2304	CA	CYS	1725		-11.056	16.570	1.00	42.33

								_					
A	ATOM 2	2305	СВ	CYS	1725	2 -							
		306	SG		1725	•		-9.7		854	1.00	41.	10
		307	C		1725 1725	30.	711	-9.7		275	1.00		
A	TOM 2	308	0		1725	32.	383	~12.0	77 15.	725	1.00		
A	TOM 2	309	N			33.		-12.0	04 15.	579	1.00		
A'	TOM 2	311			1726	31.6		-13.0		263	1.00	42.	
		312			1726	32.2		-14.1			1.00	35.	
					L726	31.3		-15.3				33.6	
		_		~~~	L726	30.0		-14.9			1.00	33.2	
					.726	30.9	81	-15.86			1.00	34.5	
					726	32.7		-13.62			1.00	25.8	
			_		726	32.2		-12.59			1.00	32.2	7
				ASN 1	727	33.6		-14.31			1.00	33.0	4
				SN 1	727	34.0					1.00	32.9	8
		_		SN 1	727	35.1		-13.85			1.00	34.9	7
AT			G A	SN 1	727	36.54		-14.68			1.00	39.8	
AT	_	-	D1 A	SN 1	727	37.04		-14.27		03	1.00	45.3	
ATO		24 N	D2 A		727	37.12	• •	-13.17			1.00	48.43	
ATO		27 C	A		727			-15.14	l 11.9	09	1.00	45.88	
ATC		28 O		•	727	32.84		-13.94		~ ~	1.00	33.97	
ATO	DM 232	29 N			28	32.64		-13.088	9.3		1.00	35.07	
ATC	OM 233	31 C	_		28	32.02		-14.973	10.4		L. 00	31.69	
ATO	M 233					30.81		-15.210	9.62		. 00		
ATO	M 233				28	30.14	1	-16.493	10.08		00	30.27	
ATO						28.93	2 .	-16.878			.00	32.53	
ATO						28.35	3.	18.190				32.81	
ATO						28.339	9 -	18.466		_		36.43	
OTA						27.908	3 -	18.945	8.82			36.75	
ATO		_	GL			29.814	l	14.049	9.68	_		41.92	
ATON		_	GL	– · -		29.234		13.655	8.66	_		28.70	
ATON	_	_	LE			29.594		13.517				28.51	
ATOM		<u>-</u>	LE	J 172	9	28.687		12.393	10.88			26.77	
ATOM			LEU	J 172	9	28.228		12.274	11.04		.00 2	26.80	
ATOM	_		LEU	J 172	9	27.233		13.355	12.490		.00 2	27.91	
				172	9	27.095		L3.345	12.913		00 3	0.71	
ATOM			LEU	172	9 .	25.885		13.345	14.428		00 3	5.79	
ATOM			LEU	172		29.319		13.141	12.253		00 2	5.70	
ATOM	,	-	LEU			28.610	-1	1.089	10.540			7.06	
ATOM	2348		TYR			30.650	- 1	0.177	10.126	1.		0.27	
ATOM	2350	CA	TYR					1.004	10.549	1.		7.03	
ATOM	2351	CB	TYR	1730		31.328 32.792		9.812	10.039	1.		5.21	
ATOM	2352	CG	TYR	1730		22./92		9.778	10.474	1.0	00 2	5.31	
ATOM	2353	CD1	TYR	1730		33.538		8.553	9.982	1.(1.89	
MOTA	2354	CE1	TYR	1730	-	33.012	-	7.270	10.169	1.0		3.59	
MOTA	2355	CD2	TYR			3.655		6.148	9.665	1.0	-		
ATOM	2356	CE2	TYR	1730		4.739	- 8	3.675	9.285	1.0		.74	
ATOM	2357	CZ		1730		5.399		7.560	8.775	1.0		.11	
MOTA	2358	OH	TYR	1730		4.853		.295	8.962			.32	
ATOM	2360		TYR	1730	3	5.484		.181	8.418	1.0		.07	
ATOM		C	TYR	1730	3	1.227		.878		1.0		.70	
ATOM	2361	0	TYR	1730	3	0.960		.875	8.509	1.0		.71	
ATOM	2362	N	MET	1731	3.	1.409	-11	.081	7.843	1.0		.05	•
	2364	CA	MET	1731		1.306	_11	.001	7.977	1.0	0 27	. 92	
ATOM	2365	CB	MET	1731	3.	1.506	-17	.355	6.548	1.00		. 89	
ATOM	2366	CG	MET	1731		068	-12	.853	6.317	1.00			
ATOM	2367	SD	MET	1731		347	-13	.379	4.975	1.00			
MOTA	2368	CE	MET	1731	ے د 7 د		-15	.167	4.865	1.00			
					32	.106	-15	. 263	3.217	1.00			
SSSD/55	145. v01										- • •	- 0	

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MOTA	2369	C	MET	1731	29.916	-10.928	6.102	1.00	27.79
MOTA	2370	0	MET	1731	29.755	-10.345	5.041	1.00	30.68
MOTA	2371	N	MET	1732	28.915	-11.203	6.932	1.00	28.02
MOTA	2373	CA	MET	1732	27.546	-10.804	6.639	1.00	25.74
MOTA	2374	CB	MET	1732	26.598	-11.317	7.718	1.00	24.94
ATOM	2375	CG	MET	1732	25.153	-10.911	7.492	1.00	22.96
ATOM	2376	SD	MET	1732	24.008	-11.593	8.684	1.00	24.39
ATOM	2377	CE	MET	1732	23.798	-13.272	8.002	1.00	18.04
MOTA	2378	С	MET	1732	27.470	-9.273	6.559	1.00	25.81
MOTA	2379	0	MET	1732	26.889	-8.729	5.620	1.00	26.85
MOTA	2380	N	MET	1733	28.068	-8.587	7.537	1.00	24.84
ATOM	2382	CA	MET	1733	28.092	-7.124	7.545	1.00	25.27
MOTA	2383	CB	MET	1733	28.931	-6.6.00	8.700	1.00	25.97
ATOM	2384	CG	MET	1733	28.342	-6.769	10.058	1.00	28.69
MOTA	2385	SD	MET	1733	29.456	-6.094	11.295	1.00	29.06
ATOM	2386	CE	MET	1733	28.927	-7.051	12.693	1.00	28.07
MOTA	2387	С	MET	1733	28.741	-6.628	6.270	1.00	26.97
MOTA	2388	0	MET	1733	28.192	-5.771	5.581	1.00	28.37
MOTA	2389	N	ARG	1734	29.922	-7.160	5.966	1.00	28.77
ATOM	2391	CA	ARG	1734	30.664	-6.775	4.762	1.00	29.66
MOTA	2392	CB	ARG	1734	32.027	-7.482	4.716	1.00	29.05
MOTA	2393	CG	ARG	1734	32.968	-7.109	5.866	1.00	25.00
MOTA	2394	CD	ARG	1734	33.247	-5.621	5.882	1.00	29.27
MOTA.	2395	NE	ARG	1734	33.911	-5.210	4.647	1.00	35.43
ATOM	2397	CZ	ARG	1.734	35.233	-5,220	4.466	1.00	38.24
MOTA	2398	NHl	ARG	1734	36.054	~5.601	5.445	1.00	36.47
MOTA	2401	NH2	ARG	1734	35.732	-4.907	3.277	1.00	38.57
MOTA	2404	С	ARG	1734	29.859	-7.034	3.478	1.00	29.57
MOTA	2405	0	ARG	1734	29.920	-6.242	2.538	1.00	29.55
MOTA	2406	N	ASP	1735	29.095	-8.124	3.448	1.00	28.07
ATOM	2408	CA	ASP	1735	28.259	-8.423	2.287	1.00	27.96
ATOM	2409	CB	ASP	1735	27.634	-9.813	2.408	1.00	28.60
MOTA	2410	CG	ASP	1735	28.664	-10.926	2.283	1.00	31.34
MOTA	2411	OD1	ASP	1735	29.785	-10.660	1.798	1.00	31.12
MOTA	2412	OD2	ASP	1735	28.356	-12.068	2.687	1.00	36.07
ATOM	2413	С	ASP	1735	27.159	-7.368	2.155	1.00	27.24
MOTA	2414	0	ASP	1735	26.846	-6.932	1.050	1.00	25.79
MOTA	2415	N	CYS	1736	26.590	-6.951	3.288	1.00	26.53
MOTA	2417	CA	CYS	1736	25.547	-5.930	3.314	1.00	24.35
MOTA	2418	CB	CYS	1736	24.968	-5.765	4.731	1.00	22.01
ATOM	2419	SG	CYS	1736	23.885	-7.101	5.281	1.00	21.52
MOTA	2420	C	CYS	1736	26.119	-4.595	2.847	1.00	24.26
MOTA	2421	0	CYS	1736	25.386	-3.725	2.368	1.00	24.19
MOTA	2422	N	TRP	1737	27.432	-4.437	3.002	1.00	22.94
MOTA	2424	CA	TRP	1737	28.104	-3.210	2.605	1.00	21.91
MOTA	2425	CB	TRP	1737	29.146	-2.820	3.640	1.00	19.26
ATOM	2426	CG	TRP	1737	28.572	-2.493	4.947	1.00	20.89
MOTA	2427	CD2	TRP	1737	29.226	-2.602	6.212	1.00	23.33
MOTA	2428	CE2	TRP	1737	28.315	-2.159	7.196	1.00	21.59
MOTA	2429	CE3	TRP	1737	30.506	-3.026	6.614	1.00	25.00
MOTA	2430	CD1	TRP	1737	27.319	-2.012	5.201	1.00	19.90
MOTA	2431	NE1	TRP	1737	27.158	-1.807	6.551	1.00	20.77
MOTA	2433	CZ2	TRP	1737	28.641	-2.127	8.563	1.00	19.89
MOTA	2434	CZ3	TRP	1737	30.825	-2.993	7.971	1.00	21.23



N CO	014								
AT					29.89	6 -2.54	3 8.92	7 1.00	3 31 60
ATO			TR	P 1737	28.75	8 -3.26			
AT(TR	• .	29.65	3 -2.47			
ATO			HI	S 1738					
ATO				S 1738					
ATO				S 1738	28.243				
ATC				3 1738	29.131				
ATC				1738	29.595				
ATC			1 HIS	1738	29.681				
ATO			1 HIS	1738	30.436				
ATO			2 HIS	1738	30.409				
ATO		_	HIS	1738	28.716				
ATO.		_	HIS	1738	27.675				
ATO		1 N	ALA		29.802	-2.564			23.96
ATO		3 CA	ALA		29.825	-1.346			26.27
ATO		4 CB	ALA	1739	31.186	-1.180		1.00	25.46
ATO		5 C	ALA	1739	28.754	-1.443			25.70
ATO	M 245	6 0	ALA	1739	28.116	-0.455		1.00	26.18
ATON	· - -	7 N	VAL	1740	28.570	-2.643		1.00	29.14
ATON		9 CA	VAL	1740	27.560	-2.875		1.00	25.71
ATON		CB	VAL	1740	28.063	-3.841	-5.802	1.00	26.12
ATOM		CG1	VAL	1740	27.102	-3.832	-6.903	1.00	25.99
ATOM		CG2	VAL	1740	29.450		-8.090	1.00	23.37
ATOM	1 2463	C	VAL	1740	26.247	-3.440	-7.349	1.00	22.07
ATOM		0	VAL	1740	26.186	-3.400	-5.191	1.00	25.43
ATOM	2465	N	PRO	1741	25.170	-4.550	-4.704	1.00	24.93
ATOM	2466	CD	PRO	1741	25.170	-2.585	-5.265	1.00	24.20
ATOM	2467	CA	PRO	1741	23.838	÷1.277	-5.953	1.00	18.88
ATOM		CB	PRO	1741	22.953	-2.914	-4.734	1.00	25.28
ATOM	2469	CG	PRO	1741	23.903	-1.788	-5.294	1.00	22.75
ATOM	2470	C	PRO	1741	23.299	-0.632	-5.398	1.00	20.99
ATOM	2471	O	PRO	1741	22.787	-4.296	-5.128	1.00	25.84
MOTA	2472	N	SER	1742	23.425	-5.036	-4.280	1.00	25.99
ATOM	2474	CA	SER	1742	22.942	-4.642	-6.407	1.00	26.48
ATOM	2475	CB	SER	1742	23.151	-5.919	-6.930	1.00	25.19
MOTA	2476	OG	SER	1742	24.530	-5.992	-8.440	1.00	25.68
MOTA	2478	С	SER	1742	23.644	-5.943	-8.769	1.00	27.46
MOTA	2479	0	SER	1742	23.124	-7.100	-6.289	1.00	25.24
MOTA	2480	N	GLN	1743	24.826	-8.218	-6.300	1.00	26.09
ATOM	2482	CA	GLN	1743	_	-6.851	-5.731	1.00	23.88
ATOM	2483	CB	GLN	1743	25.590 27.069	-7.917	-5.118		24.44
ATOM	2484	CG	GLN	1743	27.069	-7.733	-5.437	1.00	27.26
MOTA	2485	CD	GLN	1743		-7.784	-6.940		27.39
ATOM	2486	OE1	GLN	1743	26.803	-9.047	-7.581	1.00	26.46
ATOM	2487	NE2	GLŅ	1743	27.325	-10.136	-7.339	_	25.80
ATOM	2490	C	GLN	1743	25.760	-8.914	-8.393	1.00	27.42
ATOM	2491	Ō		1743	25.348	-8.151	-3.633		23.20
ATOM	2492	N		1744	25.810	-9.147	-3.083		22.90
ATOM	2494	CA			24.628	-7.243	-2.984		22.15
ATOM	2495			1744	24.318	-7.398	-1.568		21.23
ATOM	2496			1744	23.767				19.01
ATOM	2497			1744	24.705		-1.145		L7.27
ATOM	2498			1744	24.091			_	14.79
ATOM	2500			1744	24.914	-2.493	-1.157		.9.72
		-2	מאט .	1744	24.482				9.23
CCCD/FF								_	

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ATOM	2501	NH1	ARG	1744	23.201	-0.931	-1.201	1.00	15.90
MOTA	2504	NH2	ARG	1744	25.343	-0.343	-1.821	1.00	19.43
ATOM	2507	С	ARG	1744	23.259	-8.496	-1.438	1.00	21.95
ATOM	2508	0	ARG	1744	22.585	-8.827	-2.415	1.00	25.34
MOTA	2509	N	PRO	1745	23.213	-9.184	-0.292	1.00	20.82
MOTA	2510	CD	PRO	1745	24.191	-9.219	0.804	1.00	21.25
ATOM	2511	CA	PRO	1745	22.204	-10.229	-0.127	1.00	21.39
MOTA	2512	CB	PRO	1745	22.687	-10.980	1.117	1.00	21.69
MOTA	2513	CG	PRO	1745	23.418	-9.916	1.886	1.00	22.62
MOTA	2514	С	PRO	1745	20.833	-9.585	0.102	1.00	22.15
MOTA	2515	0	PRO	1745	20.739	-8.402	0.426	1.00	23.29
MOTA	2516	N	THR	1746	19.771	-10.349	-0.109	1.00	20.93
MOTA	2518	CA	THR	1746	18.440	-9.827	0.107	1.00	19.90
MOTA	2519	CB	THR	1746	17.391	-10.554	-0.783	1.00	20.21
MOTA	2520	OG1	THR	1746	17.484	-11.974	-0.584	1.00	22.03
MOTA	2522	CG2	THR	1746	17.609	-10.242	-2.255	1.00	20.82
MOTA	2523	С	THR	1746	18.112	-10.095	1.557	1.00	19.77
MOTA	2524	0	THR	1746	18.842	-10.823	2.228	1.00	19.19
MOTA	2525	N	PHE	1747	. 17.010	-9.526	2.045	1.00	23.46
MOTA	2527	CA	PHE	1747	16.582	-9.770	3.422	1.00	21.64
MOTA	2528	CB	PHE	1747	15.473	-8.794	3.827	1.00	18.89
ATOM	2529	CG	PHE	1747	15.987	-7.445	4.262	1.00	17.45
MOTA	2530	CD1	PHE	1747	16.757	-7.317	5.417	1.00	17.65
ATOM	2531	CD2	PHE	1747	15.712	-6.303	3.516	1.00	15.37
MOTA	2532	CE1	PHE	1747	17.242	-6.073	5.819	1.00	16.17
MOTA	2533	CE2	PHE	1747	16.189	-5.056	3.907	1.00	14.53
MOTA	2534	CZ	PHE	1747	16.959	-4.941	5.065	1.00	16.88
ATOM	2535	C	PHE	1747	16.118	-11.227	3.522	1.00	23.18
ATOM	2536	0	PHE	1747	16.271	-11.873	4.548	1.00	24.04
ATOM	2537	N	LYS	1748	15.570	-11.745	2.432	1.00	24.13
ATOM	2539	CA	LYS	1748	15.137	-13.132	2.385	1.00	26.35
ATOM	2540	CB	LYS LYS	1748 1748	14.502	-13.424	1.024 0.836	1.00	27.52 33.88
ATOM	2541 2542	CG CD	LYS	1748	14.034 13.598	-14.849 -15.062	-0.600	1.00	41.83
ATOM	2542 2543	CE	LYS	1748	13.190	-16.506	-0.881	1.00	50.05
MOTA MOTA	2544	NZ	LYS	1748	12.084	-16.986	0.005	1.00	55.70
ATOM	2544	C	LYS	1748	16.359	-14.037	2.636	1.00	27.50
ATOM	2549	0	LYS	1748	16.303	-14.057	3.459	1.00	31.18
MOTA	2550	Ŋ	GLN	1749	17.467	-13.761	1.949	1.00	27.24
ATOM	2552	CA	GLN	1749	18.699	-14.529	2.122	1.00	27.03
ATOM	2553	CB	GLN	1749	19.797	-14.039	1.169	1.00	31.80
ATOM	2554	CG	GLN	1749	19.501	-14.196	-0.323	1.00	38.57
ATOM	2555	CD	GLN	1749	20.460	-13.385	-1.209	1.00	39.93
ATOM	2556	OE1	GLN	1749	20.025	-12.535	-1.974	1.00	39.90
ATOM	2557	NE2	GLN	1749	21.768	-13.620	-1.068	1.00	40.23
ATOM	2560	C	GLN	1749	19.205	-14.380	3.552	1.00	25.98
ATOM	2561	0	GLN	1749	19.533	-15.371	4.198	1.00	27.18
ATOM	2562	N	LEU	1750	19.293	-13.133	4.018	1.00	25.20
ATOM	2564	CA	LEU	1750	19.774	-12.823	5.369	1.00	25.74
ATOM	2565	CB	LEU	1750	19.722	-11.317	5.631	1.00	20.99
ATOM	2566	CG	LEU	1750	20.708	-10.468	4.831	1.00	20.90
ATOM	2567	CD1	LEU	1750	20.700	-8.987	4.822	1.00	19.88
MOTA	2568	CD2	LEU	1750	22.071	-10.643	5.426	1.00	17.26
ATOM	2569	C	LEU	1750	18.985	-13.555	6.441	1.00	27.10
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	rom 2	570	0 1	LEU 17	'50 19.	E E O					
AT	COM 2	571				553	-14.(.00	27.89
ΓA	OM 2	573				672	-13.5		65 1		29.40
ΑT	'OM 2			/AL 17		798	-14.2		10 1		26.80
AT							-14.0				26.94
AT	_						-14.9				29.93
AT				'AL 17	•		-12.5	75 7.1			
AT				AL 17			-15.7				24.10
AT	_		_ *	AL 179			-16.3	59 8.2	~ - "	-	27.80
ATO				LU 175		108	-16.3	00 6.0			26.77
ATO				LU 175	52 17.7	749	-17.7				32.26
ATO				LU 175	52 17.7	721	-18.1				35.72
ATO				LU 175	16.3	06	-18.07				9.33
ATC				LU 175			-18.42				9.41
				ւՄ 175	2 15.1	41	-18.13		_	_	5.88
ATC		_	E2 GI	LU 175	2 17.1		-18.97	_			8.00
ATO		-	GI	ΔU 175	2 19.0		-18.00		_		1.03
ATO		_	GL					_			4.59
ATO			AS				-18.97			0 3	3.95
ATO		91 C	a as				-17.11			0 34	4.38
ATO			B AS				-17.23		7 1.0	0 32	2.81
ATO		3 CC	3 As				-16.22			0 31	L. 57
ATO	M 259	4 OI					-16.55			_	3.68
ATOM		5 OI					-17.75				5.14
MOTA	1 259		ASI		51		15.624		1.0	_	.44
MOTA	1 259	7 O	ASI		5,		17.058		1.0		.04
ATOM	1 259	8 N	LEU				17.837				.21
ATOM	1 260				~0.01		16.045				.00
ATOM	260						15.754				.46
ATOM				• •	02		14.426	10.598			.47
ATOM							13.309	10.318			.58
ATOM					-0.11		11.963	10.128			.46
MOTA					21.82		13.282	11.462			.18
ATOM			LEU		19.80		16.866	1.1.110	1.00		
ATOM	2607	_	LEU		20.129		17.178	12.254	1.00		
ATOM	2609		ASP		18.832	2 -]	17.471	10.445	1.00		
ATOM	2610		ASP	1755	18.116	- 1	.8.578	11.044	1.00		
ATOM	2611		ASP	1755	16.973		9.027	10.148	1.00		
ATOM	2612		ASP	.1755	16.159		0.119	10.779		38.	
ATOM	2612			1755	15.560		9.866	11.841	1.00	41.	
ATOM	2614	OD2		1755	16.142	-2	1.241	10.238	1.00	47.	
ATOM	2615	C	ASP	1755	19.114	-1	9.724	11.222	1.00	46.	
ATOM		0	ASP	1755	19.114		0.411	12.250	1.00	36.	
ATOM	2616	N	ARG	1756	19.973		9.920	10.226	1.00	38.	
	2618	CA	ARG	1756	20.982		0.969		1.00	34.8	
ATOM	2619	CB	ARG	1756	21.688		1.100	10.302	1.00	34.6	
ATOM	2620	CG	ARG	1756	22.746		2.179	8.959	1.00	34.7	
ATOM	2621	CD	ARG	1756	23.297	- 22	2.1/3	8.910	1.00	35.9	93
ATOM	2622	NE	ARG	1756	23.786		2.306	7.511	1.00	41.6	
MOTA	2624	CZ	ARG	1756	24.889		1.025	6.999	1.00	46.4	
MOTA	2625	NHl	ARG	1756	25.637		.419	7.427	1.00	48.3	
ATOM	2628	NH2	ARG	1756			.976	8.381	1.00	48.1	
ATOM	2631	С	ARG	1756	25.236		.242	6.909	1.00	46.6	
MOTA	2632	0	ARG	1756	22.002	-20	.666	11.399	1.00	36.1	
ATOM	2633	N	ILE	1757	22.372		.541	12.177	1.00	38.3	
ATOM	2635	CA	ILE		22.433		.413	11.478	1.00	37.0	
				1757	23.416	-18	.998	12.468	1.00	35.60	
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MOTA	2636	CB	ILE	1757	23.964	-17.588	12.141	1.00	35.54
MOTA	2637	CG2	ILE	1757	24.921	-17.131	13.217	1.00	32.41
MOTA	2638	CG1	ILE	1757	24.693	-17.612	10.794	1.00	33.77
MOTA	2639	CD1	ILE	1757	25.097	-16.253	10.287	1.00	33.49
MOTA	2640	C	ILE	1757	22.866	-19.048	13.891	1.00	37.28
MOTA	2641	0	ILE	1757	23.531	-19.556	14.779	1.00	38.42
MOTA	2642	N	VAL	1758	21.634	-18.585	14.088	1.00	39.19
MOTA	2644	CA	VAL	1758	21.016	-18.584	15.421	1.00	39.84
ATOM	2645	CB	VAL	1758	19.560	-18.017	15.403	1.00	37.62
MOTA	2646	CG1	VAL	1758	18.918	-18.144	16.773	1.00	38.30
ATOM	2647	CG2	VAL	1758	19.560	-16.560	15.009	1.00	39.62
MOTA	2648	С	VAL	1758	20.983	-19.997	15.988	1.00	41.98
MOTA	2649	0	VAL	1758	21.380	-20.229	17.128	1.00	43.36
MOTA	2650	N	ALA	1759	20.501	-20.932	15.182	1.00	43.31
ATOM	2652	C'A	ALA	1759	20.418	-22.325	15.589	1.00	44.00
MOTA	2653	CB	ALA	1759	19.836	-23.150	14.459	1.00	44.52
ATOM	2654	C	ALA	1759	21.784	-22.867	15.976	1.00	45.98
ATOM	2655	0	ALA	1759	21.894	-23.725	16.841	1.00	48.78
ATOM	2656	N	LEU	1760	22.823	-22.375	15.319	1.00	48.93
MOTA	2658	CA	LEU	1760	24.175	-22.831	15.592	1.00	51.47
MOTA	2659	CB	LEU	1760	24.954	-22.900	14.280	1.00	53.63
MOTA	2660	CG	LEU	1760	24.284	-23.864	13.295	1.00	57.84
MOTA	2661	CD1	LEU	1760	24.993	-23.847	11.948	1.00	61.83
MOTA.	2662	CD2	LEU	1760	24.260	-25.277	13.886	1.00	58.57
MOTA	2663	C	LEU	1760	24.911	-21.965	16.607	1.00	53.60
MOTA	2664	O	LEU	1760	26.078	-22.214	16.919	1.00	54.00
MOTA	2665	N	THR	1761	24.222	-20.963	17.141	1.00	55.77
MOTA	2667	CA	THR	1761	24.820	-20.060	18.111	1.00	56.64
ATOM	2668	CB	THR	1761	24.250	-18.627	17.979	1.00	55.76
ATOM	2669	OG1	THR	1761	24.444	-18.154	16.644	1.00	56.20
ATOM	2671	CG2	THR	1761	24.962	-17.680	18.917	1.00	55.25
MOTA	2672	С	THR	1761	24.636	-20.548	19.539	1.00	58.16
ATOM	2673	0	THR	1761	23.566	-21.021	19.919	1.00	56.85
MOTA	2674	N	SER	1762	25.706	-20.436	20.318	1.00	61.74
MOTA	2676	CA	SER	1762	25.706	-20.833	21.717	1.00	64.50
MOTA	2677	CB	SER	1762	27.155	-20.979	22.205	1.00	68.82
MOTA	2678	OG	SER	1762	27.232	-21.544	23.508	1.00	73.15
MOTA	2680	C	SER	1762	24.965	-19.775	22.547	1.00	63.87
MOTA	2681	0	SER	1762	25.080	-18.563	22.296	1.00	63.22
MOTA	3420	PA	PCP	400	62.748	10.301	7.817	1.00	90.90
MOTA	3421	01A	PCP	400	62.509	10.036	9.280	1.00	92.35
ATOM	3422	02A	PCP	400	61.832	11.180	7.038	1.00	90.49
MOTA	3423	05*	PCP	400	62.744	8.904	7.142	1.00	83.57
ATOM	3424	PB	PCP	400	65.226		8.294	1.00	101.51
MOTA	3425	OlB	PCP	400	65.246	13.015	7.264	1.00	102.85
MOTA	3426	02B	PCP	400	66.527	11.458	8.830	1.00	99.88
ATOM	3427	03A	PCP	400	64.334	10.725	7.584	1.00	96.64
ATOM	3428	C3B	PCP	400	64.345	12.502	9.635	1.00	102.94
MOTA	3429	C5*	PCP	400	62.337	8.684	5.839	1.00	71.21
ATOM	3430	C4*	PCP	400	62.479	7.204	5.587	1.00	64.48
ATOM	3431	04*	PCP	400	63.713	6.745	6.169	1.00	60.91
ATOM	3432	C1*	PCP	400	63.394	5.459	6.680	1.00	54.96
ATOM	3433	И9	PCP	400	64.326	5.101	7.712	1.00	47.26
MOTA	3434	C4	PCP	400	65.017	3.903	7.840	1.00	46.24

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A	TOM 3	435	N3	PCF	400						
A		436	C2	PCP		91.7		2.770	7.0	062 1	.00 41.02
A	_	437	N1	PCP		05.0	02 1	1.878	7.5		.00 40.72
A	том з	438	C6	PCP	-00			.917			00 37.37
A	TOM 3	439	N6	PCP				.028	9.3		00 40.23
A.	TOM 3		C5	PCP		67.57		.134	10.3		00 33.92
A:	TOM 3		N7	PCP		65.86		.091	8.9		00 44.12
A	rom 3		C8	PCP	400	65.67		.361			00 45.15
A			C2*	PCP	400 400	64.76		.894	8.7		00 44.83
ΑT				PCP		61.98		.500	7.2		
AT	OM 34			PCP	400	61.45		.153	7.2		
AT	OM 34			PCP	400	61.32	86,	.402	6.24		
AT				PCP	400	60.68		644	5.20		
AT				PCP	401	9.36		801	17.74	•	
AT				PCP	401.	9.46		736	16.70		
ATO				PCP	401	10.33		926	17.69		,
ATO				CP	401	9.427		108	19.18		
ATO			-		401	6.878	3 10.	679	16.54		
ATO		_	_	CP	401	6.223	11.		16.77		,
ATC				CP	401	6.020	9.4	486	16.40		
ATC			_	CP	401	7.868	10.4		17.81		
ATO			_	CP	401	7.790	10.8		15.15		. 0.50
ATO			_	CP	401	10.184	9.5	593	20.275	_	
ATO			_	CP	4.01	10.228	8.6		21.442		
ATO			_	CP	401	9.032	7.8		21.412		
ATO			`	CP	401	9.397	6.5		21.641		
ATO		_			401	8.386	5.6		21.044		
ATO					401	7.790	4.4		21.564		
ATON		_			401	7.982	3.8		22.732		
ATON					401	7.239	2.7		22.838		
ATOM			PC		401	6.382	2.2		22.003		
ATOM			PC		101	6.202	2.8		20.856	0.50	
ATOM			PC		101	5.327	2.41		19.975	0.50	
ATOM			PC	-	101	6.932	4.03		20.603	0.50	16.87
ATOM			PC	_	01	6.983	4.88		19.507	0.50	21.72
ATOM			PC:	-	01	7.847	5.78		19.832	0.50	24.59
ATOM					01	10.762	6.40		20.931	0.50	24.26
ATOM	,,			_	01	11.609	5.32		21.412	0.50	39.01
ATOM				_	01	11.396	7.67		21.373	0.50	43.88
ATOM	3482	03*		_	01	11.918	7.51		2.681	0.50	42.14
ATOM	3484	N	SER		61	78.844	26.05	_	4.057	0.50	44.21
ATOM	3485	CA	SER		51	79.399	24.88		3.385	1.00	43.87
ATOM	3486	CB	SER		51	78.488	23.65		3.616	1.00	43.50
ATOM		C	SER		51	79.572	25.18		1.888	1.00	39.99
ATOM	3487	0	SER		51	79.473	24.292		1.038	1.00	42.14
ATOM	3488	N	GLU		2	79.883	26.441		1.038	1.00	40.29
ATOM	3490	CA	GLU		2	80.061	26.951		1.594	1.00	43.19
	3491	CB	GLU	46	2	80.303	28.446		0.233	1.00	42.77
ATOM	3492	CG	GLU	46	2	79.209	29.301		0.250	1.00	47.75
ATOM	3493	CD	GLU	46	2	79.647	30.752		.860	1.00	60.57
ATOM	3494	OE1	GLU	46	2	80.866			061	1.00	67.56
ATOM	3495	OE2	GLU	46		78.764	31.016		.994	1.00	67.47
ATOM	3496	С	GLU	46		81.207	31.611			1.00	72.32
ATOM	3497	0	GLU	46		81.051	26.357	_		1.00	39.55
ATOM	3498	N	TYR	46:		B2.375	26.032			1.00	38.74
					•	-2.3/5	26.299	10		1.00	36.47
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ATOM	3500	CA	TYR	463	83.567	25.806	9.420	1.00	34.19
ATOM	3501	CB	TYR	463	84.702	26.828	9.505	1.00	35.55
ATOM	3502	CG	TYR	463	84.393	28.059	8.675	1.00	42.11
MOTA	3503	CD1	TYR	463	84.004	29.264	9.283	1.00	43.15
MOTA	3504	CE1	TYR	463	83.619	30.361	8.513	1.00	42.40
MOTA	3505	CD2	TYR	463	84.395	27.990	7.280	1.00	39.78
MOTA	3506	CE2	TYR	463	84.012	29.078	6.509	1.00	39.04
ATOM	3507	CZ	TYR	463	83.625	30.256	7.129	1.00	39.86
ATOM	3508	ОН	TYR	463	83.260	31.330	6.366	1.00	42.58
ATOM	3510	C	TYR	463	84.055	24.434	9.800	1.00	33.28
ATOM	3511	0	TYR	463	84.739	23.781	9.005	1.00	33.47
ATOM	3512	N	GLU	464	83.695	23.976	10.993	1.00	34.42
MOTA	3514	CA	GLU	464	84.117	22.660	11.444	1.00	36.38
ATOM	3515	CB	GLU	464	85.618	22.663	11.750	1.00	40.90
MOTA	3516	CG	GLU	464	86.041	23.755	12.729	1.00	46.29
ATOM	3517	CD	GLU	464	87.548	23.810	12.943	1.00	51.33
ATOM	3518	OE1	GLU	464	87.970	24.247	14.038	1.00	54.49
MOTA	3519	OE2	GLU	464	88.312	23.430	12.025	1.00	53.18
MOTA	3520	C	GLU	464	83.374	22.224	12.678	1.00	35.64
ATOM	3521 3522	N N	GLU LEU	464 465	83.111 82.962	23.052	13.555	1.00	37.40
ATOM ATOM	3524	CA	LEU	465 465	82.267	20.955		1.00	34.21
ATOM	3525	CB	LEU	465	81.285	19.300	13.887 13.542	1.00	34.92
ATOM	3526	CG	LEU	465	80.272	19.381	12.405	1.00	31.30 32.22
ATOM	3527	CD1	LEU	465	79.152	18.407	12.720	1.00	21.95
ATOM	3528	CD2	LEU	465	79.738	20.802	12.720	1.00	29.75
ATOM	3529	C	LEU	465	83.326	19.855	14.814	1.00	36.17
ATOM	3530	0	LEU	465	84.473	19.621	14.400	1.00	35.80
ATOM	3531	N	PRO	466	82.970	19.629	16.083	1.00	36.20
ATOM	3532	CD	PRO	466	81.722	20.018	16.758	1.00	38.17
ATOM	3533	CA	PRO	466	83.925	19.072	17.037	1.00	36.06
ATOM	3534	CB	PRO	466	83.132	19.035	18.333	1.00	35.57
MOTA	3535	CG	PRO	466	82.185	20.194	18.171	1.00	38.67
ATOM	3536	C	PRO	466	84.294	17.666	16.605	1.00	37.06
ATOM	3537	0	PRO	466	83.498	16.959	15.979	1.00	34.50
MOTA	3538	N	GLU	467	85.504	17.258	16.936	1.00	39.97
MOTA	3540	CA	GLU	467	85.951	15.932	16.587	1.00	44.69
ATOM	3541	CB	GLU	467	87.412	15.985	16.151	1.00	50.43
MOTA	3542	CG	GLU	467	87.902	14.695	15.518	1.00	60.27
ATOM	3543	CD	GLU	467	89.321	14.796	14.986	1.00	65.75
ATOM	3544	OE1	GLU	467	90.024	15.804	15.269	1.00	64.40
ATOM	3545	OE2	GLU	467	89.726	13.850	14.275	1.00	71.13
MOTA	3546	С	GLU	467	85.775	15.002	17.783	1.00	43.30
MOTA	3547	0	GLU	467	85.888	15.428	18.936	1.00	43.26
MOTA	3548	N	ASP	468	85.433	13.750	17.504	1.00	43.09
MOTA	3550	CA	ASP	468	85.254	12.739	18.545	1.00	44.15
MOTA	3551	CB	ASP	468	83.785	12.614	18.979	1.00	44.54
MOTA	3552	CG	ASP	468	83.574	11.562	20.072	1.00	41.84
ATOM	3553	OD1	ASP	468	82.405	11.244	20.368	1.00	39.81
ATOM	3554	OD2	ASP	468	84.570	11.057	20.636	1.00	42.92
ATOM	3555	C	ASP	468	85.746	11.422	17.970	1.00	44.66
ATOM	3556	0	ASP	468	84.982	10.663	17.368	1.00	44.56
MOTA	3557	N	PRO	469	87.034	11.126	18.176	1.00	44.56
MOTA	3558	CD	PRO	469	87.953	11.959	18.971	1.00	45.43



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				PRO	469	87.707	9.9	16 17.7	07 1 6	
				PRO	469	89.024				50
				PRO	469	89.300				- -
			C E	PRO	469	86.934				
			o i	PRO	469	86.935		_		
			A, V	RG	470	86.229				
			CA A	RG .	470	85.460				-0.25
			CB A	RG 4	170	84.722				
AT			G A	RG 4	170	85.579	7.61	-		
AT		69 C	D A	RG 4	70	84.764	8.20	_		
AT		70 N	E A	RG 4	70	83.581	8.45			
ATO		72 C	Z = A	RG 4	70	82.748	9.26			58.57
ATO		73 N	H1 AI		70	82.972	9.71	. –		· - · - ·
ATO	_	76 N	H2 AI		70	81.670	9.445		_	
ATO		79 C	AF		70	84.439	10.398			
ATC		80 ₀ 0	AF		70	84.166	6.924			
ATC	DM 358	31 N	TF		71	83.879	5.735			45.68
ATO		33 CZ	A TR		71	82.851	7.866			42.41
ATO		34 CF	3 TR	_	71	81.577	7 534			38.92
ATO		35 CG	3 TR		71	80.967	8.268			35.80
ATO:		6 CI)2 TR		71	80.158	7.741			37.13
ATO		7 CE	2 TR			79.723	6.569			37.26
ATO		8 CE	3 TR			79.748	6.483	19.785		38.20
ATO	•	9 CD	1 TR			81.010	5.582	17.530		35.59
ATO		0 NE	1 TR			80.260	8.300	19.584		36.42
ATON		2 CZ	2 TRI			78.896	7.553	20.462		35.89
ATON	4 359	3 CZ	3 TRI			78.934	5.454	20.239	1.00	36.18
ATOM	1 359	4 CH	2 TRE			78.514	4.561	17.978	1.00	32.81
ATOM			TRE			83.175	4.505	19.321	1.00	34.82
ATOM		5.0	TRE			82.478	7.845	15.277	1.00	39.77
ATOM	3597	7 N	GLU			84.224	7.391	14.362	1.00	39.56
ATOM		CA	GLU			84.605	8.628	15.075	1.00	39.37
MOTA		CB	GLU			85.794	9.043	13.739	1.00	38.42
MOTA		CG	GLU			85.958	9.994	13.812	1.00	37.11
ATOM		CD	GLU			84.772	10.849	12.582	1.00	34.11
ATOM		OE1				84.260	11.757	12.338	1.00	34.03
MOTA	3604	OE2	GLU	472		84.367	12.348	13.317	1.00	31.87
ATOM	3605	C	GLU	472		84.910	11.885	11 163	1.00	32.11
ATOM	3606	0	GLU	472		85.656	7.901	12.791	1.00	39.78
MOTA	3607	N	LEU	473			6.975	13.128	1.00	41.64
MOTA	3609	CA	LEU	473		84.303 84.538	7.958	11.610	1.00	37.71
MOTA	3610	CB	LEU	473		83.258	6.957	10.590	1.00	36.94
ATOM	3611	CG	LEU	473		83.438	6.196	10.265	1.00	35.38
MOTA	3612	CD1	LEU	473		84.070	5.065	9.236	1.00	37.67
ATOM	3613	CD2	LEU	473			3.845	9.903		37.28
ATOM	3614	C	LEU	473		82.106	4.687	8.598		37.87
ATOM	3615	0	LEU	473		85.035	7.664	9.330		39.31
MOTA	3616	N	PRO	474		84.484	8.697	8.938		40.55
ATOM	3617	CD	PRO	474		86.140	7.164	8.732		39.20
ATOM	3618	CA	PRO	474		87.052	6.170	9.327		37.83
ATOM	3619	CB	PRO	474		86.735	7.716	7.513		38.53
ATOM	3620	CG	PRO	474		87.914	6.777	7.282		37.16
ATOM	3621	C	PRO			88.355	6.488			34.42
ATOM	3622	Ö	PRO	474		85.733	7.607			0.25
		-	2110	474		85.220	6.523	-		0.70
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ATOM	3623	N	ARG	475	85.492	8.723	5.685	1.00	41.09
ATOM	3625	CA	ARG	475	84.534	8.746	4.590	1.00	42.26
MOTA	3626	CB	ARG	475	84.487	10.132	3.948	1.00	39.19
MOTA	3627	CG	ARG	475	83.957	11.199	4.876	1.00	35.19
MOTA	3628	CD	ARG	475	84.074	12.593	4.301	1.00	30.76
MOTA	3629	NE	ARG	475	83.796	13.567	5.345	1.00	22.86
MOTA	3631	CZ	ARG	475	82.581	13.898	5.748	1.00	21.99
MOTA	3632	NH1	ARG	475	81.529	13.350	5.165	1.00	23.39
MOTA	3635	NH2	ARG	475	82.412	14.662	6.813	1.00	22.55
MOTA	3638	C	ARG	475	84.838	7.692	3.538	1.00	45.38
ATOM	3639	0	ARG	475	83.927	7.182	2.892	1.00	47.15
MOTA	3640	N	ASP	476	86.106	7.319	3.390	1.00	47.13
MOTA	3642	CA	ASP	476	86.461	6.325	2.387	1.00	51.33
MOTA	3643	CB	ASP	476	87.973	6.294	2.134	1.00	55.23
MOTA	3644	CG	ASP	476	88.768	5.841	3.340	1.00	61.16
MOTA	3645	OD1	ASP	476	88.863	4.617	3.573	1.00	65.55
MOTA	3646	OD2	ASP	476	89.331	6.713	4.036	1.00	65.78
ATOM	3647	С	ASP	476	85.932 .	4.940	2.746	1.00	52.35
ATOM	3648	С	ASP	476	85.815	4.063	1.885	1.00	55.49
MOTA	3649	N	ARG	477	85.609	4.752	4.021	1.00	50.77
ATOM	3651	CA	ARG	477	85.080	3.482	4.508	1.00	48.65
ATOM	3652	CB	ARG	477	85.612	3.208	5.908	1.00	50.02
ATOM	3653	CG	ARG	477	87.067	2.799	5.881	1.00	55.33
ATOM	3654	CD	ARG	477	87.760	3.030	7.201	1.00	60.38
ATOM	3655	NE	ARG	477	87.238	2.207	8.285	1.00	64.36
ATOM	3657	CZ	ARG	477	87.748	2.203	9.513	1.00	69.16
ATOM	3658	NH1	ARG	477	88.794	2.968	9.814	1.00	70.73
MOTA	3661	NH2	ARG	477	. 87.190	1.459	10.459	1.00	71.59
MOTA	3664	С	ARG	477	83.546	3.414	4.484	1.00	45.25
MOTA	3665	0	ARG	477	82.957 .	2.481	5.013	1.00	46.36
MOTA	3666	N	LEU	478	82.913	4.372	3.815	1.00	42.23
MOTA	3668	CA	LEU	478	81.464	4.418	3.743	1.00	38.89
MOTA	3669	CB	LEU	478	80.938	5.537	4.657	1.00	37.17
MOTA	3670	CG	LEU	478	79.418	5.733	4.678	1.00	34.13
MOTA	3671	CD1	LEU	478	78.777	4.723	5.609	1.00	32.24
MOTA	3672	CD2	LEU	478	79.074	7.133	5.101	1.00	33.15
MOTA	3673	C	LEU	478	81.059	4.697	2.303	1.00	38.34
MOTA	3674	0	LEU	478	81.515	5.671	1.711	1.00	40.88
MOTA	3675	N	VAL	479	80.208	3.850	1.738	1.00	37.34
MOTA	3677	CA	VAL	479	79.763	4.042	0.364	1.00	37.61
MOTA	3678	CB	VAL	479	80.105	2.829	-0.563	1.00	36.57
MOTA	3679	CG1	VAL	479	79.647	3.105	-1.994	1.00	31.59
MOTA	3680	CG2	VAL	479	81.608	2.567	-0.561	1.00	36.11
MOTA	3681	С	VAL	479	78.267	4.277	0.375	1.00	39.24
MOTA	3682	0	VAL	479	77.484	3.358	0.619	1.00	39.16
MOTA	3683	N	LEU	480	77.894	5.528	0.142	1.00	41.32
MOTA	3685	CA	LEU	480	76.505	5.960	0.123	1.00	41.60
MOTA	3686	CB	LEU	480	76.446	7.480	-0.008	1.00	41.31
MOTA	3687	CG	LEU	480	77.129	8.257	1.118	1.00	39.82
MOTA	3688	CD1	LEU	480	76.985	9.737	0.856	1.00	37.96
ATOM	3689	CD2	LEU	480	76.512	7.887	2.458	1.00	37.70
MOTA	3690	С	LEU	480	75.733	5.312	-1.015	1.00	41.85
MOTA	3691	0	LEU	480	76.235	5.224	-2.131	1.00	45.02
ATOM	3692	N	GLY	481	74.501	4.897	-0.727	1.00	40.86



ATO		94 CA	GL	Y 481	73.673	4.247	- 1 70	7 7 0	
ATO		95 C	GL	Y 481	72.270				
ATC		6 0	GL.	Y 481	72.058				
ATC	M 369	7 N	LY		71.306	·	- · - -		- · · ·
ATC	M 369	9 CA	LY		69.910				
ATC	M 370	0 CB			69.061	- - ·			
ATO	M 370	1 C	LYS		69.284		-2.566		
ATO	M 370	2 0	LYS	_			-1.084	1.00	43.13
ATO	M 370	3 N	PRO		69.37.3		0.060		44.49
ATO			PRO		68.676	6.204	~1.358		43.22
ATO			PRO		68.708	6.969	-2.613	1.00	44.40
ATO			PRO		68.044	6.973	~0.290	1.00	
ATO			PRO		67.701	8.295	-0.980	1.00	
ATO	•		PRO		67.573	7.923	-2.414	1.00	
ATO					66.801	6.261	0.232	1.00	47.67
ATO			PRO		66.012	5.725	-0.547		46.76
ATO			LEU		66.650	6.242	1.552		49.68
ATON			LEU		65.514	5.598	2.196		54.51
ATOM			LEU		65.935	5.026	3.555		52.70
ATOM		_	LEU		67.132	4.066	3.530	1.00	51.83
ATOM		. – –		484	67.620	3.766	4.933	1.00	50.19
ATOM				484	66.755	2.788	2.825	1.00	52.22
			LEU	484	64.317	6.554	2.357	1.00	58.82
ATOM			LEU	484	63.158	6.138	2.244	1.00	60.07
ATOM			GLY	485	64.599	7.831	2.609	1.00	61.91
ATOM	·	CA	GLY	485	63.538	8.810	2.778	1.00	
ATOM		C	GLY	485	64.057	10.167	3.227	1.00	65.89
ATOM		0	GLY	485	65.230	10.301	3.597	1.00	69.46
ATOM		N	GLU	486	63.178	11.165	3.241	1.00	70.65
ATOM	3726	CA	GLU	486	63.563	12.521	3.624	1.00	70.72
ATOM	3727	CB	GLU	486	64.015	13.298	2.389		71.32
ATOM	3728	C	GLU	486	62.435	13.269	4.312	1.00	73.69
ATOM	3729	0	GLU	486	61.281	12.846	4.275	1.00 1.00	70.93
ATOM	3730	N	\mathtt{GLY}	487	62.781	14.404	4.909		71.58
ATOM	3732	CA	GLY	487	61.798	15.211	5.603	1.00	70.10
ATOM	3733	C	\mathtt{GLY}	487	62.218	16.669	5.598	1.00	68.11
ATOM	3734	0	\mathtt{GLY}	487	62.938	17.109	4.696	1.00	67.97
ATOM	3735	N	ALA	488	61.780	17.409	6.615	1.00	67.68
MOTA	3737	CA	ALA	488	62.106	18.826	6.737	1.00	67.26
ATOM	3738	CB	ALA	488	61.362	19.428	7.909	1.00	66.90
ATOM	3739	С	ALA	488	63.607	19.004		1.00	68.72
ATOM	3740	0	ALA	488	64.124	18.867	6.921	1.00	67.08
ATOM	3741	N	PHE	489	64.297	19.248	8.037	1.00	65.97
ATOM	3743	CA	PHE	489	65.754	19.439	5.806	1.00	66.76
ATOM	3744	CB	PHE	489	66.134	20.794	5.773	1.00	65.91
ATOM	3745	С	PHE	489	66.563		6.379	1.00	66.45
ATOM	3746	0	PHE	489	67.622	18.288	6.414	1.00	63.92
ATOM	3747	N .	GLY	490	66.067	18.503	7.031		63.16
ATOM	3749	CA	GLY	490	66.710	17.069	6.209	1.00	59.03
ATOM	3750	C	GLY	490		15.878	6.720		51.12
ATOM	3751	0		490	66.619	14.823		1.00	48.59
ATOM	3752	N		491	65.608	14.736		1.00	45.25
ATOM	3754				67.659	14.003		1.00	48.77
ATOM	3755			491	67.732	12.951			47.40
ATOM	3756			491 401	68.529	13.474	3.319	_	49.92
			אותה	491	68.653	12.514	2.155	_	56.31

MOTA	3757	CD	GLN	491	69.604	13.020	1.088	1.00	58.79
MOTA	3758	OE1	GLN	491	70.043	14.171	1.130	1.00	59.63
MOTA	3759	NE2	GLN	491	69.929	12.161	0.122	1.00	59.05
ATOM	3762	C	GLN	491	68.407	11.693	5.086	1.00	44.46
ATOM	3763	0	GLN	491	69.396	11.782	5.806	1.00	44.15
MOTA	3764	N	VAL	492	67.867	10.527	4.752	1.00	42.55
ATOM	3766	CA	VAL	492	68.416	9.247	5.205	1.00	39.22
ATOM	3767	CB	VAL	492	67.375	8.458	6.042	1.00	39.40
ATOM	3768	CG1	VAL	492	67.947	7.127	6.524	1.00	40.17
ATOM	3769	CG2	VAL	492	66.922	9.267	7.210	1.00	36.12
MOTA	3770	C	VAL	492	68.746	8.396	3.975	1.00	37.57
MOTA	3771	0	VAL	492	67.888	8.178	3.115	1.00	35.70
ATOM	3772	N	VAL	493	69.990	7.961	3.845	1.00	36.27
ATOM	3774	CA	VAL	493	70.333	7.127	2.711	1.00	37.61
ATOM	3775	CB	VAL	493	71.237	7.863	1.643	1.00	37.45
ATOM	3776	CG1	VAL	493	70.836	9.319	1.524	1.00	38.29
MOTA	3777	CG2	VAL	493	72.717	7.713	1.943	1.00	36.53
ATOM	3778	C	VAL	493	70.952	5.806	3.156	1.00	37.54
MOTA	3779	0	VAL	493	71.542	5.711.	4.233	1.00	37.32
MOTA	3780	N	LEU	494	70.691	4.763	2.380	1.00	37.67
MOTA	3782	CA	LEU	494	71.236	3.450	2.656	1.00	38.41
ATOM	3783	CB	LEU	494	70.482	2.387	1.851	1.00	39.16
MOTA	3784	CG	LEU	494	70.834	0.908	2.021	1.00	36.43
ATOM	3785	CD1	LEU	494	70.809	0.508	3.479	1.00	34.69
MOTA	3786	CD2	LEU	494	69.840	0.086	1.229	1.00	37.48
MOTA	3787	C	LEU	494	72.683	3.541	2.202	1.00	39.30
ATOM	3788	0	LEU	494	72.976	4.201	1.207	1.00	39.21
ATOM	3789	N	ALA	495	73.584	2.922	2.954	1.00	40.08
MOTA	3791	CA	ALA	495	74.996	2.954	2.619	1.00	41.70
ATOM	3792	CB	ALA	495	75.654	4.162	3.283	1.00	41.63
MOTA	3793	C	ALA	495	75.670	1.669	3.080	1.00	43.92
MOTA	3794	0	ALA	495	75.033	0.818	3.711	1.00	45.20
MOTA	3795	N	GLU	496	76.946	1.515	2.731	1.00	44.21
ATOM	3797	CA	GLU	496	77.712	0.347	3.137	1.00	43.44
MOTA	3798	CB	GLU	496	78.046	-0.538	1.943	1.00	45.87
MOTA	3799	CG	GLU	496	76.816	-1.142	1.301	1.00	53.11
ATOM	3800	CD	GLU	496	77.145	-2.262	0.339	1.00	56.68
ATOM	3801	OE1	GLU	496	76.473	-3.316	0.410	1.00	61.87
MOTA	3802	OE2	GLU	496	78.068	-2.091	-0.482	1.00	58.18
MOTA	3803	С	GLU	496	78.973	0.773	3.860	1.00	40.97
MOTA	3804	0	GLU	496	79.835	1.437	3.302	1.00	40.91
MOTA	3805	N	ALA	497	79.036	0.439	5.136	1.00	42.07
MOTA	3807	CA	ALA	497	80.173	0.786	5.959	1.00	43.69
MOTA	3808	CB	ALA	497	79.709	1.104	7.366	1.00	40.90
MOTA	3809	C	ALA	497	81.160	-0.372	5.962	1.00	46.16
MOTA	3810	0	ALA	497	80.764	-1.525	5.814	1.00	46.90
MOTA	3811	N	ILE	498	82.446	-0.059	6.090	1.00	48.78
MOTA	3813	CA	ILE	498	83.494	-1.068	6.114	1.00	49.59
ATOM	3814	CB	ILE	498	84.395	-0.993	4.858	1.00	49.46
MOTA	3815	CG2	ILE	498	85.524	-2.006	4.954	1.00	51.16
ATOM	3816	CG1	ILE	498	83.577	-1.244	3.591	1.00	48.96
MOTA	3817	CD1	ILE	498	82.924	0.009	2.998	1.00	52.50
MOTA	3818	C	ILE	498	84.352	-0.877	7.355	1.00	51.33
ATOM	3819	0	ILE	498	84.818	0.230	7.641	1.00	50.42



תי ע	OM 20		_					-	
		20 N	_	LY 499	84.50	6 -1.952	2 8.11	9 1.00	
AT				LY 499	85.31				,
AT				LY 499				_	
AT			G:	LY 499					
ATO			L	EU 500					
ATO			A LI	EU 500	82.83				
ATO		28 C	B LE	EU 500	81.339				
ATO		29 C	G LE	EU 500	80.501				• • •
ATC	OM 383	30 CI	01 LE	U 500	79.047				56.68
ATC	M 383	31 CI	02 LE		80.682				55.05
ATC	M 383	32 C	LE		83.501		055		56.30
ATC	M 383	3 0	LE			_			63.28
ATO	M 383	4 N	PR		83.623	- -	13.487		64.91
ATO	M 383	5 CI			87.387	_	10.091	1.00	82.92
ATO	M 383			-	88.522	-6.966	10.874	1.00	83.74
ATO:					87.618	-5.052	9.705	1.00	80.73
ATO					89.027	-4.770	10.247	1.00	81.95
ATO			PRO		89.655	~6.133	10.342	1.00	83.54
ATO		-	PRO		87.514	-4.794	8.205	1.00	77.60
ATO					87.445	-3.651	7.761	1.00	77.24
ATON			ASI		87.488	~5.863	7.424	1.00	75.24
ATON			ASN		87.380	-5.727	5.981	1.00	72.92
ATOM			ASN		88.435	-6.589	5.283	1.00	73.87
ATOM			ASN		85.978	-6.122	5.529	1.00	70.43
ATOM			ASN		85.719	-6.281	4.340	1.00	70.43
ATOM			ARG		85.075	-6.273	6.491	1.00	
ATOM			ARG		83.697	-6.647	6.200	1.00	68.31
ATOM			ARG		83.112	-7.429	7.378	1.00	65.59
ATOM			ARG		. 82.846	-5.413	5.941	1.00	66.34
			ARG	507	83.191	-4.313	6.375		62.97
ATOM			VAL	508	81.740	-5.599	5.231	1.00	63.16
ATOM			VAL	508	80.840	-4.495	4.947	1.00	60.02
ATOM	3856		VAL	508	80.532	··4.357	3.439	1.00	58.59
ATOM	3857	CG1	VAL	508	81.813	-4.196	2.658	1.00	58.40
ATOM	3858	CG2	\mathtt{VAL}	508	79.751	-5.553	2.938	1.00	61.14
ATOM	3859	C	VAL	508	79.537	-4.682			61.01
ATOM	3860	0	VAL	508	79.031	-5.803	5.707		57.24
ATOM	3861	N	THR	509	79.020	-3.579	5.836		58.42
ATOM	3863	CA	THR	509	77.769	-3.572	6.237		54.22
ATOM	3864	CB	THR	509	77.971	-3.100	6.973		48.99
ATOM	3865	OG1	THR	509	78.932		8.428		49.59
ATOM	3867	CG2	THR	509	76.665	-3.935	9.082		51.71
ATOM	3868	С	THR	509	76.837	-3.166	9.198		50.69
ATOM	3869	0	THR	509	77.231	-2.606	6.253		46.51
ATOM	3870	N	LYS	510	75.628	-1.503			44.91
ATOM	3872	CA	LYS	510	74.658	-3.059			15.65
ATOM	3873	CB	LYS	510		-2.208		1.00 4	13.61
ATOM	3874	CG	LYS	510	73.598	-3.058		1.00 4	15.46
MOTA	3875	CD	LYS	510	72.845	-2.306	3.568	_	4.00
ATOM	3876	CE	LYS		73.022	-2.912	2.183		8.74
ATOM	3877	NZ	LYS	510	72.194	-4.184			9.63
ATOM	3881	C		510	72.711	-5.323	_	_	1.62
ATOM	3882	0	LYS	510	74.065	-1.359			2.05
ATOM	3883		LYS	510	73.566	-1.898			1.29
ATOM	3885	N Ca	VAL	511	74.185		-		0.14
01.1	2002	CA	VAL	511	73.719				5.38
SSSD/ss	145 04								J.J0

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ATOM	3886	CB	VAL	511	74.932	1.554	8.074	1.00	33.16
MOTA	3887	CG1	VAL	511	75.761	0.501	8.795	1.00	29.24
MOTA	3888	CG2	VAL	511	75.804	2.295	7.054	1.00	30.37
MOTA	3889	С	VAL	511	72.856	2.005	6.776	1.00	33.90
MOTA	3890	0	VAL	511	72.722	2.110	5.558	1.00	32.53
MOTA	3891	N	ALA	512	72.261	2.813	7.655	1.00	31.97
MOTA	3893	CA	ALA	512	71.434	3.956	7.248	1.00	31.10
MOTA	3894	CB	ALA	512	70.088	3.945	7.952	1.00	27.38
MOTA	3895	C	ALA	512	72.225 -	5.186	7.660	1.00	30.49
MOTA	3896	0	ALA	512	72.775	5.235	8.766	1.00	30.10
MOTA	3897	N	VAL	513	72.312	6.162	6.765	1.00	30.50
MOTA	3899	CA	VAL	513	73.064	7.382	7.041	1.00	29.68
MOTA	3900	CB	VAL	513	74.204	7.593	6.015	1.00	28.89
MOTA	3901	CG1	VAL	513	74.966	8.856	6.334	1.00	26.30
MOTA	3902	CG2	VAL	513	75.134	6.389	5.987	1.00	26.66
MOTA	3903	C	VAL	513	72.171	8.607	7.012	1.00	28.50
MOTA	3904	0	VAL	513	71.536	8.893	5.994	1.00	26.27
MOTA	3905	N	LYS	514	72.091	9.282	8.154	1.00	29.18
MOTA	3907	CA	LYS	514	71.307	10.508	8.295	1.00	31.52
MOTA	3908	CB	LYS	514	70.797	10.659	9.728	1.00	33.52
MOTA	3909	CG	LYS	514	69.890	9.540	10.198	1.00	35.67
MOTA	3910	CD	LYS	514	69.439	9.831	11.618	1.00	44.89
ATOM	3911	CE	LYS	514	68.313	8.909	1.2.060	1.00	51.12
MOTA	3912	NZ	LYS	514	67.029	9.137	11.307	1.00	57.11
MOTA	3916	C	LYS	514	72.233	11.681	7.956	1.00	30.75
MOTA	3917	0	LYS	514	73.390	11.698	8.379	1.00	30.08
MOTA	3918	N	MET	515	71.724	12.651	7.201	1.00	29.45
MOTA	3920	CA	MET	515	72.511	13.814	6.786	1.00	28.74
MOTA	3921	CB	MET	515	73.342	13.466	5.552	1.00	27.72
MOTA	3922	CG	MET	515	72.487	13.034	4.378	1.00	31.56
ATOM	3923	SD	MET	515	73.442	12.549	2.945	1.90	34.98
MOTA	3924	CE	MET	515	73.730	10.878	3.330	1.00	31.23
MOTA	3925	C	MET	515	71.585	14.966	6.444	1.00	27.75
MOTA	3926	0	MET	515	70.369	14.794	6.359	1.00	29.07
MOTA	3927	N	LEU	516	72.152	16.145	6.247	1.00	28.33
MOTA	3929	CA	LEU	516	71.348	17.313	5.912	1.00	31.16
MOTA	3930	CB	LEU	516	72.052	18.605	6.339	1.00	28.70
MOTA	3931	CG	LEU	516	72.312	18.866	7.826	1.00	28.33
MOTA	3932	CD1	LEU	516	73.098	20.156	7.949	1.00	28.45
MOTA	3933	CD2	LEU	516	71.020	18.959	8.604	1.00	21.64
ATOM	3934	C	LEU	516	71.069	17.378	4.421	1.00	33.22
MOTA	3935	0	LEU	516	71.762	16.760	3.619	1.00	35.00
MOTA	3936	N	LYS	517	70.022	18.100	4.061	1.00	34.69
ATOM	3938	CA	LYS	517	69.696	18.286	2.665	1.00	34.20
MOTA	3939	CB	LYS	517	68.194	18.475	2.496	1.00	37.45
MOTA	3940	CG	LYS	517	67.403	17.264	2.950	1.00	43.71
MOTA	3941	CD	LYS	517	66.157	17.072	2.126	1.00	51.25
ATOM	3942	CE	LYS	517	65.123	18.135	2.419	1.00	58.56
ATOM	3943	NZ	LYS	517	64.010	18.049	1.438	1.00	63.12
ATOM	3947	C	LYS	517	70.482	19.533	2.259	1.00	33.81
MOTA	3948	0	LYS	517	70.991	20.244	3.130	1.00	33.17
ATOM	3949	N	SER	518	70.603	19.788	0.959	1.00	33.42
MOTA	3951	CA	SER	518	71.369	20.938	0.472	1.00	33.33
MOTA	3952	CB	SER	518	71.550	20.842	-1.042	1.00	33.23

ATO		3 OG	SE	R 518	70.306	20.624	1 -1.678	2 1 00	
ATO	M 395	5 C	SEI	7 518	70.794				
ATO	M 395	6 0	SEI	7 518	71.509				· · · -
ATO	M 395	7 N	ASI	519	69.510	22.313			
ATO		9 CA	ASI	519	68.825	23.541			
ATO		O CB	ASI	519	67.401	23.543			
ATO	M 3965	l CG	ASI	519	66.484	22.503			
ATO	M 3962	2 OD1	L ASF		66.958	21.430			
ATO	4 3963	3 OD2	2 ASP		65.261	22.754			
ATO	4 3964	l C	ASP		.68.793	23.747			
ATON	1 3965	5 0	ASP		68.114	24.648			
ATON	1 3966	N	ALA		69.538	22.931			
ATOM	1 3968	CA	ALA		69.570	23.032			31.38
ATOM	1 3969	CB	ALA		70.264	21.830			29.47
ATOM	1 3970	C	ALA		70.229	24.301			29.74
ATOM	3971	0	ALA		71.004		5.812	1.00	29.83
ATOM	3972	N	THR		69.938	24.952	5.106	1.00	30.23
ATOM	3974	CA	THR		70.487	24.616	7.071	1.00	31.57
ATOM	3975	CB	THR	521	69.361	25.793	7.742	1.00	34.56
ATOM	3976	OG1	THR	521	68.670	26.736	8.302	1.00	38.37
ATOM	3978	CG2	THR	521	68.357	26.082	9.376	1.00	41.75
ATOM	3979	С	THR	521	71.353	27.117	7.209	1.00	38.30
ATOM	3980	0	THR	521	71.333	25.363	8.916	1.00	33.22
ATOM	3981	N	GLU	522	72.092	24.207	9.327	1.00	32.31
ATOM	3983	CA	GLU	522	72.092	26.310	9.479	1.00	34.43
ATOM	3984	СВ	GLU	522	73.634	26.042	10.619	1.00	39.53
ATOM	3985	CG	GLU	522	74.398	27.340	11.068	1.00	46.35
MOTA	3986	CD	GLU	522	75.772	27271	12.402	1.00	58.03
ATOM	3987	OE1	GLU	522	76.800	26.603	12.301	1.00	63.14
ATOM	3988	OE2	GLU	522	75.824	27.321	12.404	1.00	61.75
ATOM	3989	C	GLU	522	72.130	25.359	12.158	1.00	66.35
MOTA	3990	С	GLU	522	72.130	25.428	11.765	1.00	38.40
MOTA	3991	N	LYS	523	70.853	24.622	12.543	1.00	37.92
ATOM	3993	CA	LYS	523	69.995	25.792	11.849	1.00	36.43
MOTA	3994	CB	LYS	523	68.703	25.261	12.893	1.00	36.83
ATOM	3995	CG	LYS	523	67.793	26.065	13.008	1.00	40.88
MOTA	3996	CD	LYS	523	66.584	25.636	14.152	1.00	44.55
MOTA	3997	CE	LYS	523	65.629	24.898	13.607	1.00	52.68
ATOM	3998	NZ	LYS	523	64.537	24.483	14.708	1.00	56.04
ATOM	4002	С	LYS	523	69.689	23.646	14.123	1.00	58.13
ATOM	4003	0	LYS	523	69.645	23.804	12.601	1.00	35.27
ATOM	4004	N	ASP	524	69.496	22.985	13.513	1.00	36.58
ATOM	4006	CA	ASP	524	69.235	23.473	11.326	1.00	32.27
ATOM	4007	СВ	ASP	524	68.952	22.089	10.963	1.00	27.18
ATOM	4008	CG	ASP	524	67.635	21.953	9.480	1.00	26.32
ATOM	4009	OD1	ASP	524	66.662	22.555	9.089	1.00	25.22
ATOM	4010	OD2	ASP	524		22.394	9.848	1.00	31.78
ATOM	4011	C	ASP	524	67.568	23.190	8.028		24.00
ATOM	4012	Ö	ASP	524	70.445	21.268	11.342		26.83
ATOM	4013	N	LEU	525	70.312	20.165	11.851	1.00	28.65
ATOM	4015	CA	LEU	525	71.633	21.827	11.129	1.00	28.69
ATOM	4016	CB	LEU		72.872	21.148	11.473		26.96
ATOM	4017	CG	LEU	525 525	74.077	21.981		1.00	22.80
ATOM	4018	CD1	LEU	525 525	75.445	21.355		1.00	22.32
			U 1111	525	75.522	19.883	10.858	1.00	18.89

ATOM	4019	CD2	LEU	525	76.504	22.212	10.704	1.00	17.44
MOTA	4020	C	LEU	525	72.886	20.926	12.980	1.00	28.00
MOTA	4021	0	LEU	525	73.160	19.816	13.462	1.00	28.82
ATOM	4022	N	SER	526	72.567	21.992	13.707	1.00	27.98
ATOM	4024	CA	SER	526	72.496	21.994	15.168	1.00	30.78
ATOM	4025	CB	SER	526	71.939	23.345	15.627	1.00	33.18
ATOM	4026	OG	SER	526	71.624	23.347	17.009	1.00	42.73
MOTA	4028	С	SER	526	71.599	20.865	15.704	1.00	30.56
MOTA	4029	0	SER	526	71.906	20.206	16.716	1.00	31.92
MOTA	4030	N	ASP	527	70.484	20.665	15.018	1.00	28.19
MOTA	4032	CA	ASP	527	69.516	19.651	15.366	1.00	27.41
ATOM	4033	CB	ASP	527	68.207	19.932	14.632	1.00	27.63
ATOM	4034	CG	ASP	527	67.492	21.172	15.149	1.00	27.37
ATOM	4035	OD1	ASP	527	67.870	21.728	16.211	1.00	26.70
MOTA	4036	OD2	ASP	527	66.525	21.579	14.487	1.00	33.80
MOTA	4037	C	ASP	527	70.007	18.241	15.063	1.00	27.36
MOTA	4038	0	ASP	527	69.722	17.309	15.816	1.00	30.13
ATOM	4039	N.	LEU	528	70.716	18.077	13.952	1.00	25.76
ATOM	4041	CA	LEU	528	71.245	16.765	13.588	1.00	25.29
ATOM	4042	CB	LEU	528	71.777	16.771	12.143	1.00	23.65
MOTA	4043	CG	LEU	528	72.283	15.432	11.574	1.00	25.86
MOTA	4044	CD1	LEU	528	71.234	14.341	11.770	1.00	23.35
ATOM	4045	CD2	LEU	528	72.652	15.566		1.00	17.46
ATOM	4046	С	LEU	528	72.351	16.368	14.578	1.00	25.66
ATOM	4047	С	LEU	528	72.418	15.210	15.015	1.00	24.02
MOTA	4048	N	ILE	529	73.200	17.338	14.934	1.00	26.36
ATOM	4050	CA	ILE	529	74.304	17.130	15.886	1.00	26.17
ATOM	4051	CB	ILE	529	75.192	18.381	16.003	1.00	22.72
ATOM	4052	CG2	ILE	529	76.250	18.180	17.057	1.00	21.32
ATOM	4053	CG1	ILE	529	75.876	18.666	14.685	1.00	20.71
ATOM	4054	CD1	ILE	529	76.621	19.965	14.675	1.00	25.60
MOTA	4055	C	ILE	529	73.756	16.835	17.283	1.00	29.87
ATOM	4056	0	ILE	529	74.253	15.948	17.977	1.00	32.20
ATOM	4057	N	SER	530	72.741	17.591	17.693	1.00	28.63
ATOM	4059	CA	SER	530	72.143	17.381	18.991	1.00	32.21
MOTA	4060	СВ	SER	530	71.031	18.399	19.231	1.00	37.45
MOTA	4061	OG	SER	530	70.065	18.342	18.195	1.00	49.52
ATOM	4063	С	SER	530	71.598	15.956	19.075	1.00	30.96
ATOM	4064	0	SER	530	71.728	15.301	20.105	1.00	33.05
ATOM	4065	N	GLU	531	70.996	15.476	17.996	1.00	29.13
ATOM	4067	CA	GLU	531	70.468	14.117	17.987	1.00	29.84
MOTA	4068	CB	GLU	531	69.672	13.847	16.709	1.00	30.29
ATOM	4069	CG	GLU	531	69.093	12.445	16.666	1.00	27.39
ATOM	4070	CD	GLU	531	68.521	12.074	15.331	1.00	31.34
ATOM	4071	OE1	GLU	531	67.929	10.981	15.228	1.00	35.90
MOTA	4072	OE2	GLU	531	68.660	12.860	14.376	1.00	38.37
ATOM	4073	C	GLU	531	71.600	13.081	18.109	1.00	28.48
ATOM	4074	0	GLU	531	71.468	12.094	18.822	1.00	28.17
ATOM	4075	N	MET	532	72.682	13.281	17.364	1.00	28.12
ATOM	4077	CA	MET	532	73.832	12.376	17.409	1.00	27.64
ATOM	4078	CB	MET	532	74.953	12.899	16.499	1.00	26.47
ATOM	4079	CG	MET	532	76.267	12.125	16.601	1.00	22.25
ATOM	4080	SD	MET	532	77.406	12.610	15.286	1.00	30.32
ATOM	4081	CE	MET	532	77.613	14.366	15.661	1.00	20.92
				-					20.02

ATO		32 C	MET	Г 532	74.339	12.32	0 10 02		_	
ATO		3 0	MET		74.640	11.26			_	
ATC		4 N	GLU	J 533	74.439	13.49				
ATC		6 CA	GLU	533	74.906	13.59				
ATC		7 CB	GLU	533	75.071	15.06				
ATC		8 CG	GLU		76.216	15.74				
ATO	M 408	9 CD	GLU		77.564	15.07				
ATO	M 409	0 OE:	l GLU		78.001	14.969				
ATO		1. OE2	2 GLU		78.202	14.643				
ATO		2 C	GLU		73.981	12.850				
ATO		3 0	GLU	533	74.455	12.093				
ATO	M 4094	4 N	MET	534	72.670	13.014			,	
ATO		5 CA	MET	534	71.692	12.346		-		
ATO		7 CB	MET	534	70.258	12.751	-			
OTA	M 4098	G CG	MET	534	69.311	12.594			28.95	
ATO		SD SD	MET	534	67.538	12.682			29.62	
ATOM) CE	MET	534	67.269	14.452			29.87	
ATON	4101	. C	MET	534	71.855	10.821	22.795	0.50	31.07	PRT1
MOTA	4102	0	MET	534	71.833	10.821	22.362	1.00	28.36	
MOTA	4103	N	MET	535	72.048	10.143	23.386	1.00	27.02	
ATOM		CA	MET	535	72.239	8.861	21.151	1.00	26.96	
ATOM		CB	MET	535	72.347	8.521	20.947	1.00	26.63	
ATOM		CG	MET	535	71.089	8.778	19.456	1.00	24.67	
ATOM		SD	MET	535	71.160	8.062	18.659	1.00	23.15	
ATOM	4109	CE	MET	535	71.251	9.486	17.011	1.00	24.57	
ATOM		C	MET	535	73.498	8.390	16.023	1.00	24.79	
ATOM	4111	0	MET	535	73.564	7.259	21.569	1.00	27.66	
ATOM		N	LYS	536	74.515	9.246	22.164	1.00	28.83	
MOTA		CA	LYS	536	75.757	8.918	21.698	1.00	29.13	
ATOM		CB	LYS	536	76.812	9.985	22.392 22.131	1.00	30.50	
ATOM		CG	LYS	536	77.499	9.883	20.802	1.00	29.15	
ATOM	4117	CD	LYS	536	78.377	11.100	20.602	1.00	27.71	
ATOM	4118	CE	LYS	536	79.085	11.096	19.279	1.00	28.12	
ATOM	4119	NZ	LYS	536	79.688	12.436	19.077	1.00	26.89	
ATOM	4123	C	LYS	536	75.480	8.836	23.892	1.00 1.00	27.54	
ATOM	4124	0	LYS	536	75.921	7.908	24.559	1.00	31.92	
ATOM	4125	N	MET	537	74.742	9.814	24.409		31.19	
ATOM	4127	CA	MET	537	74.384	9.881	25.822	1.00	34.02	
ATOM	4128	CB	MET	537	73.648	11.197	26.083	1.00	36.35	
ATOM	4129	CG	MET	537	73.096	11.376	27.507	1.00	43.33	
ATOM	4130	SD	MET	537	71.426	10.674	27.856	1.00	54.60 67.38	
ATOM	4131	CE	MET	537	71.684	9.813	29.440	1.00	62.03	
ATOM	4132	С	MET	537	73.507	8.705	26.253	1.00		
MOTA	4133	0	MET	537	73.744	8.069	27.275	1.00	34.53	
ATOM	4134	N	ILE	538	72.496	8.425	25.454		36.76 32.24	
ATOM	4136	CA		538	71.568	7.367	25.757	1.00		
ATOM	4137	CB		538	70.396	7.384	24.757		29.88	
ATOM	4138	CG2		538	69.582	6.096	24.842		26.98	
ATOM	4139	CG1		538	69.527	8.614			27.93	
ATOM	4140	CD1		538	68.399	8.787			22.58	
ATOM	4141	C		538	72.236	6.006			24.58	
ATOM	4142	0		538	71.983	5.227			31.83	
ATOM	4143			539	73.102	_			36.32	
ATOM	4145	CA	GLY 5	539	73.744				32.45	·
CCCD/FF	145 6:							~	32.13	

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ATOM	4146	С	\mathtt{GLY}	539	72.974	3.380	24.056	1.00	33.83
MOTA	4147	0	GLY	539	71.876	3.654	23.530	1.00	33.75
MOTA	4148	N	LYS	540	73.539	2.173	24.010	1.00	33.36
MOTA	4150	CA	LYS	540	72.980	1.054	23.256	1.00	37.04
MOTA	4151	CB	LYS	540	74.110	0.181	22.709	1.00	39.21
MOTA	4152	CG	LYS	540	74.865	0.893	21.623	1.00	48.72
MOTA	4153	CD	LYS	540	75.818	0.009	20.850	1.00	56.84
MOTA	4154	CE	LYS	540	76.225	0.693	19.516	1.00	62.14
MOTA	4155	NZ	LYS	540	77.252	-0.102	18.805	1.00	71.02
MOTA	4159	С	LYS	540	71.938	0.162	23.901	1.00	36.51
MOTA	4160	0	LYS	540	. 71.963	-0.096	25.113	1.00	38.52
MOTA	4161	N	HIS	541	71.017	-0.295	23.058	1.00	32.98
MOTA	4163	CA	HIS	541	69.963	-1.230	23.424	1.00	31.20
MOTA	4164	CB	HIS	541	68.779	-0.561	24.095	1.00	30.35
MOTA	4165	CG	HIS	541	67.815	-1.540	24.694	1.00	32.56
ATOM	4166	CD2	HIS	541	67.737	-2.058	25.941	1.00	32.45
ATOM	4167	ND1	HIS	541	66.795	-2.124	23.974	1.00	29.22
.ATOM	4169	CE1	HIS	541	66.134	-2.965	24.753	1.00	31.56
ATOM	4170	NE2	HIS	541	66.679	-2.932	25.957	1.00	32.22
MOTA	4172	С	HIS	541	69.509	-1.937	22.152	1.00	32.00
MOTA	4173	O	HIS	541	69.409	-1.324	21.095	1.00	32.84
MOTA	4174	N	LYS	542	69.187	-3.222	22.273	1.00	33.61
ATOM	4176	CA	LYS	542	68.786	-4.061	21.154	1.00	31.54
ATOM	4177	CB	LYS	542	68.653	-5.516	21.596	1.00	33.94
ATOM	4178	CG	LYS	542	6.8.322	-6.451	20.437	1.00	42.34
ATOM	4179	CD	LYS	542	68.083	-7.885	20.856	1.00	47.57
ATOM.	4180	CE	LYS	542	67.634	-8.726	19.658	1.00	52.70
ATOM	4181	NZ	LYS	542	67.402	-10.146	20.023	1.00	59.51
ATOM	4185	C	LYS	542	67.495	-3.611	20.487	1.00	29.57
ATOM	4186	0	LYS	542	67.268	-3.884	19.305	1.00	27.99
MOTA	4187	N	ASN	543	66.649	-2.931	21.253	1.00	28.32
MOTA	4189	CA	ASN	543	65.378	-2.476	20.714	1.00	28.86
ATOM	4190	CB	ASN	543	64.231	-2.947	21.601	1.00	29.33
MOTA	4191	CG	ASN	543	64.247	-4.452	21.811	1.00	29.64
MOTA	4192	OD1	ASN	543	64.437	-4.926	22.930	1.00	33.86
MOTA	4193	ND2	ASN	543	64.106	-5.206	20.732	1.00	28.02
MOTA	4196	С	ASN	543	65.252	-0.983	20.378	1.00	29.69
MOTA	4197	0	ASN	543	64.159	-0.413	20.457	1.00	30.02
ATOM	4198	N	ILE	544	66.372	-0.357	20.011	1.00	27.35
ATOM	4200	CA	ILE	544	66.382	1.046	19.593	1.00	25.95
MOTA	4201	CB	ILE	544	66.898	2.030	20.706	1.00	25.56
MOTA	4202	CG2	ILE	544	66.148	1.819	22.037	1.00	21.06
MOTA	4203	CG1	ILE	544	68.406	1.901	20.902	1.00	25.61
MOTA	4204	CD1	ILE	544	68.952	2.818	21.976	1.00	25.89
MOTA	4205	С	ILE	544	67.341	1.083	18.399	1.00	25.97
MOTA	4206	0	ILE	544	68.126	0.152	18.227	1.00	25.69
ATOM	4207	N	ILE	545	67.226	2.095	17.537	1.00	27.27
MOTA	4209	CA	ILE	545	68.129	2.243	16.384	1.00	27.02
ATOM	4210	CB	ILE	545	67.541	3.194	15.307	1.00	27.30
ATOM	4211	CG2	ILE	545	68.592	3.553	14.269	1.00	26.52
ATOM	4212	CG1	ILE	545	66.309	2.570	14.638	1.00	22.63
ATOM	4213	CD1	ILE	545	66.605	1.447	13.665	1.00	17.57
ATOM	4214	С	ILE	545	69.383	2.873	16.979	1.00	28.55
ATOM	4215	0	ILE	545	69.346	4.014	17.451	1.00	29.47

ATOM 4216 N ASN 546 70.482 2.123 16.965 1.00 ATOM 30.90 4218 CA ASN 546 71.748 2.564 17.560 1.00 ATOM 29.56 4219 CB ASN 546 72.497 1.365 18.159 1.00 MOTA 26.32 4220 CG ASN 546 71.732 0.695 19.281 1.00 23.81 ATOM 4221 OD1 ASN 546 71.580 1.252 20.362 1.00 ATOM 27.34 4222 ND2 ASN 546 71.267 -0.515 19.039 1.00 ATOM 4225 23.49 C ASN 546 72.700 3.330 16.653 1.00 ATOM 4226 30.99 0 ASN 546 72.679 3.169 15.430 1.00 MOTA 30.98 4227 N LEU 547 73.543 4.148 17.286 1.00 ATOM 32.29 4229 CA LEU 547 74.570 4.948 16.610 1.00 30.93 ATOM 4230 CB LEU 547 75.043 6.076 17.542 1.00 ATOM 4231 25.97 CG LEU 547 76.075 7.088 17.021 1.00 ATOM 4232 22.12 CD1 LEU 547 75.553 7.815 15.765 1.00 ATOM 22.10 4233 CD2 LEU 547 76.415 8.089 18.112 1.00 ATOM 18.67 4234 C LEU 547 75.756 4.039 16.264 1.00 30.70 ATOM 4235 O LEU 547 76.284 3.361 17.137 1.00 ATOM 34.46 4236 N LEU 548 76.141 3.993 14.992 1.00 30.97 ATOM 4238 CA LEU 548 77.262 3.165 14.562 1.00 30.73 MOTA 4239 CB LEU 548 76.929 2.406 13.281 1.00 29.24 MOTA 4240 CG LEU 548 75.788 1.394 13.371 1.00 28.77 MOTA 4241 CD1 LEU 548 75.924 0.460 12.209 1.00 MOTA 26.55 4242 CD2 LEU 548 75.839 0.616 14.683 1.00 23.48 MOTA 4243 С LEU 548 78.522 3.982 14.347 1.00 ATOM 33.00 4244 0 LEU 548 79.640 3.500 14.558 1.00 ATOM. 35.92 4245 N GLY 549 78.351 5.215 13.901 1.00 32.52 MOTA 4247 CA GLY 549 79.503 6.051 13.673 1.00 ATOM 32.76 4248 C GLY 549 79.092 7.411 13.180 ATOM 1.00 33.72 4249 0 GLY 549 77.895 7.707 13.092 ATOM 1.00 35.01 4250 N ALA 550 80.089 8.226 12.840 1.00 ATOM 33.47 4252 CA ALA 550 79.848 9.566 12.337 1.00 ATOM 30.69 4253 CB ALA 550 79.555 10.509 13.497 1.00 ATOM 28.66 4254 C ALA 550 81.022 10.099 11,523 1.00 ATOM 30.41 4255 0 ALA 550 82.181 9.780 11.808 1.00 ATOM 29.13 4256 N CYS 551 80.695 10.817 10.446 1.00 30.29 ATOM 4258 CA CYS 551 81.675 11.490 9.584 1.00 ATOM 4259 28.44 CB CYS 551 81.432 11.214 8.096 1.00 ATOM 4260 27.25 SG CYS 551 81.639 9.508 7.566 1.00 ATOM 28.89 4261 C CYS 551 81.337 12.950 9.883 1.00 ATOM 27.07 4262 0 CYS 551 80.293 13.441 9.467 1.00 ATOM 29.86 4263 N THR 552 82.184 13.616 10.658 1.00 25.10 ATOM 4265 CA THR 552 81.952 14.997 11.047 1.00 MOTA 24.37 4266 CB THR 552 81.959 15.091 12.569 1.00 ATOM 27.67 4267 OG1 THR 552 83.271 14.760 13.052 1.00 MOTA 26.11 4269 CG₂ THR 552 80.951 14.120 13.164 1.00 ATOM 30.41 4270 C THR 552 83.003 15.980 10.557 1.00 ATOM 24.51 4271 О THR 552 82.804 17.194 10.604 1.00 ATOM 21.56 4272 N GLN 553 84.151 15.441 10.162 1.00 27.13 MOTA 4274 CA GLN 553 85.284 16.243 9.710 1.00 26.64 MOTA 4275 CB GLN 553 15.679 86.592 10.283 1.00 ATOM 25.24 4276 CG GLN 553 86.641 15.561 11.809 1.00 ATOM 22.38 4277 CD GLN 553 86.464 16.897 12.515 1.00 24.04 ATOM 4278 OE1 GLN 553 87.267 17.815 12.344 1.00 MOTA 31.50 4279 NE₂ GLN 553 85.403 17.017 13.304 1.00 ATOM 21.59 4282 C GLN 553 85.384 16.276 8.206 1.00 28.02

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MOTA	4283	0	GLN	553	85.069	15.293	7.537	1.00	30.20
ATOM	4284	N	ASP	554	85.794	17.430	7.695	1.00	28.08
MOTA	4286	CA	ASP	554	86.000	17.652	6.263	1.00	30.14
MOTA	4287	CB	ASP	554	87.330	<i>†</i> 17.034	5.833	1.00	29.82
MOTA	4288	CG	ASP	554	88.451	17.470	6.707	1.00	31.79
MOTA	4289	OD1	ASP	554	88.699	18.666	6.767	1.00	36.45
MOTA	4290	OD2	ASP	554	89.066	16.623	7.364	1.00	33.06
MOTA	4291	C	ASP	554	84.895	17.217	5.317	1.00	29.52
MOTA	4292	0	ASP	554	85.128	16.411	4.424	1.00	33.67
MOTA	4293	N	GLY	555	83.709	17.793	5.488	1.00	29.02
ATOM	4295	CA	GLY	555	82.586	17.476	4.621	1.00	26.05
MOTA	4296	C	GLY	555	81.286	17.447	5.405	1.00	23.80
MOTA	4297	0	GLY	555	81.269	17.751	6.597	1.00	24.09
ATOM	4298	N	PRO	556	80.175	17.117	4.740	1.00	23.29
ATOM	4299	CD	PRO	556	80.094	16.804	3.304	1.00	18.93
MOTA	4300	CA	PRO	556	78.860	17.045	5.378	1.00	23.45
MOTA	4301	CB	PRO	556	77.943	16.643	4.226	1.00	22.35
MOTA	4302	CG	PRO	556	78.889	15.931	3.261	1.00	24.94
MOTA	4303	С	PRO	556	78.806	16.019	6.503	1.00	26.66
MOTA	4304	0	PRO	556	79.488	14.984	6.464	1.00	27.76
MOTA	4305	N	LEU	557	78.006	16.324	7.522	1.00	29.14
ATOM	4307	CA	LEU	557	77.842	15.440	8.676	1.00	30.83
MOTA	4308	CB	LEU	557	77.173	16.181	9.842	1.00	28.40
MOTA	4309	ĆĠ	LEU	557	76.775	15.393	11.097	1.00	22.93
ATOM	4310	CD1	LEU	557	77.989	14.897	11.835	1.00	23.02
MOTA	4311	CD2	LEU	557	75.970	16.285	11.984	1.00	23.53
MOTA	4312	С	LEU	557	77.028	14.200	8.321	1.00	31.04
MOTA	4313	0	LEU	557	75.968	14.293	7.694	1.00	31.89
MOTA	4314	N	TYR	558.	77.552	13.041	8.700	1.00	29.88
MOTA	4316	CA	TYR	558	76.891	11.773	8.460	1.00	27.80
ATOM	4317	CB	TYR	558	77.741	10.878	7.562	1.00	28.04
ATOM	4318	CG	TYR	558	77.895	11.339	6.122	1.00	29.98
ATOM	4319	CD1	TYR	558	78.843	10.751	5.289	1.00	31.81
ATOM	4320	CE1	TYR	558	78.980	11.140	3.956	1.00	32.22
ATOM	4321	CD2	TYR	558	77.086	12.335	5.584	1.00	31.50
ATOM	4322	CE2	TYR	558	77.214	12.729	4.256	1.00	31.57
ATOM	4323	CZ	TYR	558	78.166	12.125	3.449	1.00	32.04
ATOM	4324	OH	TYR	558	78.317	12.511	2.134	1.00	33.34
ATOM	4326	C	TYR	558	76.715	11.099	9.809	1.00	27.34
ATOM	4327	0	TYR	558	77.678	10.937	10.558	1.00	25.80
MOTA	4328	N	VAL	559	75.464	10.798	10.147	1.00	28.06
ATOM	4330	CA	VAL	559	75.118	10.118	11.394	1.00	26.67
ATOM	4331	CB	VAL	559	73.930	10.816	12.129	1.00	26.22
ATOM	4332	CG1	VAL	559	73.590	10.079	13.425	1.00	22.58
ATOM	4333	CG2	VAL	559	74.298	12.278	12.440	1.00	23.09
ATOM	4334	C	VAL	559	74.745	8.715	10.943	1.00	24.32
MOTA	4335	0	VAL	559	73.665	8.464	10.412	1.00	26.37
ATOM	4336	N	ILE	560	75.689	7.815	11.095	1.00	23.63
ATOM	4338	CA	ILE	560	75.514	6.448	10.664	1.00	24.67
ATOM	4339	CB	ILE	560	76.901	5.859	10.299	1.00	24.62
ATOM	4340	CG2	ILE	560	76.753	4.507	9.646	1.00	30.13
MOTA	4341	CG1	ILE	560	77.627	6.810	9.326	1.00	21.87
MOTA	4342	CD1	ILE	560	79.114	6.538	9.162	1.00	22.25
ATOM	4343	C	ILE	560	74.814	5.621	11.737	1.00	27.30
ATOM	434J	-		200	,1.011	5.021	,_,	00	250

								•					
		344	0	ILE	560	75.3	06		_				
		345	N		561	73.6		5.50	_		1.00	28.	80
		347	CA		561	72.89		5.09	:		1.00	26.	80
		348	CB		561	71.5		4.27			1.00	26.	
		349	CG1		561	71.86		4.95			1.00	24.	
		350	CG2	_	561	70.67		6.20			1.00		
		351	C 1		561	72.57		5.25			1.00	21.9	
		352	7 0		561	72.85		2.90			1.00	27.9	
			N G		662	71.99		2.632	_		1.00	26.4	
			CA G		62	71.60		2.039	-		1.00	28.8	
AT	'OM 43	356 (62			0.685		19	1.00	28.2	
AT	OM 43	57 (62	71.09		-0.068			1.00	25.8	
AT	OM 43	58 (62	72.17		-0.392		24	1.00	27.0	
AT	OM 43	59 (· — -	_	62	71.64		-0.969			1.00	28.3	
AT	OM 43	60 C			62	72.389		1.714			1.00	33.3	
ATO	OM 43	61 C			62	70.49		0.665	16.09		1.00	31.60	
ATO	OM 43	62 O			52	70.529		0.720	11.17		1.00	29.67	
ATO	DM 436				53	69.581		1.489	11.28		1.00	32.53	
ATC	OM 436					70.666		0.126	10.16	_	1.00	30.70	
ATC	OM 436					69.699		0.209	9.08	_	L.00	30.65	
ATC						70.419		0.621	7.80		00		
ATO	M 436		D1 TY			69.510		0.905	6.63		.00	30.83	
ATO						68.545		0.018	6.23			32.10	
ATO						67.715	(0.227	5.16		.00	.33.24	
ATO	M 437					69.609	2	2.098	5.92		.00	34.65	
ATO				•		68.779	- 2	2.353	4.838	_	.00	31.04	
ATO				- •		67.831	1	.413	4.470		.00	33.12	
ATO			TYI			67.902	1	650	3.400		. 00	34.22	
ATON		_	TY			68.592	1	.223	9.406			34.76	
ATOM		-	ALA			68.855	-2	.325	9.884			34.39	
ATOM			ALA			67.356	-0	.861	9.091			34.87	
ATOM			ALA			66.212	-1	.726	9.324			35.49	
ATOM			ALA			65.213	-1	.000	10.210			35.41	
ATOM			ALA			65.585	-2	.056	7.962			35.93	
ATOM	4383					64.789	-1	.276	7.434			37.19	
ATOM			SER SER			65.931		211	7.401	1.		38.08	
ATOM	4386		SER			65.433	-3.	616	6.080	1.	_	37.14	
ATOM	4387		SER	565		66.151	-4.	88.1	5.614	1.	_	86.83	
ATOM	4389	C	SER	565		66.105	-5.	873	6.619	1.0		5.24	
ATOM	4390	0	SER	565		63.932	-3.	782	5.886	1.0		4.96	
ATOM	4391	N		565		63.428	-3.	617	4.760	1.0		8.65	
MOTA	4393	CA	LYS LYS	566		63.212	-4.	077	6.964	1.0		7.80 8.96	
ATOM	4394	CB		566		61.772	-4.	271	6.851	1.0			
ATOM	4395	CG	LYS	566		61.357	-5.	495	7.655	1.0	_	7.83	
ATOM	4396	CD	LYS	566		61.954	-б. [°]	765	7.078	1.0		9.07	
ATOM	4397	CE	LYS	566		61.813	~7.		7.996			3.73	
ATOM	4398	NZ	LYS	566		62.258	-9.2		7.299	1.0		7.07	
ATOM	4402	C	LYS	566	(52.361	-10.3		8.278	1.0	_	7.77	
ATOM	4403		LYS	566	•	50.899	-3.0		7.165	1.0		48	
ATOM	4404	O	LYS	566	5	9.702	-3.1		7.442	1.0		7.53	
ATOM	4406	N	GLY	567	ϵ	1.496	-1.8		7.066	1.00		.55	
ATOM	4406	CA	GLY	567		0.788	-0.6		7.305	1.00	_	.23	
ATOM	4407	C	GLY	567		0.120	-0.4		8.656	1.00	_	.64	
ATOM		0	GLY	567		0.518	-1.1		9.627	1.00		.24	
	4409	N	ASN	568		9.120	0.3			1.00		.80	
							5		9.716	1.00	31	.65	



MOTA	4411	CA	ASN	568	58.407	0.623	9.952	1.00	33.38
MOTA	4412	CB	ASN	568	57.831	2.055	10.025	1.00	37.10
MOTA	4413	CG	ASN	568	56.624	2.272	9.116	1.00	37.78
MOTA	4414	OD1	ASN	568	55.552	1.708	9.337	1.00	41.15
ATOM	4415	ND2	ASN	568	56.780	3.147	8.124	1.00	35.74
MOTA	4418	C	ASN	568	57.357	-0.435	10.263	1.00	33.33
ATOM	4419	0	ASN	568	56.917	-1.178	9.384	1.00	32.54
MOTA	4420	N	LEU	569	56.971	-0.490	11.532	1.00	33.35
MOTA	4422	CA	LEU	569	56.004	-1.455	12.040	1.00	32.38
MOTA	4423	CB	LEU	569	55.838	-1.263	13.552	1.00	27.50
MOTA	4424	CG	LEU	569	54.954	-2.259	14.291	1.00	26.34
MOTA	4425	CD1	LEU	569	55.452	-3.671	14.007	1.00	24.19
MOTA	4426	CD2	LEU	569	54.968	-1.951	15.787	1.00	21.44
ATOM	4427	C	LEU	569	54.641	-1.433	11.355	1.00	33.35
MOTA	4428	0	LEU	569	54.060	-2.484	11.095	1.00	34.99
ATOM	4429	N	ARG	570	54.130	-0.239	11.083	1.00	34.36
ATOM	4431	CA	ARG	570	52.827	-0.091	10.445	1.00	36.82
ATOM	4432	СВ	ARG	570	52.548	1.393	10.188	1.00	37.28
ATOM	4433	CG	ARG	570	51.210	1.689	9.539	1.00	43.90
ATOM	4434	CD	ARG	570	51.212	3.099	8.967	1.00	50.39
ATOM	4435	NE	ARG	570	52.273	3.268	7.973	1.00	54.99
ATOM	4437	CZ	ARG	570	53.075	4.328	7.887	1.00	54.96
ATOM	4438	NHl	ARG	570		5.343	8.735	1.00	54.71
ATOM	4441	NH2	ARG	570	54.030	4.357	6.966	1.00	56.12
ATOM	4444	С	ARG	570	52.818	-0.877	9.133	1.00	36.53
ATOM	4445	0	ARG	570	51.968	-1.737	8.909	1.00	34.68
ATOM	4446	N	GLU	571	53.830	-0.611	8.320	1.00	37.14
ATOM	4448	CA	GLU	571	53.994	-1.253	7.031	1.00	37.94
ATOM	4449	CB	GLU	571	55.126	-0.558	5.274	1.00	39.71
ATOM	4450	CG	GLU	571	54.834	0.916	6.062	1.00	44.69
ATOM	4451	CD	GLU	571	55.934	1.665	5.346	1.00	52.22
ATOM	4452	OE1	GLU	571	57.098	1.196	5.358	1.00	54.87
ATOM	4453	OE2	GLU	571	55.629	2.743	4.777	1.00	56.37
ATOM	4454	С	GLU	571	54.258	-2.744	7.164	1.00	36.53
ATOM	4455	0	GLU	571	53.692	-3.550	6.426	1.00	36.35
MOTA	4456	N	TYR	572	55.105	-3.105	8.120	1.00	35.77
MOTA	4458	CA	TYR	572	55.456	-4.499	8.371	1.00	36.28
MOTA	4459	CB	TYR	572	56.446	-4.555	9.534	1.00	30.27
ATOM	4460	CG	TYR	572	56.859	-5.925	10.006	1.00	31.65
MOTA	4461	CD1	TYR	572	57.889	-6.626	9.371	1.00	29.40
ATOM	4462	CE1	TYR	572	58.354	-7.839	9.883	1.00	29.32
MOTA	4463	CD2	TYR	572	56.292	-6.480	11.161	1.00	35.17
MOTA	4464	CE2	TYR	572	56.749	-7.696	11.680	1.00	33.08
ATOM	4465	CZ	TYR	572	57.780	-8.366	11.038	1.00	35.15
ATOM	4466	ОН	TYR	572	58.234	-9.559	11.558	1.00	36.91
MOTA	4468	С	TYR	572	54.189	-5.321	8.672	1.00	37.70
MOTA	4469	0	TYR	572	53.942	-6.369	8.068	1.00	36.82
ATOM	4470	N	LEU	573	53.368	-4.799	9.576	1.00	37.64
ATOM	4472	CA	LEU	573	52.126	-5.442	9.970	1.00	36.03
ATOM	4473	CB	LEU	573	51.497	-4.659	11.122	1.00	36.17
ATOM	4474	CG	LEU	573	52.257	-4.641	12.445	1.00	36.39
ATOM	4475	CD1	LEU	573	51.590	-3.665	13.412	1.00	36.17
ATOM	4476	CD2	LEU	573	52.311	-6.042	13.032	1.00	32.13
ATOM	4477	C	LEU	573	51.117	-5.562	8.822	1.00	36.33
		_	~			502			55.55



						200			
AT	OM 44	78 0	LE	EU 573	50.47	77 6 5	26		
AT	OM 44	79 N	GI		50.97				
ATO	OM 448	81 C <i>I</i>			50.02				
ATO	OM 448	32 CE			49.79		-		
ATO	OM 448	33 CG		_	48.89				43.82
ATO	OM 448	34 CD			48.87				45.42
ATO	OM 448	35 OE			49.45	-			49.56
ATC	OM 448	6 NE			48.20			_	52.22
ATC	M 448	9 C	GL		50.40				54.86
ATC	M 449	0 0	GL						42.89
ATO	M 449	1 N	AL	· · · -	49.53				46.15
ATO	M 449	3 CA	AL		51.69		_		42.39
ATO	M 449		ALA		52.16			2 1.00	40.19
ATO	M 449		ALA		53.59				40.68
ATO	M 449		ALA		52.088	_			40.49
ATO	M 449		ARG		52.437			1.00	43.34
ATO	M 449		ARG	•	51.630				38.76
ATOI	M 4500		ARG	· -	51.538			1.00	38.44
ATO	M 4501		ARG		52.600			1.00	34.26
ATON	4502		ARG		53.991				37.16
ATON	4503		ARG		55.052			1.00	36.38
ATOM	4505		ARG		56.384				36.98
ATOM					56.897			1.00	38.62
ATOM	1 4509				56.204				41.41
ATOM			ARG	_	58.112			1.00	37.48
ATOM			ARG	576 576	50.165			1.00	40.55
ATOM	4514		ARG	577	50.013	-10.746		1.00	43.20
ATOM			ARG	577	49.156	-9.146	6.844	1.00.	41.98
ATOM		CB	ARG	577	47.794	-9.372	7.309	1.00	43.12
ATOM	4518	CG	ARG	577	46.896	-8.226	6.851	1.00	44.21
ATOM	4519	CD	ARG	577	47.206	-6.910	7.525	1.00	45.21
ATOM		NE	ARG	577	46.402	-5.766	6.941	1.00	47.50
ATOM	4522	CZ	ARG	577	46.172	-4.734	7.948	1.00	47.58
ATOM	4523	NH1	ARG	577	45.447	-3.641	7.752	1.00	47.63
ATOM	4526	NH2	ARG	577	44.882	-3.421	6.574	1.00	49.05
ATOM	4529	C	ARG	577	45.256	-2.789	8.747	1.00	49.88
ATOM	4530	0	ARG	577	47.241	-10.715	6.821	1.00	43.10
MOTA	4531	N	GLN	594	47.297	-11.015	5.627	1.00	43.86
ATOM	4533	CA	GLN	594	53.448	-13.666	7.976	1.00	64.97
ATOM	4534	СВ	GLN	594	52.231	-13.872	8.759	1.00	66.30
ATOM	4535	C	GLN	594	51.419	-15.042	8.200		67.44
ATOM	4536	0	GLN	594	52.582	-14.116	10.224	1.00	66.02
ATOM	4537	N	LEU	595	53.162	-15.145	10.583		67.47
ATOM	4539	CA	LEU	595 595	52.218	-13.151	11.058		62.86
ATOM	4540	СВ	LEU	595 595	52.499	-13.187	12.480		59.77
ATOM	4541	CG	LEU	595 595	52.597	-11.751	12.987	_	59.35
ATOM	4542	CD1	LEU		53.471	-10.905	12.051	_	61.70
ATOM	4543	CD2	LEU	595 505	53.307	-9.427	12.322	_	64.61
ATOM	4544	C	LEU	595	54.923	-11.324	12.175	_	52.38
ATOM	4545	0	LEU	595	51.482	-13.985	13.290		57.49
ATOM	4546	И		595	50.302	-14.026	12.951		56.36
ATOM	4548	CA	SER	596	51.969	-14.647			55.62
ATOM	4549	CB	SER	596	51.134	-15.447			34.72
ATOM	4550		SER	596	51.905	-16.669			55.13
	1330	<u> </u>	SER	596	52.871	-16.309			4.98
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ATOM	4552	C	SER	596	50.723	-14.597	16.415	1.00	54.73	
MOTA	4553	0	SER	596	51.348	-13.579	16.704	1.00	53.29	
ATOM	4554	N	SER	597	49.704	-15.051	17.137	1.00	55.09	
MOTA	4556	CA	SER	597	49.215	-14.337	18.307	1.00	56.44	
ATOM	4557	CB	SER	597	48.178	-15.185	19.044	1.00	59.14	
MOTA	4558	OG	SER	597	47.455	-16.009	18.138	1.00	65.57	
MOTA	4560	С	SER	597	50.387	-14.026	19.238	1.00	55.64	
MOTA	4561	0	SER	597	50.430	-12.966	19.856	1.00	56.04	
MOTA	4562	N	LYS	598	51.345	-14.948	19.315	1.00	54.91	
ATOM	4564	CA	LYS	598	52.528	-14.773	20.161	1.00	54.25	
MOTA	4565	CB	LYS	598	53.287	-16.096	20.311	1.00	54.23	
MOTA	4566	CG	LYS	598	54.236	-16.138	21.494	1.00	55.12	
MOTA	4567	CD	LYS	598	55.009	-17.448	21.523	1.00	59.41	
ATOM	4568	CE	LYS	598	55.711	-17.679	22.858	1.00	58.10	
ATOM	4569	NZ	LYS	598	54.750	-17.983	23.959	1.00	56.10	
ATOM	4573	С	LYS	598	53.439	-13.716	19.536	1.00	52.32	
ATOM	4574	0	LYS	598	53.986	-12.869	20.249	1.00	52.23	
MOTA	4575	N	ASP	599	53.573	-13.768	18.208	1.00	47.57	
ATOM	4577	CA	ASP	599	54.389	-12.818	17.466	1.00	45.47	
ATOM	4578	CB	ASP	599	54.324	-13.101	15.959	1.00	49.05	
ATOM	4579	CG	ASP	599	55.245	-14.238	15.525	1.00	54.16	
ATOM	4580	OD1	ASP	599	56.242	-14.503	16.223	1.00	61.34	
ATOM	4581	OD2	ASP	599	54.992	-14.863	14.471	1.00	55.80	
MOTA	4582	C	ASP	599	53.933	-11.383	17.721	1.00	43.55	
ATOM	4583	0	ASP	599	54.762	-10.491	17.895	1.00	44.34	
ATOM	4584	N	LEU	600	52.622	-11.160	17.751	1.00	39.73	
ATOM	4586	CA	LEU	600	52.104	-9.821	17.989	1.00	37.64	
ATOM	4587	CB	LEU	600	50.597	-9.743	17,719	1.00	35.42	
ATOM	4588	CG	LEU	600	50.075	··9.951	16.287	1.00	33.95	
ATOM	4589	CD1	LEU	600	48.621	-9.552	16.262	1.00	36.59	
MOTA	4590	CD2	LEU	600	50.841	-9.139	15.265	1.00	28.40	
ATOM	4591	C	LEU	600	52.429	-9.347	19.402	1.00	38.24	
MOTA	4592	0	LEU	600	52.817	-8.193	19.590	1.00	38.28	
ATOM	4593	N	VAL	601	52.305	-10.235	20.391	1.00	38.77	
ATOM	4595	CA	VAL	601	52.610	-9.855	21.772	1.00	38.87	
ATOM	4596	CB	VAL	601	52.121	-10.906	22.812	1.00	38.03	
ATOM	4597	CG1	VAL	601	52.150	-10.303	24.223	1.00	36.21	
ATOM	4598	CG2	VAL	601	50.710	-11.332	22.504	1.00	39.07	
ATOM	4599	С	VAL	601	54.123	-9.662	21.887	1.00	38.98	
ATOM	4600	0	VAL	601	54.601	-8.757	22.580	1.00	39.93	
ATOM	4601	N	SER	602	54.861	-10.488	21.155	1.00	37.35	
ATOM	4603	CA	SER	602	56.311	-10.422	21.126	1.00	37.11	
ATOM	4604	CB	SER	602	56.853	-11.469	20.154	1.00	39.38	
ATOM	4605	OG	SER	602	58.265	-11.413	20.061	1.00	46.76	
ATOM	4607	C	SER	602	56.695	-9.020	20.664	1.00	35.43	
ATOM	4608	0	SER	602	57.493	-8.339	21.315	1.00	35.01	
MOTA	4609	N	CYS	603	56.091	-8.586	19.561	1.00	33.42	
MOTA	4611	CA	CYS	603	56.329	-7.254	19.015	1.00	32.18	
MOTA	4612	CB	CYS	603	55.449	-7.035	17.790	1.00	32.38	
MOTA	4613	SG	CYS	603	55.440	-5.365	17.123	0.50	35.11	PRT1
MOTA	4614	С	CYS	603	56.074	-6.167	20.059	1.00	31.20	
ATOM	4615	0	CYS	603	56.862	-5.234	20.185	1.00	32.44	
ATOM	4616	N	ALA	604	55.001	-6.321	20.828	1.00	29.74	
MOTA	4618	CA	ALA	604	54.640	-5.363	21.872	1.00	32.26	



ATOM	4619	CB	ALA	604	53.232	-5.675	22.412	1.00	31.75
ATOM	4620	С	ALA	604	55.656	-5.365	23.019	1.00	33.71
ATOM		0	ALA	604		-4.326	23.621	1.00	33.49
MOTA	4622	N	TYR	605	56.186	-6.544	23.326	1.00	35.56
ATOM	4624	CA	TYR	605	57.176	-6.709	24.388	1.00	35.49
ATOM	4625	CB	TYR	605	57.447	-8.206	24.617	1.00	36.12
ATOM	4626	CG	TYR	605	58.562	-8.495	25.591	1.00	34.75
ATOM	4627	CD1	TYR	605	58.415	-8.237	26.954	1.00	
ATOM	4628	CE1	TYR	605	59.444	-8.499	27.853	1.00	34.30 36.26
MOTA	4629	CD2	TYR	605	59.773	-9.021	25.150	1.00	
MOTA	4630	CE2	TYR	605	60.812	-9.288	26.040	1.00	37.39
ATOM	4631	CZ	TYR	605	60.641	-9.027	27.388	1.00	37.81
ATOM	4632	OH	TYR	605	61.662	-9.324	28.265	1.00	38.34
ATOM	4634	С	TYR	605	58.475	-5.972	24.027	1.00	42.09
ATOM	4635	Q	TYR	605	58.981	-5.171	24.822	1.00	34.98
ATOM	4636	N	GLN	606	58.996	-6.247	22.828	1.00	35.83
ATOM	4638	CA	GLN	606	60.218	-5.620	22.315	1.00	33.99 33.60
ATOM	4639	CB	GLN	606	60.506	-6.111	20.894	1.00	31.37
ATOM	4640	CG	GLN	606	60.858	-7.584	20.786	1.00	
MOTA	4641	CD	GLN	606	61.175	-8.015	19.354	1.00	32.05 30.33
ATOM	4642	OE1	GLN	606	62.145	-7.558	18.754	1.00	
ATOM	4643	NE2	GLN	606	60.353	-8.895	18.810	1.00	30.84
ATOM	4646	C	GLN	606	60.123	-4.079	22.321	1.00	33.75
ATOM	4647	O	GLN	606	61.070	-3.390	22.702	1.00	34.86 37.54
ATOM	4648	N	VAL	607	58.975	-3.555	21.904	1.00	32.89
MOTA	4650	CA	VAL	607	58.748	-2.114	21.883	1.00	30.80
MOTA	4651	CB	VAL	607	57.426	-1.777	21.120	1.00	28.82
MOTA	4652	CG1	VAL	607	57.121	-0.299	21.191	1.00	25.36
MOTA	4653	CG2	VAL	607	57.541	-2.204	19.661	1.00	23.37
ATOM	4654	C	VAL	607	58.747	-1.532	23.312	1.00	30.48
ATOM	4655	O	VAL	607	59.359	-0.485	23.563	1.00	29.42
MOTA	4656	N	ALA	608	58.106	-2,225	24.255	1.00	30.07
MOTA	4658	CA	ALA	608	58.064	-1.761	25.646	1.00	30.14
MOTA	4659	CB	ALA	608	57.027	-2.548	26.452	1.00	28.49
MOTA	4660	С	ALA	608	59.455	-1.849	26.305	1.00	31.25
MOTA	4661	0	ALA	608	59.791	-1.054	27.198	1.00	28.90
MOTA	4662	N	ARG	609	60.257	-2.819	25.870	1.00	31.61
MOTA	4664	CA	ARG	609	61.608	-2.979	26.393	1.00	31.99
ATOM	4665	CB	ARG	609	62.253	-4.245	25.856	1.00	34.93
ATOM	4666	CG	ARG	609	61.606	-5.507	26.317	1.00	40.82
ATOM	4667	CD	ARG	609	62.633	-6.606	26.397	1.00	42.68
ATOM	4668	NE	ARG	609	63.275	-6.621	27.705	1.00	43.85
ATOM	4670	CZ	ARG	609	64.332	-7.364	28.019	1.00	44.73
MOTA	4671	NH1	ARG	609	64.889	-8.162	27.108	1.00	41.40
ATOM	4674	NH2	ARG	609	64.803	-7.341	29.260	1.00	44.85
ATOM	4677	C	ARG	609	62.459	-1.796	25.966	1.00	33.70
MOTA	4678	0	ARG	609	63.130	-1.174	26.793	1.00	35.94
MOTA	4679	N	GLY	610	62.459	-1.511	24.663	1.00	31.22
MOTA	4681	CA	GLY	610	63.232	-0.391	24.157	1.00	27.21
MOTA	4682	C	GLY	610	62.819	0.875	24.865	1.00	25.81
MOTA	4683	0	GLY	610	63.665	1.652	25.300	1.00	26.21
MOTA	4684	N	MET	611	61.511	1.056	25.015	1.00	27.12
MOTA	4686	CA	MET	611	60.969	2.222	25.695	1.00	28.82
MOTA	4687	CB	MET	611	59.457	2.288	25.524	1.00	29.29
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MOTA	4688	CG	MET	611	59.004	2.706	24.135	1.00	31.07
MOTA	4689	SD	MET	611	59.732	4.286	23.617	1.00	28.38
MOTA	4690	CE	MET	611	59.155	5.431	24.922	1.00	28.34
MOTA	4691	С	MET	611	61.341	2.261	27.178	1.00	30.34
MOTA	4692	0	MET	611	61.596	3.334	27.730	1.00	31.73
ATOM	4693	N	GLU	612	61.347	1.109	27.837	1.00	32.72
MOTA	4695	CA	GLU	612	61.723	1.057	29.253	1.00	35.46
MOTA	4696	CB	GLU	612	61.603	-0.370	29.792	1.00	34.70
MOTA	4697	CG	GLU	612	62.029	-0.516	31.237	1.00	32.31
MOTA	4698	CD	GLU	612	62.135	-1.968	31.688	1.00	33.14
MOTA	4699	OE1	GLU	612	62.546	-2.834	30.883	1.00	30.79
MOTA	4700	OE2	GLU	612	61.826	-2.240	32.867	1.00	36.13
ATOM	4701	C	GLU	612	63.178	1.544	29.353	1.00	36.43
ATOM	4702	0	GLU	612	63.534	2.319	30.261	1.00	35.38
ATOM	4703	N	TYR	613	63.999	1.107	28.391	1.00	35.47
ATOM	4705	CA	TYR	613	65.403	1.507	28.334	1.00	33.16
MOTA	4706	CB	TYR	613	66.156	0.743	27.241	1.00	31.33
MOTA	4707	CG	TYR	613	67.612	1.146	27.132	1.00	33.03
MOTA	4708	CD1	TYR	613	68.584	0.544	27.931	1.00	36.69
MOTA	4709	CE1	TYR	613	69.930	0.927	27.851	1.00	36.82
MOTA	4710	CD2	TYR	613	68.021	2.148	26.247	1.00	33.49
MOTA	4711	CE2	TYR	613	69.352	2.540	26.157	1.00	34.73
MOTA	4712	CZ	TYR	613	70.307	1.927	26.963	1.00	37.07
MOTA	4713	OH	TYR	613	71.632	2.318	26.896	1.00	36.77
ATOM	4715	С	TYR	613	65.539	3.005	28.088	1.00	31.82
ATOM	4716	0	TYR	613	66.256	3.682	28.814	1.00	34.76
ATOM	4717	N	LEU	614	64.836	3.536	27.090	1.00	28.44
MOTA	4719	CA	LEU	614	64.931	4.956	26.793	1.00	25.67
MOTA	4720	CB	LEU	614	64.089	5.319	25.569	1.00	24.75
MOTA	4721	CG	LEU	614	64.545	4.778	24.208	1.00	23.73
MOTA	4722	CD1	LEU	614	63.594	5.257	23.125	1.00	20.54
MOTA	4723	CD2	LEU	614	65.983	5.213	23.894	1.00	23.21
MOTA	4724	C	LEU	614	64.499	5.761	28.001	1.00	28.30
MOTA	4725	0	LEU	614	65.110	6.770	28.345	1.00	27.09
MOTA	4726	И	ALA	615	63.470	5.272	28.683	1.00	32.73
MOTA	4728	CA	ALA	615	62.955	5.945	29.871	1.00	34.10
MOTA	4729	CB	ALA	615	61.625	5.314	30.314	1.00	33.68
MOTA	4730	C	ALA	615	63.986	5.913	31.007	1.00	33.84
MOTA	4731	0	ALA	615	64.112	6.885	31.753	1.00	34.95
MOTA	4732	N	SER	616	64.722	4.809	31.134	1.00	32.69
MOTA	4734	CA	SER	616	65.738	4.703	32.175	1.00	33.50
MOTA	4735	CB	SER	616	66.287	3.277	32.285	1.00	28.27
MOTA	4736	OG	SER	616	67.076	2.935	31.165	1.00	25.54
MOTA	4738	C	SER	616	66.870	5.678	31.865	1.00	35.43
ATOM	4739	0	SER	616	67.637	6.061	32.755	1.00	37.32
MOTA	4740	N	LYS	617	66.971	6.060	30.592	1.00	34.80
MOTA	4742	CA	LYS		67.975	7.010	30.143	1.00	33.01
ATOM	4743	CB	LYS	617	68.508	6.620	28.776	1.00	33.18
MOTA	4744	CG	LYS	617	69.224	5.302	28.797	1.00	35.64
MOTA	4745	CD	LYS	617	70.423	5.380	29.710	1.00	40.31
MOTA	4746	CE	LYS	617	71.075	4.025	29.863	1.00	43.03
MOTA	4747	NZ	LYS	617	72.426	4.152	30.449	1.00	45.54
MOTA	4751	C	LYS	617	67.360	8.397	30.102	1.00	32.87
MOTA	4752	0	LYS	617	67.892	9.308	29.470	1.00	34.06

MOTA 4753 N LYS 618 66.221 8.542 30.772 1.00 33.53 MOTA 4755 CA LYS 618 65.500 9.808 30.872 1.00 33.28 ATOM 4756 CB LYS 618 66.384 10.842 31.558 1.00 37.22 ATOM 4757 CG LYS 618 66.968 10.367 32.869 1.00 43.11 MOTA 4758 CD LYS 618 65.927 10.278 33.957 1.00 49.82 MOTA 4759 CE LYS 618 66.520 9.636 35.199 1.00 55.20 MOTA 4760 NZ LYS 618 65.669 9.853 36.415 1.00 61.31 ATOM 4764 С LYS 618 65.012 10.359 29.542 1.00 31.57 MOTA 4765 0 LYS 618 64.651 11.530 29.455 1.00 31.10 ATOM 4766 N CYS 619 64.953 9.506 28.524 1.00 31.04 ATOM 4768 CA CYS 619 64.519 9.922 27.196 1.00 29.21 MOTA 4769 CB CYS 619 65.213 9.065 26.125 1.00 28.55 MOTA 4770 SG CYS 619 64.782 9.400 24.392 1.00 26.31 MOTA 4771 C CYS 619 62.999 9.849 27.051 1.00 30.91 MOTA 4772 0 CYS 619 62.376 8.827 27.364 1.00 31.18 MOTA 4773 N ILE 620 62.411 10.967 26.632 1.00 29.48 ATOM 4775 CA ILE 620 60.981 11.073 26.416 1.00 29.34 ATOM 4776 CBILE 620 60.402 12.344 27.060 1.00 28.12 ATOM 4777 CG2 ILE 620 58.944 12.535 26.645 1.00 28.76 MOTA 4778 CG1 ILE 620 60.521 12.267 28.581 1.00 28.36 MOTA 4779 CD1 ILE 620 60.062 13.522 29.270 1.00 25.55 ATOM 4780 C ILE 620 60.852 11.188 24.908 1.00 30.97 ATOM 4781 0 ILE 620 61.254 12.193 24.336 1.00 33.88 ATOM 4782 N HIS 621 60.307 10.147 24.284 1.00 31.55 ATOM 4784 CA HIS 621 60.148 10.080 22.831 1.00 31.85 ATOM 4785 CB HIS 621 59.721 8.668 22.425 1.00 28.27 ATOM 4786 CG HIS 521 59.913 8.373 20.979 1.00 24.68 **ATOM** 4787 CD2 HIS 621 60.608 7.383 20.356 1.00 24.39 MOTA 4788 ND1 HIS 621 59.354 .9.130 19.973 1.00 25.87 ATOM 4790 HIS CE1 621 59.691 8.623 . 18.798 1.00 27.65 ATOM 4791 NE₂ HIS 621 60.444 7.571 19.007 1.00 25.80 ATOM 4793 C HIS 621 59.187 11.096 22.224 1.00 34.38 ATOM 4794 0 HIS 621 59.387 11.539 21.104 1.00 38.74 ATOM 4795 N ARG 622 58.080 11.374 22.898 1.00 37.17 MOTA 4797 CA ARG 622 57.093 12.346 22.425 1.00 37.27 ATOM 4798 CBARG 622 57.718 13.746 22.298 1.00 38.63 MOTA 4799 CG ARG 622 58.261 14.271 23.601 1.00 40.47 ATOM 4800 CD ARG 622 58.661 15.739 23.530 1.00 44.76 ATOM 4801 NE ARG 622 59.129 16.174 24.842 1.00 52.09 ATOM 4803 CZARG 622 60.299 15.821 25.375 1.00 56.86 ATOM 4804 NH1 ARG 622 61.132 15.041 24.699 1.00 61.20 MOTA 4807 NH2 ARG 622 60.606 16.167 26.624 1.00 58.19 ATOM 4810 C ARG 622 56.324 11.994 21.151 1.00 37.23 ATOM 4811 0 ARG 622 55.300 12.614 20.867 1.00 38.45 MOTA 4812 N ASP 623 56.805 11.035 20.364 1.00 36.55 ATOM 4814 CA ASP 623 56.075 10.652 19.160 1.00 36.52 ATOM 4815 CB ASP 623 56.581 11.403 17.910 1.00 39.68 ATOM 4816 CG ASP 623 55.635 11.247 16.687 1.00 48.75 MOTA 4817 OD1 ASP 623 56.077 11.491 15.538 1.00 49.98 ATOM 4818 OD2 ASP 623 54.445 10.879 16.872 1.00 49.65 MOTA 4819 C ASP 623 56.126 9.143 18.967 1.00 33.37 MOTA 4820 О ASP 623 56.325 8.650 17.864 1.00 31.77 ATOM 4821 N LEU 624 55.999 8.404 20.059 1.00 30.45 **ATOM** 4823 CA LEU 624 56.014 6.954 19.950 1.00 30.77

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4824 CB LEU 624 55.983 6.307 21.342 1.00 27.43 ATOM 4.778 21.441 1.00 28.69 4825 CG LEU 624 55.949 ATOM 1.00 4826 CD1 LEU 624 57.139 4.132 20.731 24.75 MOTA 4827 CD2 LEU 624 . 55.927 4.389 22.894 1.00 27.39 MOTA LEU 6.532 19.109 1.00 MOTA 4828 С 624 54.803 31.22 ATOM 4829 0 LEU 624 53.680 6.952 19.380 1.00 33.44 ATOM 4830 N ALA 625 55.053 5.763 18.054 1.00 28.85 ALA 625 54.009 5.286 17.159 1.00 26.93 MOTA 4832 CA CB ATOM 4833 ALA 625 53.559 6.400 16.227 1.00 25.03 625 16.356 1.00 ATOM 4834 С ALA 54.642 4.162 28.44 625 4.065 16.317 1.00 MOTA 4835 0 ALA 55.863 31.32 MOTA 4836 N ALA 626 53.828 3.329 15.705 1.00 29.14 ATOM 4838 CA ALA 626 54.344 2.205 14.905 1.00 28.42 ATOM 4839 CB ALA 626 53.192 1.357 14.353 1.00 27.37 MOTA 4840 C ALA 626 55.231 2.698 13.771 1.00 26.38 ATOM 4841 О ALA 626 56.195 2.041 13.395 1.00 26.12 MOTA 4842 ARG 627 54.890 3.861 13.230 1.00 27.16 MOTA 4844 CA ARG 627 55.669 4.474 12.158 1.00 28.44 4845 CB ARG 627 5.794 11.733 1.00 28.19 ATOM 55.022 **ATOM** 4846 CG ARG 627 54.889 6.793 12.867 1.00 30.34 ATOM 4847 CD ARG 627 54.456 8.155 12.361 1.00 34.08 **ATOM** 4848 NE ARG 627 54.081 9.024 13.471 1.00 35.58 ATOM 4850 CZARG 627 52.849 9.123 13.950 1.00 35.55 MOTA 4851 NH1 ARG 627 51.860 8.422 13.420 1.00 35.67 ATOM 4854 NH2 ARG 627 52.618 9.898 14.993 1.00 40.81 MOTA 4857 С ARG 627 57.108 4.733 12.630 1.00 28.06 MOTA 4858 0 ARG 627 58.044 4.737 11.825 1.00 29.80 MOTA 4859 Ν ASN 628 57.272 4.935 13.940 1.00 28.50 MOTA 4861 CA ASN 628 58.582 5.195 14.544 1.00 26.14 MOTA 4862 CB ASN 628 58.494 6.340 15.551 1.00 23.55 MOTA 4863 CG ASN 628 58.319 7.681 14.874 1.00 27.48 MOTA 4864 OD1 ASN 628 58.874 7.919 13.800 1.00 34.12 ATOM 4865 ND2 ASN 628 57.543 8.556 15.479 1.00 23.21 MOTA 4868 С ASN 628 59.263 3.965 15.153 1.00 26.76 MOTA 4869 0 ASN 628 60.202 4.078 15.948 1.00 26.90 MOTA 4870 N VAL 629 58.774 2.794 14.767 1.00 27.02 MOTA 4872 CA VAL 629 59.344 1.523 15.186 1.00 27.81 MOTA 4873 CB VAL 629 58.298 0.622 15.864 1.00 26.83 MOTA 4874 CG1 VAL 629 58.876 -0.766 16.115 1.00 20.74 MOTA 4875 CG2 VAL 629 57.836 1.259 17.165 1.00 22.49 VAL 629 59.781 0.895 13.861 1.00 28.61 MOTA 4876 C MOTA 4877 О VAL 629 58.983 0.809 12.924 1.00 28.76 630 61.059 0.557 13.746 1.00 MOTA 4878 N LEU 30.35 MOTA 4880 CA LEU 630 61.576 -0.033 12.514 1.00 32.42 ATOM LEU 62.824 0.725 12.040 1.00 32.28 4881 CB 630 **ATOM** 4882 LEU 630 62.697 2.249 11.880 1.00 27.75 CG LEU 630 64.019 2.860 11.469 1.00 24.71 MOTA 4883 CD1 1.00 4884 CD2 LEU 630 2.582 10.872 27.70 ATOM 61.611 **ATOM** 4885 LEU 630 61.895 -1.488 12.799 1.00 32.89 C O LEU 630 -1.838 13.943 1.00 32.32 MOTA 4886 62.167 1.00 ATOM N VAL 631 -2.336 11.774 34.81 4887 61.831 ATOM 4889 CA VAL 631 62.087 -3.772 11.943 1.00 33.87 ATOM 4890 CB VAL 631 60.818 -4.616 11.597 1.00 31.60 VAL -6.004 1.00 30.84 MOTA 4891 CG1 631 60.929 12.197

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VAL -3.916 12.089 1.00 CG2 631 59.545 25.53 MOTA 4892 VAL 631 -4.256 11.109 1.00 MOTA 4893 C 63.286 34.95 VAL -4.009 9.892 1.00 ATOM 4894 0 631 63.365 37.01 11.770 1.00 MOTA 4895 N THR 632 64.215 -4.942 35.08 THR 1.00 MOTA 4897 CA 632 65.418 -5.444 11.104 35.96 4898 THR -5.711 12.116 1.00 MOTA CB 632 66.541 34.29 4899 OG1 THR 12.953 1.00 MOTA 632 66.187 -6.818 32.35 4901 CG2 THR 66.750 -4.488 12.985 1.00 MOTA 632 33.42 4902 C THR 632 -6.712 10.300 1.00 MOTA 65.162 39.32 4903 0 THR 632 64.078 -7.302 10.382 1.00 MOTA 41.24 GLU 4904 633 66.153 -7.123 9.511 1.00 42.32 MOTA Ν MOTA 4906 CA GLU 633 66.030 -8.335 8.703 1.00 44.34 MOTA 4907 CB GLU 633 67.314 -8.609 7.912 1.00 46.06 GLU -9.767 6.898 1.00 MOTA 4908 CG 633 67.205 49.87 MOTA 4909 CD GLU 633 66.380 -9.445 5.629 1.00 53.04 1.00 MOTA 4910 OE1 GLU 633 65.637 -8.430 5.570 51.31 1.00 MOTA 4911 OE₂ GLU 633 66.479 -10.226 4.667 55.48 MOTA 4912 C GLU 633 65.708 -9.526 9.600 1.00 44.58 MOTA 4913 0 GLU 633 64.974 -10.423 9.207 1.00 46.56 44.12 MOTA 4914 N ASP 634 66.201 -9.493 10.833 1.00 4916 ASP 65.961 -10.583 11.759 1.00 MOTA CA 634 44.23 12.580 ATOM 4917 CB ASP 634 67.221 -10.867 1.00 50.17 ASP 11.697 1.00 MOTA 4918 CG 634 68.443 -11.181 56.79 OD1 ASP -12.113 10.857 1.00 59.62 MOTA 4919 634 68.363 1.00 MOTA 4920 OD2 ASP 634 69.482 -10.490 11.837 58.62 MOTA 4921 C ASP 634 64.756 -10.331 12.644 1.00 43.26 MOTA 4922 0 ASP 634 64.652 -10.879 13.733 1.00 43.58 MOTA 4923 N ASN 635 63.858 -9.475 12.166 1.00 43.97 MOTA 4925 CA ASN 635 62.612 -9.126 12.847 1.00 43.66 MOTA 4926 CB ASN 635 61.698 -10.355 12.930 1.00 46.94 MOTA 4927 CG ASN 635 61.413 -10.958 11.572 1.00 48.19 MOTA 4928 OD1 ASN 635 60.831 -10.314 10.702 1.00 51.42 MOTA 4929 ND2 ASN 635 61.832 -12.198 11.380 1.00 49.44 MOTA 4932 C ASN 635 62.694 -8.463 14.216 1.00 43.03 MOTA 4933 0 ASN 635 61.774 -8.596 15.031 1.00 43.03 ATOM 4934 VAL 63.763 -7.712 14.467 1.00 N 636 42.69 MOTA 4936 CA VAL 636 63.915 -7.034 15.756 1.00 38.30 ATOM 4937 CB VAL 636 65.406 -6.861 16.134 1.00 37.92 MOTA 4938 CG1 VAL 636 65.555 -6.040 17.421 1.00 37.14 ATOM 4939 CG2 VAL 636 66.052 -8.226 16.306 1.00 37.55 ATOM 4940 C VAL 636 63.251 -5.673 15.688 1.00 35.75 ATOM 4941 0 VAL 636 63.486 -4.926 14.746 1.00 36.28 16.628 1.00 MOTA 4942 N MET 637 62.355 -5.396 34.73 637 -4.103 16.680 1.00 ATOM 4944 CA MET 61.672 33.22 637 17.608 1.00 MOTA 4945 CB MET 60.456 -4.152 34.83 17.231 1.00 MOTA 4946 CG MET 637 59.364 -5.148 34.41 MOTA 4947 MET 637 -4.926 15.589 1.00 SD 58.661 33.19 4948 CE MET -6.584 14.913 1.00 MOTA 637 58.869 29.73 4949 MET -3.107 17.250 1.00 MOTA С 637 62.677 33.75 -3.357 18.308 1.00 MOTA 4950 0 MET 637 63.281 31.79 -1.980 16.558 1.00 MOTA 4951 N LYS 638 62.839 31.83 MOTA 4953 CA LYS 638 63.774 -0.939 16.965 1.00 28.17 CB LYS 638 -0.930 16.038 1.00 MOTA 4954 64.986 24.98 LYS 638 -1.967 16.400 1.00 ATOM 4955 CG 66.006 23.17

MOTA	4956	CD	LYS	638	67.193	-1.916	15.470	1.00	25.04
MOTA	4957	CE	LYS	638	68.212	-2.969	15.847	1.00	24.79
ATOM	4958	NZ	LYS	638	68.747	-2.765	17.220	1.00	24.91
MOTA	4962	C	LYS	638	63.165	0.445	16.986	1.00	26.04
MOTA	4963	0	LYS	638	62.803	0.958	15.936	1.00	24.44
MOTA	4964	N	ILE	639	63.052	1.031	18.181	1.00	25.14
MOTA	4966	CA	ILE	639	62.508	2.376	18.351	1.00	25.68
MOTA	4967	CB	ILE	639	62.589	2.863	19.839	1.00	27.40
MOTA	4968	CG2	ILE	639	61.875	4.189	19.984	1.00	,18.94
MOTA	4969	CG1	ILE	639	62.019	1.827	20.826	1.00	26.05
MOTA	4970	CD1	ILE	639	60.517	1.667	20.792	1.00	25.07
MOTA	4971	C	ILE	639	63.387	3.338	17.543	1.00	25.82
MOTA	4972	0	ILE	639	64.619	3.283	17.642	1.00	25.76
MOTA	4973	N	ALA	640	62.758	4.231	16.783	1.00	25.92
ATOM	4975	CA	ALA	640	63.477	5.218	15.976	1.00	26.12
MOTA	4976	CB	ALA	640	63.222	4.964	14.506	1.00	26.54
ATOM	4977	С	ALA	640	63.042	6.643	16.344	1.00	26.33
MOTA	4978	Ο.	ALA	640	61.996	6.828	16.974	1.00	26.20
ATOM	4979	Ŋ	ASP	641	63.863	7.637	15.993	1.00	26.59
ATOM	4981	CA	ASP	641	63.545	9.052	16.245	1.00	28.09
MOTA	4982	CB	ASP	641	62.217	9.443	15.593	1.00	31.43
ATOM	4983	CG	ASP	641	62.346	9.762	14.107	1.00	36.81
ATOM	4984	OD1	ASP	641	63.409	9.478	13.500	1.00	40.24
ATOM	4985	OD2	ASP	641	61.356	10.299	13.548	1.00	40.49
MOTA	4986	C	ASP	641	63.455	9.442	17.700	1.00	28.40
ATOM	4987	0	ASP	641	62.825	10.446	18.041	1.00	29.30
ATOM	4988	N CA	PHE PHE	642 642	64.080	8.658	18.564	1.00	30.27
ATOM ATOM	4990 4991	CB	PHE	642	64.044 64.327	8.943 7.664	19.992 20.787	1.00 1.00	30.97 24.64
ATOM	4992	CG	PHE	642	65.673	7.063	20.767	1.00	20.96
ATOM	4993	CD1	PHE	642	66.812	7.539	21.163	1.00	16.89
ATOM	4994	CD2	PHE	642	65.806	6.026	19.576	1.00	16.23
ATOM	4995	CE1	PHE	642	68.072	6.990	20.900	1.00	18.35
ATOM	4996	CE2	PHE	642	67.051	5.471	19.305	1.00	18.76
ATOM	4997	CZ	PHE	642	68.195	5.954	19.970	1.00	17.91
ATOM	4998	C	PHE	642	65.024	10.045	20.414	1.00	34.53
MOTA	4999	0	PHE	642	64.990	10.503	21.563	1.00	35.23
ATOM	5000	N	GLY	643	65.910	10.433	19.500	1.00	36.40
MOTA	5002	CA	GLY	643	66.888	11.455	19.799	1.00	38.28
ATOM	5003	С	GLY	643	66.634	12.768	19.093	1.00	41.44
ATOM	5004	0	GLY	643	67.482	13.652	19.132	1.00	44.10
ATOM	5005	N	LEU	644	65.461	12.921	18.484	1.00	45.44
MOTA	5007	CA	LEU	644	65.131	14.144	17.748	1.00	49.14
ATOM	5008	CB	LEU	644	63.832	13.975	16.969	1.00	46.26
MOTA	5009	CG	LEU	644	63.823	12.967	15.836	1.00	42.90
ATOM	5010	CD1	LEU	644	62.527	13.134	15.070	1.00	42.68
ATOM	5011	CD2	LEU	644	65.004	13.228	14.934	1.00	45.15
MOTA	5012	С	LEU	644	65.027	15.396	18.605	1.00	53.90
MOTA	5013	0	LEU	644	64.488	15.356	19.715	1.00	56.54
ATOM	5014	N	ALA	645	65.534	16.505	18.068	1.00	57.59
MOTA	5016	CA	ALA	645	65.505	17.794	18.759	1.00	60.15
MOTA	5017	CB	ALA	645	66.539	18.741	18.156	1.00	59.55
MOTA	5018	С	ALA	645	64.112	18.407	18.667	1.00	61.90
MOTA	5019	0	ALA	645	63.393	18.500	19.663	1.00	63.83

ATOM	5020	N	ASP	652	52.090	22.191	14.865	1.00	89.91
ATOM	5022	CA	ASP	652	50.913	22.199	14.007	1.00	89.75
ATOM	5023	CB	ASP	652	51.314	22.428	12.537	1.00	88.08
ATOM	5024	CG	ASP	652	50.109	22.557	11.607	1.00	87.09
ATOM	5025	OD1	ASP	652	49.028	22.996	12.052	1.00	86.85
ATOM	5026	OD2	ASP	652	50.252	22.222	10.411	1.00	86.69
ATOM	5027	C	ASP	652	50.145	20.890	14.156	1.00	89.98
ATOM	5028	0	ASP	652	50.434	19.899	13.483	1.00	90.19
ATOM	5029	N	TYR	653	49.145	20.905	15.027	1.00	90.26
ATOM	5031	CA	TYR	653	48.318	19.730	15.277	1.00	90.78
MOTA	5032	CB	TYR	653	47.272	20.048	16.344	1 00	91.65
MOTA	5033	CG	TYR	653	47.804	20.185	17.755	1.00	93.43
ATOM ATOM	5034 5035	CD1 CE1	TYR	653	47.017	20.757	18.752	1.00	94.60
ATOM	5035		TYR	6.53	47.477	20.885	20.058	1.00	95.35
ATOM	5037	CD2 CE2	TYR	653	49.083	19.738	18.101	1.00	93.46
ATOM	5037	CZ	TYR	653	49.558	19.860	19.406	1.00	94.36
ATOM	5038	OH	TYR TYR	653	48.748	20.435	20.378	1.00	95.26
MOTA	5041	C		653	49.220	20.554	21.669	1.00	95.00
ATOM	5041	0	TYR	653 653	47.602	19.231	14.021	1.00	90.47
ATOM	5042	И	TYR TYR	653	47.045	18.131	14.012	1.00	91.33
ATOM	5045	CA	TYR	654 654	47.632	20.031	12.962	1.00	89.21
ATOM	5045	CB	TYR	654 654	46.954	19.673	11.727	1.00	89.09
ATOM	5040	CG CG		654 654	46.205	20.893	11.188	1.00	88.23
ATOM	5047	CD1	TYR TYR	654		., 21.499	12.209	1.00	87.65
ATOM	5049	CE1	TYR	654 654	45.776	22.140	13.343	1.00	86.76
ATOM	5050	CD2	TYR	654	44.929 43.895	22.655		1.00	87.17
ATOM	5050 5051	CE2	TYR	654	43.895	21.396	12.067	1.00	88.61
ATOM	5052	CZ	TYR	654	43.557	21.912	13.033	1.00	89.32
ATOM	5053	ОН	TYR	654	42.710	22.538 23.034	14.153	1.00	88.66
ATOM	5055	. c	TYR	654	47.857	19.080	15.117	1.00	89.39
ATOM	5056	Ö	TYR	654	47.396	18.772	10.651 9.552	1.00	89.49
ATOM	5057	N	LYS	655	49.139	18.919	10.959	1.00 1.00	88.37 90.80
ATOM	5059	CA	LYS	655	50.056	18.356	9.982	1.00	93.18
ATOM	5060	СВ	LYS	655	51.508	18.713	10.311	1.00	95.66
ATOM	5061	CG	LYS	655	52.504	18.133	9.315	1.00	99.82
ATOM	5062	CD	LYS	655	53.932	18.585	9.562	1.001	
ATOM	5063	CE	LYS	655	54.898	17.833	8.637	1.001	
ATOM	5064	NZ	LYS	655	56.325	18.246	8.821	1.001	
MOTA	5068	С	LYS	655	49.884	16.847	9.935	1.00	93.56
ATOM	5069	0	LYS	655	49.904	16.182	10.972	1.00	93.72
MOTA	5070	N	LYS	656	49.670	16.320	8.735	1.00	94.19
MOTA	5072	CA	LYS	656	49.500	14.886	8.545	1.00	94.84
MOTA	5073	CB	LYS	656	48.628	14.620	7.320	1.00	94.64
ATOM	5074	CG	LYS	656	47.155	14.874	7.542	1.00	95.54
MOTA	5075	CD	LYS	656	46.402	14.709	6.241	1.00	99.56
ATOM	5076	CE	LYS	656	44.926	14.449	6.473	1.0010	
ATOM	5077	NZ	LYS	656	44.202	14.327	5.173	1.0010	
MOTA	5081	С	LYS	656	50.859	14.225	8.368	1.00	95.18
ATOM	5082	0	LYS	656	51.823	14.878	7.956	1.00	95.74
ATOM	5083	N	GLY	660	48.651	9.665	5.782	1.00	58.76
MOTA	5085	CA	GLY	660	47.932	10.910	6.012	1.00	56.04
ATOM	5086	С	GLY	660	47.241	10.937	7.364	1.00	53.90
MOTA	5087	0	GLY	660	46.183	11.552	7.525	1.00	53.92
									

ATOM	5088	N	ARG	661	47.838	10.243	8.328	1.00	51.87
ATOM	5090	CA	ARG	661	47.297	10.177	9.679	1.00	48.23
ATOM	5091	CB	ARG	661	47.755	8.891	10.377	1.00	49.74
ATOM	5092	CG	ARG	661	47.506	7.620	9.566	1.00	47.59
ATOM	5093	CD	ARG	661	47.561	6.390	10.446	1.00	51.85
ATOM	5094	NE	ARG	661	47.584	5.155	9.663	1.00	52.94
ATOM	5096	CZ	ARG	661	48.035	3.988	10.117	1.00	52.19
ATOM	5097	NH1	ARG	661	48.503	3.884	11.356	1.00	52.10
ATOM	5100	NH2	ARG	661	48.036	2.926	9.327	1.00	54.43
ATOM	5103	С	ARG	661	47.722	11.401	10.483	1.00	43.67
ATOM	5104	0	ARG	661	48.658	12.103	10.104	1.00	41.45
ATOM	5105	N	LEU	662	47.019	11.656	11.579	1.00	40.27
ATOM	5107	CA	LEU	662	47.310	12.799	12.437	1.00	37.15
ATOM	5108	СВ	LEU	662	46.021	13.533	12.783	1.00	37.39
ATOM	5109	CG	LEU	662	45.301	14.149	11.588	1.00	
ATOM	5110	CD1	LEU	662	43.852	14.428	11.937	1.00	35.38
ATOM	5111	CD2	LEU	662	46.041	15.407	11.163	1.00	39.79
ATOM	5112	С	LEU	662	47.973	12.330	13.716	1.00	34.68
ATOM	5113	0	LEU	662	47.327	11.718	14.568	1.00	33.33
ATOM	5114	N	PRO	663	49.260	12.655	13.892	100	34.11
MOTA	51 15	CD	PRO	663	50.086	13.389	12.924	1.00	33.67
ATOM	5116	CA	PRO	663	50:052	12.281	15.068	1.00	33.55
ATOM	5117	СВ	PRO	663	51.367	13.003	14.833	1.00	32.99
ATOM	5118	CG	PRO	663	51.479	12.966	13.328	1.00	36.09
MOTA	5119	C	PRO	663	49.412	12.665	16.399	1.00	33.55
ATOM	5120	0	PRO	663	49.683	1.2.036	17.426	1.00	34.11
ATOM	5121	N	VAL .	664	48.566	13.697	16.387	1.00	32.63
ATOM	5123	CA	VAL	664	47.874	14.092	17.613	1.00	32.24
ATOM	5124	CB	VAL	664	46.953	15.327	17.396	1.60	33.24
ATOM	5125	CG1	VAL	664	47.779	16.583	17.252	1.00	35.01
ATOM	5126	CG2	VAL	664	46.089	15.154	16.155	1.00	35.44
MOTA	5127	C	VAL	664	47.072	12.896	18.150	1.00	31.08
MOTA	5128	0	VAL	664	46.866	12.760	19.360	1.00	31.49
ATOM	5129	N	LYS	665	46.710	11.978	17.255	1.00	29.75
ATOM	5131	CA	LYS	665	45.956	10.788	17.638	1.00	28.83
ATOM	.5132	СВ	LYS	665	45.411	10.083	16.397	1.00	29.52
ATOM	5133	CG	LYS	665	44.242	10.835	15.797	1.00	27.21
MOTA	5134	CD	LYS	665	43.905	10.431	14.397	1.00	27.25
ATOM	51 35	CE	LYS	665	42.684	11.228	13.931	1.00	28.63
ATOM	5136	NZ	LYS	665	42.266	10.902	12.545	1.00	25.33
ATOM	5140	С	LYS	665	46.718	9.830	18.537	1.00	29.03
ATOM	5141	0	LYS	665	46.152	8.869	19.046	1.00	28.37
MOTA	5142	N	TRP	666	47.994	10.123	18.765	1.00	30.40
ATOM	5144	CA	TRP	666	48.825	9.296	19.628	1.00	31.10
ATOM	5145	СВ	TRP	666	50.123	8.906	18.917	1.00	29.53
ATOM	5146	CG	TRP	666	49.946	7.781	17.966	1.00	27.03
ATOM	5147	CD2	TRP	666	49.407	7.853	16.638	1.00	25.06
MOTA	5148	CE2	TRP	666	49.418	6.546	16.116	1.00	23.83
ATOM	5149	CE3	TRP	666	48.924	8.899	15.835	1.00	26.08
ATOM	5150	CD1	TRP	666	50.257	6.475	18.186	1.00	20.75
ATOM	5151	NE1	TRP	666	49.937	5.729	17.086	1.00	24.92
ATOM	5153	CZ2	TRP	666	48.962	6.245	14.832	1.00	23.95
ATOM	5154	CZ3	TRP	666	48.466	8.604	14.548	1.00	29.09
ATOM	5155	CH2	TRP	666	48.491	7.282	14.060	1.00	29.22
									·

							2/0					
A	TOM 5	156	C	TRP	666	40 -						
A'		157		TRP	666	49.1		10.049		96 1.	00 3	3.20
A'	TOM 5	158		MET		49.7		9.469	21.8			4.39
A:	TOM 5			MET	667	48.86		11.340	20.9		_	4.82
				MET	667	49.16		12.175	22.0			
					667	49.20)5 1	.3.645				6.31
				/ET	667	50.47	'5 1	4.047				0.08
				/ET	667	50.55		5.818				2.41
			~	IET	667	50.95		5.928				1.31
			_	ET	667	48.29		2.003				5.44
				ET	667	47.08		1.871	23.28			7.81
	_		1 A	LA	668	48.95		1.964	23.19			.91
AT			CA A	LA	668	48.28			24.44		0 36	.47
ATC	_		B A	LA	668	49.30		1.846	25.71		0 37	.06
ATO		71 C	A	_	668	47.548		1.654	26.83		0 35	.76
AT(72 O	A		668	48.000		3.161	25.89		0 38	.76
ATO	DM 51	73 N			669			201	25.41			.04
ATO		74 C	_		569	46.416		.142	26.60	8 1.0	_	.60
ATC	DM 51	75 C.			569	45.819		.981	27.282	2 1.0		.64
ATC	M 517				69	45.614		.347	26.84	1 1.0		
ATO	M 517			_		44.478		.827	27.718			
ATO		-	PR	_	69	44.383		.368	27.325			
ATO				-	69	46.390	15.	. 486	27.526			
ATO		_	PR	-	69	46.304		.644	27.111			
ATO			GL	-	70	47.135		.164	28.580			
ATO				_	70	47.905		.195	29.266			
ATO				_	70	48.596		637	30.509	_		
ATO				_	70	49.858		819	30.243			
ATON				J 6'	70	49.588		345		_		
ATOM				J 6'	70	50.512		552	30.070			
	-		2 GLU	J 67	70	48.458		975.	30.327	1.00		
ATOM			GLU	7 67	70	48.942			29.700	1.00	52.7	70
ATOM		_	GLU	67	70	49.174		802	28.320	1.00	45.6	;3
ATOM			ALA			49.546	18.		28.340	1.00	44.7	['] 5
ATOM		CA	ALA			50.555	15.		27.482	1.00	46.1	
ATOM		CB	ALA			51.218	16.		26.531	1.00	46.4	
ATOM		C	ALA				15.2		25.860	1.00	43.2	
ATOM		0	ALA			49.931	17.3		25.483	1.00	47.8	
ATOM	5196	N	LEU			50.485	18.3		25.150	1.00	47.6	
ATOM	5198	CA	LEU	67:		48.748	16.9	928 2	25.018	1.00	51.4	
ATOM	5199	CB	LEU	672		48.010	17.6		23.990	1.00	54.29	
ATOM	5200	CG	LEU			46.996	16.7	05 2	23.346	1.00	55.60	
ATOM	5201	CD1	LEU	672		46.202	17.1		2.105	1.00	58.92	
ATOM	5202	CD2		672		47.114	17.4		0.932	1.00		
ATOM	5203		LEU	672		45.269	15.9		1.753		58.60	
ATOM	5204	C	LEU	672		47.315	18.9		4.514	1.00	60.32	
ATOM	5205	0	LEU	672		47.289	19.9		3.837	1.00	55.91	
ATOM		N	PHE	673		46.782	18.84		5.730	1.00	55.72	
	5207	CA	PHE	673		46.089	19.9			1.00	57.88	
ATOM	5208	CB	PHE	673		44.873	19.48		6.342	1.00	60.07	
ATOM	5209	CG	PHE	673		43.876			7.127	1.00	57.08	
ATOM	5210	CD1	PHE	673		43.191	18.74			1.00	56.39	
ATOM	5211	CD2	PHE	673		43.633	17.65		5.813	1.00	57.67	
ATOM	5212	CE1	PHE	673			19.11			1.00	55.36	
ATOM	5213	CE2	PHE	673		42.281	16.93				57.42	
ATOM	5214	CZ	PHE	673		42.724	18.41				55.91	
ATOM	5215	C	PHE			42.049	17.31				56.42	
		-		673	4	16.974	20.85				63.00	
SSSD/55	145 v01								-		-3.00	



MOTA	5216	0	PHE	673	46.926	22.085	27.155	1.00	65.31
ATOM	5217	N	ASP	674	47.786	20.223	28.081	1.00	64.08
MOTA	5219	CA	ASP	674	48.656	20.954	28.999	1.00	64.97
MOTA	5220	CB	ASP	674	48.545	20.375	30.409	1.00	65.13
ATOM	5221	CG	ASP	674	47.128	20.358	30.923	1.00	67.33
ATOM	5222	OD1	ASP	674	46.684	19.283	31.372	1.00	66.68
ATOM	5223	OD2	ASP	674	46.462	21.416	30.869	1.00	69.20
MOTA	5224	С	ASP	674	50.132	20.971	28.603	1.00	66.38
MOTA	5225	0	ASP	674	50.984	21.304	29.434	1.00	68.44
MOTA	5226	N	ARG	675	50.441	20.585	27.365	1.00	65.68
MOTA	5228	CA	ARG	675	51.829	20.550	26.883	1.00	63.71
ATOM	5229	CB	ARG	675	52.321	21.970	26.576	1.00	63.67
MOTA	5230	CG	ARG	675	51.491	22.685	25.531	1.00	67.65
MOTA	5231	CD	ARG	675	52.094	24.034	25.146	1.00	73.20
MOTA	5232	NE	ARG	675	53.382	23.911	24.457	1.00	74.09
MOTA	5234	CZ	ARG	675	54.159	24.939	24.122	1.00	73.41
MOTA	5235	NH1	ARG	675	53.788	26.182	24.408	1.00	72.90
MOTA	5238	NH2	ARG	675	55.324	24.720	23.524	1.00	71.96
MOTA	5241	С	ARG	675	52.780	19.864	27.876	1.00	61.41
MOTA	5242	0	ARG	675	53.960	20.208	27.966	1.00	62.62
MOTA	5243	N	ILE	676	52.248	18.903	28.627	1.00	59.15
MOTA	5245	CA	ILE	676	53.016	18.162	29.623	1.00	56.88
ATOM	5246	CB	ILE	676	52.175	17.904	30.891	1.00	56.26
MOTA	5247	CG2	ILE	675	52.871	16.904	31.807	1.00	53.11
MOTA	5248	CG1	ILE	676	51.920	19.224	31.614	1.00	57.86
MOTA	5249	CD1	ILE	676	51.038	19.096	32.835	1.00	61.05
MOTA	5250	C	ILE	676	53.494	16.828	29.070	1.00	56.58
MOTA	5251	0	ILE	676	52.727	15.869	28.985	1.00	58.12
MOTA	5252	N	TYR	677	54.760	16.773	28.680	1.00	54.34
MOTA	5254	CA	TYR	677	55.340	15.556	28.143	1.00	51.14
MOTA	5255	CB	TYR	677	56.240	15.868	26.954	1.00	52.37
MOTA	5256	CG	TYR	677	55.488	16.315	25.719	1.00	56.21
ATOM	5257	CD1	TYR	677	55.187	17.660	25.512	1.00	56.78
ATOM	5258	CE1	TYR	677	54.534	18.086	24.353	1.00	57.54
MOTA	5259	CD2	TYR	677	55.113	15.395	24.738	1.00	57.82
ATOM	5260	CE2	TYR	677	54.458	15.809	23.571	1.00	59.32
MOTA	5261	CZ	TYR	677	54.177	17.159	23.385	1.00	59.59
MOTA	5262	OH	TYR	677	53.557	17.589	22.230	1.00	60.15
MOTA	5264	C	TYR	677	56.124	14.854	29.224	1.00	48.64
MOTA	5265	0	TYR	677	57.040	15.430	29.812	1.00	50.45
ATOM	5266	N	THR	678	55.733	13.621	29.510	1.00	44.59
MOTA	5268	CA	THR	678	56.397	12.834	30.524	1.00	42.21
MOTA	5269	СВ	THR	678	55.524	12.726	31.791	1.00	43.55
ATOM	5270	OG1	THR	678	54.302	12.045	31.475	1.00	47.42
ATOM	5272	CG2	THR	678	55.190	14.105	32.327	1.00	48.74
ATOM	5273	C	THR	678	56.634	11.432	29.992	1.00	39.94
MOTA	5274	0	THR	678	56.207	11.085	28.892	1.00	39.34
ATOM	5275	N	HIS	679	57.312	10.616	30.784	1.00	38.54
ATOM	5277	CA	HIS	679	57.532	9.248	30.390	1.00	38.29
MOTA	5278	CB	HIS	679	58.441	8.546	31.391	1.00	39.51
ATOM	5279	CG	HIS	679	59.869	8.997	31.331	1.00	43.13
ATOM	5280	CD2	HIS	679	60.630	9.668	32.233	1.00	43.49
MOTA	5281	ND1	HIS	679	60.694	8.726	30.263	1.00	43.00
MOTA	5283	CE1	HIS	679	61.903	9.201	30.510	1.00	43.62



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1	MOTA	5284	NE2	HIS	670	_					
P	MOTA	5286	C	HIS	679 679	92.00		778 3	1.695	1.00	11 60
A	TOM !	5287	0	HIS	679	30.19	7 8.		0.359	1.00	
A	TOM	5288	N	GLN	680	22.03			9.593	1.00	
A	TOM 5	5290	CA	GLN		55.22	8. 9.		1.142	1.00	40.00
A	TOM 5	291	СВ	GLN	680	53.86			1.209	1.00	38.96
A ^c	TOM 5	292	CG		680	53.21	49.		2.543		38.84
A'		293		GLN	680	53.83	58.		3.732	1.00	40.90
	~~.			GLN	680	53.67	76.		3.660	1.00	44.42
				GLN	680	52.59			3.908	1.00	44.47
			_	GLN	680	54.767	6.0		3.348	1.00	45.52
			_	GLN	680	53.013				1.00	42.06
				GLN	680	51.968			.036	1.00	38.25
				SER	681	53.427			.758	1.00	39.27
				SER	681	52.665			.349	1.00	37.00
				ER	681	52.929			.182	1.00	38.02
AT	•••		OG S	ER	681	54.307			.813	1.00	40.29
ATO		06 (: s	ER	681	53.066			.620	1.00	47.29
ATO		07 C) s	ER	681	52.289	9.6		.051	1.00	37.43
ATO		08 M	A		682	54.281	9.36		136	1.00	37.86
ATO		_	A A		682		9.0		162	1.00	35.23
ATC		11 C	B A		682	54.800	8.10			1.00	33.24
ATC		12 C			682	56.284	7.82	26.			31.85
ATO		13 OI	DI AS		582	57.224	8.73	2 25.			34.18
ATO		L4 O.	02 AS		582	58.445	8.53	7 25.		_	31.79
ATO		.5 C	AS		82	56.763	9.62	0 24.			
ATO	M 531		AS		82	54.015	6.81	0 26.	_		29.15
ATO	M 531	7 <u>N</u>	VA		83	53.788	6.08	7 25.			31.52
ATO	M 531					53.653	6.49	9 27.6			31.93
ATON	1 532				83	52.879	5.29	3 27.9			33.14
ATOM	1 532				83	52.725	5.095	5 29.4			32.79
ATOM	532			-	83	51.653	4.059	29.7			4.55
ATOM			VA:	_	83	54.050	4.649				2.39
ATOM		-			83	51.506	5.338				8.08
ATOM		_	VAI		33	51.008	4.311				1.45
MOTA	5327		TRI			50.919	6.531				0.37
ATOM			TRI			49.638	6.686				1.04
ATOM	5329		TRE			49.158	8.137				1.23
ATOM	5330		TRE			47.913	8.423	25.69			1.14
ATOM	5331					46.573	8.593	26.18			7.17
ATOM	5332			68	4	45.755	8.888			00 38	1.61
ATOM	5333	CE3	TRP	68		45.978	8.528	25.06			.91
ATOM	5334	CD1	TRP	68		47.850	8.612	27.45			.63
ATOM		NE1	TRP	684	4	46.560	8.894	24.33		00 37	.39
ATOM	5336	CZ2	TRP	684	1	44.380	9.118	23.95		00 34	.76
ATOM	5337	CZ3	TRP	684	Į.	44.611		25.18			. 79
	5338	CH2	TRP	684		43.830	8.759	27.56			. 53
ATOM	5339	C	TRP	684		49.876	9.048	26.42			. 59
ATOM	5340	0	TRP	684		49.254	6.294	25.01		0 29.	
ATOM	5341	N	SER	685		50.815	5.356	24.503	3 1.0		
ATOM	5343	CA	SER	685			6.992	24.380	1.0		
ATOM	5344	CB	SER	685		51.174	6.738	22.986	1.0		
ATOM	5345	OG	SER	685		2.444	7.504	22.631	_	_	
ATOM	5347	C	SER	685		2.355	8.874	22.986			
ATOM	5348	0	SER			1.399	5.249	22.737			
MOTA	5349	N	PHE	685		0.968	4.709	21.713			
			- 41E	686	5	2.065		23.676	1.00		
SSSD/551	145. v01							•	4.00	26.4	± 7

MOTA	5351	CA	PHE	686	52.325	3.151	23.563	1.00	26.35
MOTA	5352	CB	PHE	686	53.167	2.668	24.754	1.00	25.01
MOTA	5353	CG	PHE	686	53.447	1.182	24.742	1.00	27.24
MOTA	5354	CD1	PHE	686	54.187	0.600	23.712	1.00	24.88
MOTA	5355	CD2	PHE	686	52.915	0.351	25.729	1.00	24.99
MOTA	5356	CE1	PHE	686	54.389	-0.783	23.655	1.00	22.77
ATOM	5357	CE2	PHE	686	53.113	-1.036	25.679	1.00	28.39
MOTA	5358	CZ	PHE	686	53.853	-1.601	24.631	1.00	22.71
ATOM	5359	C	PHE	686	50.997	2.366	23.466	1.00	28.82
MOTA	5360	0	PHE	686	50.892	1.398	22.696	1.00	26.41
MOTA	5361	N	GLY	687	49.988	2.797	24.229	1.00	29.65
MOTA	5363	CA	GLY	687	48.692	2.134	24.194	1.00	29.88
ATOM	5364	С	GLY	687	48.099	2.158	22.794	1.00	29.57
MOTA	5365	o	GLY	687	47.560	1.165	22.300	1.00	30.38
MOTA	5366	N	VAL	688	48.222	3.310	22.147	1.00	29.19
MOTA	5368	CA	VAL	688	47.718	3.478	20.795	1.00	25.09
MOTA	5369	CB	VAL	688	47.747	4.956	20.359	1.00	22.52
MOTA	5370	CG1	VAL	688	47.106	5.115	18.985	1.00	21.13
MOTA	5371	CG2	VAL	688	47.001	5.810	21.366	1.00	22.50
MOTA	5372	С	VAL	688	48.574	2.636	19.865	1.00	23.82
ATOM	5373	0	VAL	688	48.080	2.132	18.871	1.00	25.39
MOTA	5374	N	LEU	689	49.849	2.463	20.208	1.00	24.46
MOTA	5376	CA	LEU	689	50.764	1.655	19.401	1.00	25.68
ATOM	5377	CB	LEU	689	52.222	1.893	19.834	1.00	25.93
MOTA	5378	CG	LEU	689	53.374	1.307	19.004	1.00	25.01
ATOM	5379	CD1	LEU	689	54.655	2.080	19.257	1.00	25.86
ATOM	5380	CD2	LEU	689	53.593	-0.145	19.318	1.00	24.90
MOTA	5381	C	LEU	689 .	50.374	0.171	19.531	1.00	26.50
MOTA	5382	0	LEU	689	50.464	-0.578	18.558	1.00	27.13
MOTA	5383	И	LEU	690	49.927	-0.234	20.724	1.00	27.76
MOTA	5385	CA	LEU	690	49.481	-1.610	20.980	1.00	28.59
MOTA	5386	CB	LEU	690	49.087	-1.800	22.447	1.00	30.38
MOTA	5387	CG	LEU	690	50.121	-2.065	23.545	1.00	29.57
MOTA	5388	CD1	LEU	690	49.435	-1.966	24.907	1.00	27.40
MOTA	5389	CD2	LEU	690	50.744	-3.431	23.360	1.00	28.79
MOTA	5390	C	LEU	690	48.242	-1.849	20.134	1.00	28.77
MOTA	5391	0	LEU	690	48.055 .	-2.922	19.573	1.00	28.07
ATOM	5392	N	TRP	691	47.383	-0.838	20.075	1.00	29.58
MOTA	5394	CA	TRP	691	46.166	-0.921	19.275	1.00	30.53
MOTA	5395	CB	TRP	691	45.327	0.349	19.451	1.00	28.28
MOTA	5396	CG	TRP	691	43.985	0.300	18.769	1.00	25.86
ATOM	5397	CD2	TRP	691	43.702	0.689	17.421	1.00	23.99
MOTA	5398	CE2	TRP	691	42.321	0.498		1.00	25.08
MOTA	5399	CE3	TRP	691	44.487	1.165	16.367	1.00	20.88
MOTA	5400	CD1	TRP	691	42.791	-0.090	19.314	1.00	23.72
MOTA	5401	NE1	TRP	691	41.786	0.031	18.389	1.00	26.15
ATOM	5403	CZ2	TRP	691	41.704	0.788	15.997	1.00	25.07
MOTA	5404	CZ3	TRP	691	43.883	1.448	15.163	1.00	22.80
ATOM	5405	CH2	TRP	691	42.501	1.251	14.982	1.00	24.95
MOTA	5406	С	TRP	691	46.566	-1.116	17.811	1.00	30.63
MOTA	5407	0	TRP	691	45.943	-1.892	17.093	1.00	33.02
MOTA	5408	N	GLU	692	47.625	-0.431	17.386	1.00	31.00
MOTA	5410	CA	GLU	692	48.130	-0.545	16.018	1.00	29.00
MOTA	5411	CB	GLU	692	49.285	0.426	15.778	1.00	26.55

		412	CG	GLU 69	2 48.87	73 7 0	76		
			CD (GLU 69	,				29.90
		414	OE1 (GLU 69	01				29.83
		415	OE2 (GLU 69					32.18
		1 16 (2 (GLU 69					31.57
		117 () (ELU 69:			_		29.02
AT		118 1	_	LE 69	-01	_			29.22
AT	OM 54	20 (LE 693					29.54
ATO	-	21 (LE 693	-2.750		_		31.01
ATO	OM 54	22 C		LE 693					32.36
ATO	OM 54	23 C		LE 693	02.000				34.39
ATC		24 C		LE 693					30.30
ATC	OM 54	25 C		LE 693				2 1.00	25.66
ATC		26 O		LE 693	-0.050				30.63
ATO	M 54:	27 N		HE 694	40.033			1.00	31.10
ATO		29 C			-7.044			1.00	32.60
ATO		30 CI			46.543			1.00	33.86
ATO	M 543	31 C			45.938	_		1.00	35.66
ATO	M 543				46.941	-6.499			35.70
ATO	M 543	3 CI			47.460	-5.684		1.00	37.18
ATOI	M 543				47.449	-7.794		1.00	34.37
ATO	M 543				48,473	-6.150	21.392	1.00	36.90
ATON	M 543				48.456	-8.265	20.255	1.00	31.89
ATOM	1 543		PH		48.970	-7.446	21.234	1.00	34.95
ATOM	1 543		PH		45.532	-5.576	16.049	1.00	34.26
ATOM	1 543	9 N	THI		44.702	-6.442	15.787	1.00	37.52
ATOM	544	l CA			45.636	-4.441	15.359		32.23
ATOM	5442	2 CB	THE		44.775	-4.160	14.215		28.08
ATOM		G:				-2.728	14.241		25.71
ATOM	5445	CG2		•	45.237	-1.762	14.228		24.94
ATOM	5446	С	THR		43.353	-2.528	15.468		23.07
ATOM	5447	0	THR		45.615	-4.348	12.955		27.53
ATOM	5448	N	LEU	•	45.166	-4.066	11.845		30.89
MOTA	5450	CA	LEU		46.833	-4.848	13.145		27.73
ATOM	5451	CB	LEU		47.781	-5.081	12.061		8.99
ATOM	5452	CG	LEU		47.370	-6.297	11.226		7.78
ATOM	5453	CD1		696	47.379	-7.591	12.047		9.89
MOTA	5454	CD2	LEU	696	47.251	-8.823	11.164		9.96
MOTA	5455	C	LEU	696	48.668	-7.656	12.803		0.20
ATOM	5456	0	LEU	696	48.044	-3.853	11.179		0.33
ATOM	5457	N	GLY	697	48.006	-3.926	9.948	_	9.41
ATOM	5459	CA	GLY	697	48.374 48.655	-2.738	11.831		0.92
MOTA	5460	C	GLY	697		-1.503	11.113		0.35
ATOM	5461	0	GLY	697	47.420	-0.650	10.912		0.65
MOTA	5462	N	GLY	698	47.359		10.000		0.01
ATOM	5464	CA	GLY	698	46.428		11.772		0.50
MOTA	5465	C	GLY	698	45.209		11.656).36
MOTA	5466	Ó	GLY	698	45.416	1.415	11.930		0.07
ATOM	5467	N	SER	699	46.320	1.809			.56
MOTA	5469	CA	SER	699	44.554				.65
ATOM	5470	CB	SER		44.597	3.674		_	.42
ATOM	5471	OG	SER	699	44.263				.61
ATOM	5473	C	SER	699	43.960				.25
MOTA	5474	o	SER	699	43.621			_	.25
	_	-	Car	699	42.406				.14
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			1.682 13.675 1.00 29.29
лиом 5475 N	PRO 700		1.682 13.073
AIOM 31.	PRO 700		1.867 13.22
ATOM 5476 CD	PRO 700		5.155 14.70
ATOM 5477 CA	PRO 700		5.624 15.525 1 00 27.85
ATOM 5478 CB	PRO 700	45.531	5.982 14.500
ATOM 5479 CG	PRO 700	42.413	6.305 14.500 - 21.38
ATOM 5480 C	PRO 700	42.800	7.096 13.110
ATOM 5481 O		41.204	6.357 14.032
ATOM 5482 N		40.246	7.419 14.545
ATOM 5484 CA		40.559	8.64/
ATOM 5485 CB		40.321	8.413 10.000
ATOM 5486 CG		41.323	8.638 17.000
ATOM 5487 CD1		41.092	8.412 19.130
ATOM 5488 CE1		39.084	7.965 17.31
ATOM 5489 CD2	T.O.1	38.845	7.738 18.033 -
ATOM 5490 CE2		39.845	7.963 17.57
ATOM 5491 CZ	TYR 701	39.584	7.716 20.307
ATOM 5492 OH	TYR 701	40.173	7.829 13.000
ATOM 5494 C	TYR 701	40.356.	9.001 12.760 1.00 29.03
ATOM 5495 O	TYR 701	39.901	6.867 12.191 1.00 28.05
ATOM 5496 N	PRO 702	39.671	5.430 12.417 1.00 26.30
ATOM 5497 CD	PRO 702	39.815	- 103 10 764 1.00. 27.40
ATOM 5498 CA	PRO 702	39.610	5.807 10.119 1.00 27.00
ATOM 5499 CB	PRO 702	39.610	5.036 11.169 1.00 28.28
ATOM 5500 CG		38.689	2 145 10 440 1.00 26.81
ATOM 5501 C	PRO 702		7.953 10.865 1.00 28.20
ATOM 5502 O	PRO 702	37.554	9 693 1.00 28.48
ATOM 5503 N	GLY 703	39.035	10 217 9.295 1.00 26.54
ATOM 5505 CA		38.085	11 285 10.351 1.00 28.03
ATOM 5506 C	GLY 703	37.862	10 227 10 108 1.00 28.93
ATOM 5507 O	GLY 703	37.110	22 240 11 505 1.00 28.16
ATOM 5508 N	VAL 704	38.518	12 001 12 619 1.00 29.55
ATOM 5510 C	A VAL 704	38.369	13 984 1.00 28.50
ATOM 5511 C	B VAL 704	38.473	12 350 15.135 1.00 28.07
AIOM 5522	G1 VAL 704	38.330	12 205 14 091 1.00 29.78
ATOM SOL	G2 VAL 704	37.403	12 588 1.00 32.00
AIOI.	1	39.375	13.227
AIOM 5524	701	40.578	13.020
AION 3325	-DO 70E	38.888	11 906 1.00 33.69
AION 5525	D PRO 705	37.512	14.703 22.65
AIOM SSE	CA PRO 705	39.745	200 34 10
	CB PRO 705	38.863	10.04, 1 00 36 38
ATOM 33-	CG PRO 705	37.478	10.430 1 00 33 22
ATOM SSE	C PRO 705	40.164	10.001
AION	O PRO 705	39.549	15.700 14.000
AIOM 5522	704	5 41.198	16.912 13
AION 33-1			17.41/ 14.55
ATOM 5525			18.52/ 14.07
ATOM 5526		403	18.941 15.957 1.00
ATOM 5527			18.038 13.670 1.00 12.0
ATOM 5528			17.934 15.969 1.00 38 42
ATOM 5529	~~~~ 70		17.536 17.136 1.00 40 43
ATOM 5530	O VAL 70	02/	1 18.796 15.517 1.00 40.43
ATOM 5531	N GLU 70		3 19.375 16.395 1.00 40.00
ATOM 5533	CA GLU 70	07	1E 621 L.UU 43.40
ATOM 5534	CB GLU 70	07 37.97.	-

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Z	MOTA	5535	С	GLU	707	77.0					
P	MOTA	5536	0	GLU	707	37.5		316 17	.028	1.00	41.03
A	TOM !	5537	N	GLU	708			370 18	.231	1.00	41.52
A	TOM 9	5539	CA	GLU.		37.5			.224	1.00	41.62
		540	_	GLU	708	36.70			. 700	1.00	
		541			708	36.13	79 15.		523		41.06
		_		GLU	708	35.28	31 16.		571	1.00	45.19
		-		GLU	708	34.06	16.	-	258	1.00	48.74
	_			GLU	708	33.52				1.00	57.18
				GLU	708	33.64			207	1.00	54.30
				3LU	708	37.44				1.00	61.76
				3LU	708	36.86	_	-		1.00	38.39
			N I	EU	709	38.72				1.00	36.76
		54.9 (CA I	ĿΕU	709					1.00	37.78
ΑT	'OM 55	550 (ΈU	709	39.55	-			1.00	38.13
AT	OM 55	51 0		ΕU	709	41.00		55 17.8		1.00	35.45
AT	OM 55					41.984		60 18.7		1.00	
AT	_				709	41.825		49 18.7		00	35.57
AT		_			709	43.407	7- 13.9				32.33
ATO		_	_		709	39.550	14.9			.00	31.98
ATO	- •				709	39.362	14.2			.00	38.31
				HE .	710	39.776				.00	38.16
ATC					710	39.807			_	.00	40.09
ATC		59 CI	B PF	IE 7	10	39.997		_			43.61
ATC		50 C	G PF		10	41.328					48.22
ATC		51 CI	01 PH		10						51.77
ATO	M 556	2 CI			10	42.395	17.93		31 1		52.94
ATO	M 556	3 CE			10	41.513	20.07				53.99
ATO	M 556			`		43.632	18.27	5 19.67			
ATO	M 556			-	10	42.746	20.42	2 19.02			6.48
ATO					10	43.807	19.51				55.72
ATO		_	PH.		10	38.519	16.72		_		7.84
ATON		_	PH		LO	38.539	16.424				3.35
ATON		_	LY	S '7:	L1	37.399	16.804		_		3.22
ATOM			LYS	3 71	1	36.095	16.587		_	-	4.68
ATOM			LYS	71	.1	34.977	16.878			_	3.47
			LYS	71	1	33.601				00 4	4.33
ATOM			LYS	71	1	32.510	16.765			00 4	7.63
ATOM			LYS			31.158	17.206			00 4	9.97
ATOM		NZ	LYS				16.873				1.70
MOTA		_	LYS			30.038	17.412	20.150	1.0		7.55
MOTA	5580	0	LYS			35.986	15.173	22.261	1.0		2.72
ATOM	5581	N	LEU		_	35.589	14.999	23.420			16
ATOM	5583	CA	LEU			36.392	14.176	21.471	1.0		
ATOM	5584	СВ	LEU	712		36.361	12.770	21.898			.52
ATOM	5585	CG		712		36.922	11.843	20.809		_	.52
ATOM	5586		LEU	712		36.090	11.528	19.560			.56
ATOM	5587	CD1	LEU	712	:	36.902	10.620	18.636	1.0		.87
ATOM		CD2	LEU	712		34.760	10.868		1.0		.28
	5588	C	LEU	712		37.158		19.951	1.00		.19
ATOM	5589	0	LEU	712		36.697	12.564	23.180	1.00		. 34
ATOM	5590	N	LEU	713		38.366	11.886	24.107	1.00	40	
ATOM	5592	CA	LEU	713			13.121	23.208	1.00		
ATOM	5593	CB	LEU	713		39.240	13.025	24.371	1.00		
MOTA	5594	CG	LEU	713		40.581	13.710	24.100	1.00		
ATOM	5595	CD1	LEU			11.418	13.114	22.963	1.00		
ATOM	5596	CD2		713	4	12.676	13.945	22.750	1.00	-	
ATOM	5597	CD2	LEU	713	4	11.757	11.660	23.282			
	/	_	LEU	713	3	88.571	13.654	25.591	1.00		
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MOTA	5598	0	LEU	713	38.562	13.051	26.662	1.00	45.70
ATOM	5599	N	LYS	714	37.980	14.839	25.418	1.00	43.05
ATOM	5601	CA	LYS	714	37.300	15.510	26.524	1.00	42.19
MOTA	5602	CB	LYS	714	36.884	16.921	26.127	1.00	42.41
ATOM	5603	CG	LYS	714	38.076	17.828	25.918	1.00	46.10
ATOM	5604	CD	LYS	714	37.684	19.259	25.589	1.00	49.86
ATOM	5605	CE	LYS	714	38.939	20.097	25.292	1.00	52.55
ATOM	5606	NZ	LYS	714	39.889	20.148	26.459	1.00	50.17
ATOM	5610	С	LYS	714	36.104	14.728	27.054	1.00	42.39
ATOM	5611	0	LYS	714	35.767	14.824	28.237	1.00	43.44
ATOM	5612	N	GLU	715	35.480	13.934	26.192	1.00	40.44
ATOM	5614	CA	GLU	715	34.342	13.118	26.593	1.00	37.90
MOTA	5615	CB	GLU	715	33.408	12.893	25.411	1.00	39.54
ATOM	5616	CG	GLU	715	32.800	14.174	24.846	1.00	45.20
ATOM	5617	CD	GLU	715	32.032	13.936	23.563	1.00	47.85
ATOM	5618	OE1	GLU	715	32.409	13.008	22.810	1.00	50.00
MOTA	5619	OE2	GLU	715	31.061	14.677	23.304	1.00	50.41
ATOM	5620	С	GLU	715	34.793	11.773	27.157	1.00	37.31
MOTA	5621	0	GLU	715	33.970	10.907	27.450	1.00	36.79
ATOM	5622	N	GLY	716	36.102	11.585	27.286	1.00	36.60
ATOM	5624	CA	GLY	716	36.623	10.336	27.819	1.00	37.11
ATOM	5625	C	GLY	716	36.503	9.140	26.887	1.00	38.30
ATOM	5626	0	GLY	716	36.603	7.994	27.34C	1.00	36.84
ATOM	5627	N	HIS	717	36.307	9.404	25.592	1.00	40.24
ATOM	5629	CA	HIS	717	36.167	8.353	24.579	1.00	42.63
ATOM	5630	СВ	HIS	717	35.800	8.951	23.217	1.00	43.11
ATOM	5631	CG	HIS	717	35.745	. 7.941	22.112	1.00	44.69
ATOM	5632	CD2	HIS	717	34.756	7.101	21.717	1.00	45.13
ATOM	5633	ND1	HIS	717	36.818	7.683	21.283	1.00	47.31
ATOM	5635	CE1	HIS	717	36.494	6.728	20.425	1.00	47.61
ATOM	5636	NE2	HIS	717	35.250	6.357	20.670	1.00	44.95
ATOM	5638	C	HIS	717	37.451	7.567	24.413	1.00	44.84
ATOM	5639	0	HIS	717	38.528	8.152	24.295	1.00	46.79
ATOM	5640	N	ARG	718	37.313	6.247	24.337	1.00	45.44
ATOM	5642	CA	ARG	718	38.440	5.345	24.170	1.00	45.36
ATOM	5643	CB	ARG	718	38.614	4.496	25.434	1.00	43.82
ATOM	5644	CG	ARG	718	38.976	5.308	26.687	1.00	44.52
ATOM	5645	CD	ARG	718	40.284	6.065	26.476	1.00	45.02
MOTA	5646	NE	ARG	718	40.718	6.856	27.630	1.00	43.12
ATOM	5648	CZ	ARG	718	40.550	8.173	27.744	1.00	44.77
ATOM	5649	NH1	ARG	718	39.940	8.859	26.784	1.00	44.67
ATOM	5652	NH2	ARG	718	41.067	8.826	28.777	1.00	46.39
ATOM	5655	С	ARG	718	38.124	4.474	22.952	1.00	45.94
MOTA	5656	0	ARG	718	36.953	4.243	22.645	1.00	47.59
ATOM	5657	N	MET	719	39.145	4.077	22.204	1.00	45.34
MOTA	5659	CA	MET	719	38.925	3.253	21.029	1.00	44.28
ATOM	5660	СВ	MET	719	40.198	3.125	20.185	1.00	42.30
MOTA	5661	CG	MET	719	40.575	4.399	19.441	1.00	38.44
ATOM	5662	SD	MET	719	42.000	4.225	18.368	1.00	36.97
ATOM	5663	CE	MET	719	43.317	4.219	19.511	1.00	36.09
ATOM	5664	C	MET	719		1.877	21.418	1.00	46.21
MOTA	5665	0	MET	719	38.708	1.393	22.517	1.00	43.29
ATOM	5666	N	ASP	720	37.659	1.267	20.498	1.00	48.79
ATOM	5668	CA	ASP	720	37.069	-0.063	20.456	1.00	48.87
01.1	2000	J.,	. 10 1	, 20	57.005	5.005	20.000		-0.07

								_				
		669	CB	ASP	720) 26	000					
A:	rom 5	670	CG	ASP	720			-0.		.513	1.00	54.01
ΑT	rom 5	671	OD1	ASP	720				374 19	.632	1.00	59.30
ΑT	COM 5	672		ASP				1.9		.981	1.00	62.96
ΡA	OM 5	673		ASP	720	55.		-0.2		.354	1.00	
AT			_		720			-1.1		.688	1.00	58.64
				ASP	720			-0.9		.125		46.10
		-		LYS	721	,		-2.2		.322	1.00	44.13
AT				LYS	721	38.6	89	-3.4		404	1.00	45.27
AT				LYS	721	38.1		-4.4			1.00	43.25
AT				LYS	721	39.0		-5.6		416	1.00	42.02
				LYS	721	38.6		-6.5		557	1.00	46.57
ATO			CE I	YS.	721	38.3				666	1.00	49.96
ATO				YS	721	37.9		-7.9		141	1.00	51.80
ATC		86 (L	YS	721	38.76		8.9		240	1.00	56.08
ATC		87 C	L	YS	721			-4.05		031	1.00	43.67
ATC	DM 56	88 M		RO	722	37.73		-4.31		394	1.00	44.02
ATO	M 56	89 C		RO	722	39.99		-4.23		513	1.00	43.94
ATO	M 56	90 C	_	RO	722	41.28		-3.71		001	1.00	45.90
ATO	M 569				722	40.15		-4.85	3 18.		1.00	43.96
ATO	M 569			30		41.66		-4.72	0 17.9		1.00	
ATO		_			722	42.04	6	-3.50	9 18.7		1.00	43.11
ATO				_	722	.39.77		-6.31			1.00	45.16
ATO		_	PI		722	39.76		~6.88				43.09
ATON		,	SE	_	723	39.382	2 .	-6.90			1.00	41.32
ATON		_			723	39.044	4	-8.31				45.79
ATOM					723	38.303		-8.664				46.67
ATOM			~~		723	39.131		-8.414				44.69
ATOM	_		SE		723	40.422		-8.961				19.79
ATOM		-	SE	R 7	723	41.360		-8.411				16.90
		_	AS:	N 7	24	40.540		1.0.131		_		18.81
ATOM			AS	N 7	24	41.826					00 4	19.28
ATOM			ASI	7	24	42.480		10.804			.00 5	2.10
ATOM			ASI		24	41.774		10.947				5.86
ATOM	5708	OD:	L ASN		24	41.686		1.957				8.72
MOTA	5709	ND2	ASN		24	41.258	~ .)	.3.140				2.28
ATOM	5712	C	ASN		24			1.503	14.44			9.56
ATOM	5713	0	ASN		24	42.665		9.931	18.77	_		1.97
ATOM	5714	N	CYS	_	25	43.621		9.274	18.36		_	3.85
MOTA	5716	CA	CYS			42.202		9.859	20.00			1.02
ATOM	5717	CB	CYS	72		42.853	-	9.094	21.04	_ `	_	0.18
ATOM	5718	SG	CYS			42.708	-	7.583	20.81			
ATOM	5719	C	CYS	72		43.424	-	6.577	22.130			7.75
ATOM	5720	0		72		42.131	:	9.507	22.31		_	.37
ATOM	5721	N	CYS	72		40.916	- 9	9.371	22.417			.31
ATOM	5723		THR	72		42.866		0.088	23.249			.90
ATOM		CA	THR	72	6	42.262).541	24.490			.52
ATOM	5724	CB	THR	72	6	43.251	-11	.444			00 49	
	5725	OG1	THR	726	5	44.236		.648	25.291			.84
ATOM	5727	CG2	THR	726	5	43.982			25.976			.05
ATOM	5728	C	THR	726		41.788		.363	24.352	1.0	00 47	. 96
ATOM	5729	0	THR	726		42.305		.369	25.356	1.0		. 93
ATOM	5730	N	ASN	727				.256	25.244	1.0		. 55
ATOM	5732	CA	ASN	727		40.829		.622	26.242	1.0		
ATOM	5733	CB	ASN	727		40.335		.577	27.144	1.0		
ATOM	5734	CG	ASN			39.190		.099	28.016	1.0		
	5735	OD1	ASN	727		39.533		.409	28.714	1.0	-	
	_		ADIA.	727		40.709	-10	786	28.833	1.0	_	
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MOTA	5736	ND2	ASN	727	38.500	-11.122	29.175	1.00	68.43
MOTA	5739	C	ASN	727	41.491	-8.091	28.023	1.00	50.29
MOTA	5740	0	ASN	727	41.467	-6.976	28.540	1.00	49.88
MOTA	5741	N	GLU	728	42.518	-8.927	28.163	1.00	50.60
MOTA	5743	CA	GLU	728	43.700	-8.597	28.956	1.00	49.33
MOTA	5744	CB	GLU	728	44.529	-9.859	29.220	1.00	50.44
MOTA	5745	CG	GLU	728	45.802	-9.600	30.008	1.00	55.30
MOTA	5746	CD	GLU	728	46.577	-10.862	30.354	1.00	57.40
MOTA	5747	OE1	GLU	728	46.716	-11.754	29.489	1.00	56.75
MOTA	5748	OE2	GLU	728	47.062	-10.950	31.502	1.00	59.85
MOTA	5749	C	GLU	728	44.539	-7.552	28.212	1.00	47.08
MOTA	5750	0	GLU	728	44.888	-6.512	28.776	1.00	48.02
MOTA	5751	N	LEU	729	44.846	-7.821	26.945	1.00	43.34
MOTA	5753	CA	LEU	729	45.630	-6.891	26.129	1.00	42.01
ATOM	5754	CB	LEU	729	45.899	-7.500	24.751	1.00	39.46
ATOM	5755	CG	LEU	729	46.911	-8.639	24.772	1.00	40.31
MOTA	5756	CD1	LEU	729	46.782	-9.482	23.531	1.00	42.21
MOTA	5757	CD2	LEU	729	48.314	-8.068	24.900	1.00	42.49
MOTA	5758	C	LEU	729	44.901	-5,557	25.980	1.00	40.61
ATOM	5759	0	LEU	729	45.510	-4.481	25.953	1.00	38.33
MOTA	5760	N	TYR	730	43.580	-5.637.	25.909	1.00	39.07
A.TOM	5762	CA	TYR	730	42.761	-4.455	25.773	1.00	38.61
MOTA	5763	CB	TYR	730	41.341	~4.837	25.369	1.00	36.79
MOTA	5764	CG	TYR	730	40.454	-3.646	25.125	1.00	37.08
MOTA	5765	CD1	TYR	730	40.760	-2.721	24.127	1.00	32.86
ATOM	5766	CE1	TYR	730	39.961	-1.616	23.912	1.00	29.79
MOTA	5767	CD2	TYR	730	39.328	-3.420	25.916	1.00	36.99
MOTA	5768	CE2	TYR	730	38.522	-2.312	25.704	1.00	36.69
ATOM	5769	CZ	TYR	730	38.853	-1.412	24.706	1.00	32.69
ATOM	5770	OH	TYR	730	38.044	-0.320	24.492	1.00	38.80
MOTA	5772	С	TYR	730	42.767	-3.662	27.080	1.00	39.75
MOTA	5773	0	TYR	730	42.781	-2.430	27.065	1.00	40.53
MOTA	5774	N	MET	731	42.738	-4.360	28.210	1.00	41.88
MOTA	5776	CA	MET	731	42.778	-3.684	29.509	1.00	45.34
MOTA	5777	CB	MET	731	42.658	-4.697	30.646	1.00	53.46
MOTA	5778	CG	MET	731	41.253	-5.248	30.836	1.00	64.30
MOTA	5779	SD	MET	731	40.134	-4.095	31.653	1.00	75.78
MOTA	5780	CE	MET	731	40.657	-4.338	33.370	1.00	69.70
MOTA	5781	C	MET	731	44.099	-2.927	29.614	1.00	41.53
MOTA	5782	0	MET	731	44.157	-1.814	30.138	1.00	37.91
MOTA	5783	N	MET	732	45.156	-3.545	29.098	1.00	40.48
MOTA	5785	CA	MET	732 .	46.478	-2.937	29.091	1.00	40.23
MOTA	5786	CB	MET	732	47.508	-3.872	28.436	1.00	40.29
MOTA	5787	CG	MET	732	48.929	-3.307	28.390	1.00	38.07
MOTA	5788	SD	MET	732	50.171	-4.522	27.908	1.00	37.65
MOTA	5789	CE	MET	732	50.407	-5.343	29.431	1.00	37.90
ATOM	5790	C	MET	732	46.378	-1.623	28.317	1.00	38.96
MOTA	5791	0	MET	732	46.843	-0.591	28.790	1.00	41.36
ATOM	5792	N	MET	733	45.744	-1.663	27.148	1.00	36.94
MOTA	5794	CA	MET	733	45.574	-0.463	26.340	1.00	35.19
MOTA	5795	CB	MET	733	44.796	-0.769	25.070	1.00	36.07
MOTA	5796	CG	MET	733	45.549	-1.577	24.048	1.00	35.99
MOTA	5797	SD	MET	733	44.471	-1.851	22.641	1.00	40.05
ATOM	5798	CE	MET	733	45.244	-3.351	21.909	1.00	33.13



	7.000.						28	0			
	ATOM	5799	_	MET	733	4.4					
	ATOM	5800	-	MET	733	44	.800	0.560	27.141	1.00	2
	MOTA	5801	N	ARG	734	43	.207	1.719	27.245	1.00	
	ATOM	5803	CA	ARG	734	43	.690	0.125	27.735	1.00	
	ATOM	5804	CB	ARG	734	42	.849	1.014	28.532	1.00	
	ATOM	5805	CG	ARG	734	41	.577	0.297	28.993		
	ATOM	5806	CD	ARG	734	40	.699	-0.225	27.856	1.00	40.33
	ATOM	5807	NE	ARG	734	40.	256	0.877	26.909	1.00	38.02
	ATOM	5809	CZ	ARG	734	39.	443	1.898	27.567	1.00	42.72
	ATOM	5810	NH1	ARG	734	38.	120	1.838	27.700	1.00	48.85
	ATOM	5813	NH2	ARG	734	37.	435	0.811	27.222	1.00	52.35
	ATOM	5816	C	ARG	734	37.	477	2.804	28.338	1.00	54.79
	ATOM	5817	0		734	43.	627	1.587	29.715	1.00	54.69
		5818	N	2		43.4	145	2.757	30.068	1.00	38.70
		5820	CA	3 ~ -	735	44.5	530	_	30.276	1.00	40.92
	ATOM	5821	CB	> ~ -	735	45.3	79	_	31.399	1.00	38.76
	MOTA	5822	CG	3	735	46.3	25 (_	- ·	1.00	38.60
	TOM !	823	OD1	3	735	45.6	22 - 3	_	30	1.00	41.34
A	TOM 5		OD2	· '	735	46.0	48 -2			1.00	44.66
	TOM 5		_	3.0-	35	44.6	57 -ე			1.00	43.15
A'	TOM 5	000	_		35	46.2	15 2	_		1.00	44.46
	TOM 5		-	~·-	35	46.23	35 3			r.00	37.76
	rom 5			~~ ·	36	46.89	90 2			1.00	36.35
	TOM 5	~ ~ ~		· ·	36	47.73	0 3		0 70-	.00	35.39
	'OM 58				36	48.37	92			.00 3	4.77
AT	'OM 58	332 C				49.45	3 1		- .	.00 3	0.62
AT	OM 58	33 o	_			46.93	84.			.00 з	0.96
AT	OM 58	34 N	_			47.516	5.			.00 3	5.98
AT			_ ^			45.620) 4.			. 00 з	7.38
ATO						44.772	5.			.00 3	8.50
ATC						43.791	5.	_		00 40	0.16
ATC.						44.453	4.			00 38	3.41
ATO	M 584					43.893	3.7			00 39	.33
ATO	M 584	1 CE			-	44.852	3.5	_		00 39	.64
. ATO	M 584			,	7	12.672	3.0		.992 1.		. 97
ATO	M 584			,	4	15.695	4.9		900 1.	00 37	.06
ATO	M 584			,	4	5.941	4.3		556 1.0	و3 00	. 56
ATON	1 584			_ , , ,	4	4.627	2.7		343 1.0	00 38	.61
ATOM				,	4	2.452	2.2		859 1.0	00 38.	
ATOM	5848			,	4	3.426	2.14			0 38.	90
ATOM			TRI TRI		4	4.028	6.02			0 38.	18
ATOM	5850				42	2.979	6.65			0 41.	30
MOTA		-	HIS		44	1.575	5.87	_		0 41.	45
ATOM	5853		HIS	0	43	3.932	6.42			9 43.	01
ATOM	5854		HIS	, 50	44	.454	5.73			44.	
ATOM	5855	CD2	HIS	738	43	.742	6.15			46.2	
ATOM	5856	ND1	HIS	738	43	. 473	7.379			50.3	15
ATOM	5858		HIS	738	43	.220	5.244			49.0	
ATOM	5859	CE1	HIS	738	42	. 659			⁵⁵ 1.00	49.9	
ATOM	5861	NE2	HIS	738	42	. 798	5.899		57 1.00		
ATOM	5862	C	HIS	738	44	174	7.194		1.00	46.9	
ATOM	5863	0	HIS	738	45.	314	7.921		7 1.00	45.2	- 5
ATOM	5865	N	ALA	739	43	099	8.356		1 1.00	45.3	
ATOM	5866	CA	ALA	739	43	155	8.686	32.22	4 1.00	46.6	
	2006	CB	ALA	739	41.	823	10.150	32.32	2 1.00	48.49	
SSSD/55	145				,	- 4 5	10.681	32.79	0 1.00	49.69	
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ATOM	5867	С	ALA	739	44.272	10.682	33.224	1.00	50.77
MOTA	5868	0	ALA	739	45.004	11.601	32.846	1.00	51.77
MOTA	5869	N	VAL	740	44.336	10.138	34.439	1.00	51.47
ATOM	5871	CA	VAL	740	45.352	10.485	35.439	1.00	51.09
MOTA	5872	CB	VAL	740	44.897	10.075	36.850	1.00	52.40
ATOM	5873	CG1	VAL	740	45.847	10.624	37.878	1.00	53.38
ATOM	5874	CG2	VAL	740	43.485	10.544	37.105	1.00	55.18
MOTA	5875	С	VAL	740	46.649	9.727	35.130	1.00	48.99
ATOM	5876	0	VAL	740	46.773	8.534	35.440	1.00	47.72
ATOM	5877	N	PRO	741	47.646	10.421	34.565	1.00	48.31
MOTA	5878	CD	PRO	741	47.603	11.861	34.253	1.00	47.84
ATOM	5879	CA	PRO	741	48.949	9.852	34.197	1.00	48.51
MOTA	5880	CB	PRO	741	49.762	11.087	33.828	1.00	46.83
ATOM	5881	CG	PRO	741	48.714	12.000	33.255	1.00	46.21
MOTA	5882	C	PRO	741	49.641	9.016	35.275	1.00	49.12
ATOM	5883	O	PRO	741	50.449	8.139	34.955	1.00	46.57
ATOM	5884	N	SER	742	49.327	9.290	36.541	1.00	49.47
ATOM	5886	CA	SER	742	49.928	8.557	37.651	1.00	49.50
ATOM	5887	CB	SER	742	49.760	9.326	38.963	1.00	51.06
ATOM	5888	OG	SER	742	48.403	9.638	39.209	1.00	53.81
ATOM	5890	С	SER	742	49.339	7.159	37.787	1.00	48.81
ATOM	5891	0	SER	742	49.926	6.284	38.427	1.00	49.45
ATOM	5892	N	GLN	743	48.164	6.959	37.203	1.00	47.82
ATOM	5894	CA	GLN	743	47.529	5.658	37.273	1.00	46.34
ATOM	5895	СВ	GLN	743	46.022	5.791	37.432	1.00	49.74
ATOM	5896	CG	GLN	743	45.519	5.305	38.784	1.00	55.41
ATOM	5897	CD	GLN	743	46.178	5.030	39.947	1.00	59.15
ATOM	5898	OE1	GLN	743	46.905	5.425	40.748	1.00	59.02
ATOM	5899	NE2	GLN	743	45.922	7.338	40.052	1.00	60.03
ATOM	5902	С	GLN	743	47.874	4.768	36.095	1.00	44.34
MOTA	5903	0	GLN	743	47.548	3.578	36.114	1.00	44.64
MOTA	5904	N	ARG	744	48.497	5.339	35.059	1.00	4.2.83
MOTA	5906	CA	ARG	744	48.914	4.559	33.880	1.00	40.34
ATOM	5907	CB	ARG	744	49.349	5.469	32.724	1.00	35.84
ATOM	5908	CG	ARG	744	48.296	6.406	32.190	1.00	28.25
MOTA	5909	CD	ARG	744	48.906	7.383	31.216	1.00	22.56
ATOM	5910	NE	ARG	744	47.948	8.437	30.922	1.00	28.09
ATOM	5912	CZ	ARG	744	48.258	9.658	30.493	1.00	32.83
ATOM	5913	NH1	ARG	744	49.524	10.001	30.278	1.00	34.44
MOTA	5916	NH2	ARG	744	47.307	10.569	30.360	1.00	32.00
ATOM	5919	C	ARG	744	50.110	3.712	34.295	1.00	41.58
MOTA	5920	0	ARG	744	50.906	4.124	35.145	1.00	45.48
ATOM	5921	N	PRO	745	50.223	2.489	33.754	1.00	40.97
ATOM	5922	CD	PRO	745	49.345	1.749	32.831	1.00	39.90
MOTA	5923	CA	PRO	745	51.381	1.685	34.157	1.00	39.77
ATOM	5924	СВ	PRO	745	51.063	0.311	33.558	1.00	39.31
ATOM	5925	CG	PRO	745	50.255	0.642	32.344	1.00	40.98
MOTA	5926	С	PRO	745	52.664	2.269	33.573	1.00	38.44
ATOM	5927	0	PRO	745	52.631	3.009	32.595	1.00	39.64
ATOM	5928	N	THR	746	53.783	2.001	34.224	1.00	37.50
ATOM	5930	CA	THR	746	55.066	2.462	33.728	1.00	37.56
ATOM	5931	CB	THR	746	56.108	2.571	34.869	1.00	38.58
ATOM	5932	OG1	THR	746	56.286	1.285	35.487	1.00	43.28
MOTA	5934	CG2	THR	746	55.666	3.567	35.899	1.00	34.64



Δ	TOM 5		_									
		935	C	THR	746	55.5	46	7	393 32	770	<u>.</u> .	
		936		THR	746	55.1				739	1.0	
	_	937		PHE	747	56.4	 53			.817	1.0	
		939	CA	PHE	747	56.99				.839	1.00	35.27
			CB	PHE	747	58.02				.880	1.00	33.48
			CG ;	PHE	747	57.41		1.4		.970	1.00	
		942	CD1]	PHE	747			.2.3		.920	1.00	
			CD2 I	PHE	747	56.71		1.8		.856	1.00	30.69
ΑT	OM 59	944		HE	747	57.51		3.7		.018	1.00	
AT	OM 59	945 (HE	747	56.12		2.6		907	1.00	
AT	'OM 59	946 (HE	747	56.92		4.5		072	1.00	
AT	OM 59	947 (HE	747	56.22		4.0		015	1.00	31.50
AT	OM 59	48 (HE		57.62		-0.3		606	1.00	34.65
AT	OM 59	49 N	_	YS	747	57.61		-1.4		099	1.00	
AT				YS	748	58.142	2	-0.12		808	1.00	36.34
ATO		-	_		748	58.748	3	-1.20)5 33.		1.00	37.75
ATO				YS	748	59.382		-0.66			1.00	39.67
ATO		_	_	YS	748	59 .95 8	3	-1.75				43.06
ATO					748	60.750)	-1.20			1.00	48.96
ATC			_		748	61.183		-2.34			1.00	52.20
ATC					748	62.057		-1.89			1.00	53.62
ATO			LY		748	57.680		-2.26			1.00	54.82
ATO	•		LY		748	57.902		-3.45			1.00	39.65
ATO			GL		749	56.503		-1.81			1.00	38.91
		_			749	55.402		-2.742			1.00	39.39
ATO				N 7	749 .	54.177		-1.991			1.00	40.70
ATO				N ?	49	54.395		-1.149			1.00	43.82
ATO				N '7	49	53.175					1.00	50.97
ATO	_		1 GL	N 7	49	53.272	•	-0.304			1.00	55.53
ATON			2 GLi	1 7	49	52.012		0.914			.00	55.80
ATON		2 C	GL1		49	55.009		0.940			1.00	60.05
ATOM	,	3 0	GLM		49 .	54.903		3.455			00	40.03
ATOM	, .		LEU		50	54.802		4.679			.00	40.26
ATOM			LEU		50			2.666			.00	39.18
ATOM	5977	CB	LEU		50	54.400		3.171	30.96			36.65
ATOM	5978	CG	LEU		50	54.369		2.039	29.92			34.58
ATOM	5979	CD1				53.355	-	0.910	30.11	_		32.52
ATOM	5980		_	_		53.644		0.210	29.12			31.67
ATOM	5981	С	LEU			51.947		1.435	29.93			31.37
ATOM	5982	0	LEU			55.321	~ 4	1.255	30.47			35.81
ATOM	5983	N	VAL	75		54.856	- 5	5.267	29.96			35.81
ATOM	5985	CA	VAL	75		56.626		.035	30.62			
ATOM	5986	CB	VAL	75		57.607	~ 5	.029	30.19			37.38
ATOM	5987	CG1		75		59.077	-4	.545	30.41			8.66
ATOM	5988	CG2	VAL	75		60.075	- 5	.646	30.04			5.42
ATOM	5989	C	VAL	75		59.342		.324	29.559	-		9.83
ATOM	5990		VAL	75:		57.337	-6	.314	30.974			9.95
ATOM	5991	0	VAL	75:		57.312		.401	30.396			1.63
ATOM		N ~-	GLU	752	3	57.051		.174				2.43
ATOM	5993	CA	GLU	752	2	56.766		.329	32.267	_		3.35
ATOM	5994	CB	GLU	752	?	56.674		.914	33.111			7.39
	5995	CG	GLU	752	:	57.950		243	34.587			0.66
ATOM	5996	CD	GLU	752		58.006			35.101	1.(1.77
ATOM	5997	OE1	GLU	752		58.246	-6.	101	36.612	1.0		5.14
ATOM	5998	OE2	GLU	752		57.844		972	37.102	1.0	0 54	.14
ATOM	5999	C	GLU	752		55.496		131	37.308	1.0	0 57	.73
CCC= :				_		-2.470	~8.	068	32.655	1.0		.00
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6000 GLU ATOM 0 752 55.548 -9.261 32.328 1.00 46.25 6001 ASP 753 MOTA N 54.380 -7.346 32.601 1.00 44.35 MOTA 6003 CA ASP 753 53.099 -7.912 32.180 1.00 44.19 MOTA 6004 CB ASP 753 52.059 -6.814 31.985 1.00 46.22 CG ASP 753 MOTA 6005 51.512 -6.279 33.278 1.00 50.48 ATOM 6006 OD1 ASP 753 51.396 -7.062 34.248 1.00 52.15 ATOM 6007 OD2 ASP 753 33.306 1.00 51.170 -5.069 52.20 6008 ASP MOTA C 753 53.244 -8.608 30.849 1.00 44.54 MOTA 6009 0 ASP 753 52.770 -9.724 30.674 1.00 46.03 ATOM 6010 N LEU 754 53.880 -7.918 29.906 1.00 44.43 MOTA 6012 CA LEU 754 54.079 -8.438 28.563 1.00 43.70 MOTA 6013 CB LEU 754 54.570 -7.339 27.618 1.00 43.48 MOTA 6014 CG LEU 754 53.481 -6.350 27.201 1.00 44.67 MOTA 6015 CD1 LEU 754 54.095 -5.218 26.399 1.00 44.51 MOTA 601.6 CD2 LEU 754 52.384 -7.069 26.408 1.00 42.07 MOTA 6017 С LEU 754 54.993 -9.642 28.512 1.00 43.14 6018 0 LEU 754 ATOM 54.795 -10.536 27.697 1.00 41.32 MOTA 6019 N ASP 755 55.990 -9.671 29.383 1.00 44.74 6021 MOTA CA ASP 755 56.897 -10.800 29.426 1.00 47.24 6022 755 MOTA CB ASP 30.517 57.942 -10.575 1.00 51.26 MOTA 6023 .CG ASP 755 59.121 -11.518 30.407 1.00 55.39 MOTA 6024 OD1 ASP 755 59.739 -11.793 31.455 1.00 60.61 MOTA 6025 OD2 ASP 755 59.443 -11.970 29.283 1.00 57.16 6026 MOTA C. ASP 755 . 56.023 -12.005 29.771 1.00 47.67 ATOM 6027 0 ASP 755 56.041 -13.032 29.081 1.00 45.99 55.186 MOTA 6028 N ARG 756 -11.816 30.789 1.00 46.72 MOTA 6030 CA 756 ARG 54.272 -12.851 31..256 1.00 46.25 MOTA 6031 CB ARG 756 53.519 -12.368 32.499 1.00 46.31 MOTA 6032 ARG 756 CG 52.391 -13.287 32.953 1.00 46.99 MOTA 6033 CD ARG 756 51.733 -12.776 34.227 1.00 48.10 MOTA 6034 NE ARG 756 51.320 -11.379 34.118 1.00 53.67 ATOM 6036 CZ ARG 756 50.294 -10.951 33.385 1.00 55.35 MOTA 6037 NH1 ARG 756 -11.812 32.684 49.562 1.00 54.10 MOTA ARG 756 6040 NH2 50.008 -9.654 33.344 1.00 56.02 MOTA 6043 C ARG 756 53.282 -13.261 30.175 1.00 45.05 MOTA ARG 6044 0 756 53.213 -14.429 29.806 1.00 47.19 ILE MOTA 6045 N 757 52.550 -12.289 29.647 1.00 43.47 6047 ILE 757 MOTA CA 51.552 -12.55328.617 1.00 43.80 MOTA 6048 757 CB ILE 50.842 -11.241 28.161 1.00 42.02 -11.536 MOTA 6049 CG2 ILE 757 49.811 27.086 1.00 39.63 MOTA 6050 CG1 ILE 757 50.154 -10.578 29.361 1.00 40.00 MOTA 6051 CD1 ILE 757 49.600 -9.212 29.086 1.00 42.68 6052 ILE 757 MOTA C 52.148 -13.296 27.428 1.00 46.03 ATOM 6053 0 ILE 757 51.549 -14.250 26.947 1.00 47.78 MOTA 6054 N VAL 758 53.359 -12.925 27.015 1.00 49.03 MOTA 6056 CA VAL 758 54.015 -13.584 25.884 1.00 51.51 MOTA 6057 CB VAL 758 55.412 -12.971 25.556 1.00 50.75 MOTA 6058 CG1 VAL 758 56.105 -13.780 24.470 1.00 50.31 MOTA 6059 CG2 VAL 758 55.269 -11.541 25.081 1.00 52.52 ATOM 6060 C VAL 758 54.209 -15.050 26.212 1.00 54.30 53.991 MOTA 6061 0 VAL 758 -15.915 25.369 1.00 54.80 ATOM 6062 N ALA 759 54.617 -15.311 27.450 1.00 57.65 MOTA 6064 CA ALA 759 54.858 -16.667 27.919 1.00 60.62 MOTA 6065 CB ALA 759 55.423 -16.637 29.327 1.00 60.32

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ATOM 6066 C ALA	750
ATOM 6067 0	759 53.571 -17.478 27.889 1.00
ATOM 6068 N	53.568 -18.639 25 4.00 63.25
ATOM 6070 CA	760 52.475 -16.856 27.478 1.00 65.81
ATOM 6071	760 51 191 17 28.305 1.00 63 56
ATOM CO LEU 7	60 50 302 28.333 1.00 64 25
ATOM CO LEU 7	60 50 894
- CDI LEU 7	60 15.962 30.820 1.00
7 60/4 CD2 LEU 7	50 -16.246 31.809 1.00
ATOM 6075 C LEII 7	-18.410 31.227 1 00
ATOM 6076 0	50.483 -17.535 26 004
ATOM 6077 N	49.390 -18.088 36 363 1.00 64.89
ATOM 6079 CA	51.103 -16 923 05 1.00 66.37
ATOM 6080 CB 76	50.516 -16.883 25.9/3 1.00 65.24
ATOM 6001 000	1 50 920 24.534 1.00 64 44
ATTOM OF THE 76	1 50 247 23.939 23.925 1.00 62 95
ATOM 55-	1 24.463 24.669 1 00
76 THR 76	1 -15.525 22.521 1 00
76 THR 76	1 -18.044 23.769 1 00
ATOM 6086 SG CVC 16	32.202 -18.201 32 53
ATOM 6087 CG MET 53	18.536 -8.818 20 305
ATOM 6088 SD MET 55	69.178 12.159 22.000 0.50 33.97 PRT2
ATOM 6089 CE 1534	68.892 13 130 0.50 31.30 PRT2
ATOM 6090 SC 534	70.060 12.456 05 0.50 33.06 PRT2
ATOM 2602 000 CIS 603	56: 041 25.568 0.50 34 33 ppms
ATOM 2685 cm	71 788 25 15.319 0.50 37 82 ppms
ATOM 2500	40 000 25.340 2.479 1.00 24.10
ATOM 255-	4.089 16.127 7 20
- Onz 1703 A	19.577 10.510 1 00 = 1.09
ATOM 2694 OH2 TIP3 5	20.163 7.482 1.00 27.38
2697 OH2 TIP3 6	75.022 16.439
ATOM 2700 OH2 TTD2 -	86.308 19.567 0.00 33.15
ATOM 2703 OH2 TIP2	51.888 11.346 34 11.00 33.55
ATOM 2706 OH2 TIP2	55.125 9.616 33.400 34.30
ATOM 2709 OTTO	57.087 4 825 22.499 1.00 21.44
ATOM OFFEE	52 142 1.00 28 70
ATOM 2715 000	47 313 - 13.180 1.00 21 14
ATOM 2710 271	45 003
ATOM 2002 TIP3 13	64 600 21.6/1 1.00 37 00
- OHZ TIPS 1A	75 - 20.003 1 00
TIP3 15	77.132 13.199 23.753 1 00 22
ATOM 2727 OH2 TIP3 16	17.296 17.997 1 00 22
A10M 2730 OH2 TIP3 17	02.988 11.608 15 745
A10M 2733 OH2 WIDE -	±±.096
ATOM 2736 OH2 TIP3 10	38.325 0 249 5 1.00 23.53
ATOM 2739 OH2 TID	26.939 6.001 1.00 43.17
ATOM OF 1	34.305 ~1 616 30.00
ATOM STATES 21	20 300 - 10.994 1.00 44 92
ATOM 2742	50 996 27.798 1.00 45 22
ATOM 2002 TIP3 23	17 361
ATOM 277 11P3 24	-1.444 1 00 07
1110M 2/54 OH2 TIP3 25	8.124 14.996 1 00 22
2/5/ OH2 TIP3 26	0.294 6.872 1.00
2/60 OH2 TTD3 27	20.90/ -12.815 28.161 1 00
ATOM 2763 OH2 TIP2 20	28.705 -17.192 13.262 49.20
ATOM 2766 OTTO 28	88.639 13.953 7 600 1.00 30.16
ATOM 2750	-2.328 -3.576 11.00c 1.00 41.04
ATOM 2555	34 910 44 90
ATOM 2777 31	80 124 17 13.070 1.00 53 72
ATOM 2775 OH2 TIP3 32	5 417 3.324 1.00 20 00
SSSD/55145. v01	5.417 3.492 10.771 1.00 34.07
	34. 0/

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TIP3 33 2778 OH2 -10.718 11.542 1.00 30.81 MOTA 4.889 2781 OH2 TIP3 34 29.486 -8.823 20.599 1.00 51.35 MOTA 3.065 2784 OH2 TIP3 35 13.821 1.00 **ATOM** 6.151 34.56 ATOM 2787 OH2 TIP3 36 31.907 2.919 0.361 1.00 48.13 ATOM 2790 OH2 TIP3 37 19.974 1.928 -3.873 1.00 30.12 MOTA 2793 OH2 TIP3 38 61.976 2.660 32.604 1.00 36.01 OH2 TIP3 39 ATOM 2796 21.084 -7.119 -3.759 1.00 20.12 MOTA 2799 OH2 TIP3 40 -15.729 8.693 22.468 1.00 54.88 ATOM 2802 OH2 TIP3 41 40.160 2.461 8.734 1.00 37.95 2805 OH2 TIP3 42 0.190 ATOM 19.248 11.349 1.00 37.63 2808 TIP3 43 17.185 MOTA OH2 66.856 9.143 1.00 27.91 **MOTA** 2811 OH2 TIP3 44 87.262 19.150 18.734 1.00 57.83 2814 OH2 TIP3 45 ATOM 74.597 17.144 3.987 1.00 42.19 MOTA 2817 OH2 TIP3 46 10.582 1.00 29.192 16.988 37.28 MOTA 2820 OH2 TIP3 47 66.415 7.073 14.829 1.00 34.86 2823 OH2 TIP3 48 21.453 5.510 1.00 ATOM 85.063 27.42 ATOM 2826 OH2 TIP3 49 -4.716 2.835 2.998 1.00 40.54 ATOM 2829 OH2 TIP3 50 5.069 4.888 1.00 19.369 38.40 34.750 MOTA 2832 OH2 TIP3 51 5.517 24.999 1.00 29.11 32.68 MOTA 2835 OH2 TIP3 52 34.740 -16.765 14.093 1.00 MOTA 2838 OH2 TIP3 53 59.994 7.555 27.844 1.00 32.60 1.00 ATOM 2841 OH2 TIP3 54 -7.401 -1.595 6.080 43.73 MOTA 2844 OH2 TIP3 55 55.257 12.084 25.108 1.00 44.32 TIP3 56 MOTA 2847 OH2 68.239 6.953 16.647 1.00 44.46 MOTA 2850 OH2 TIP3 57 73.621 20.852 18.820 1.00 29.47 TIP3 58 OH2 -8.210 1.00 22.31 MOTA 2853 3.399 -3.294 MOTA 2856 OH2 TIP3 59 37:999 10.824 5.505 1.00 31.62 -9.515 MOTA 2859 OH2 TIP3 60 29.779 -1.395 1.00 40.76 MOTA 2862 OH2 TIP3 61 1.00 49.114 1.432 12.261 29.92 MOTA 2865 OH2 TIP3 62 41.257 4.012 29.005 1.00 39.24 OH2 TIP3 63 MOTA 2868 11.113 -12.848 1.296 1.00 34.36 TIP3 64 MOTA 2871 OH2 -1.221 -4.593 21.504 1.00 34.24 MOTA 2874 OH2 TIP3 65 30.002 16.453 13.258 1.00 49.66 MOTA 2877 OH2 TIP3 66 8.212 4.106 3.434 1.00 36.54 18.807 MOTA 2880 OH2 TIP3 67 72.868 22.589 1.00 38.26 **ATOM** 2883 OH2 TIP3 68 -8.056 -3.666 25.021 1.00 39.81 ATOM 2886 OH2 TIP3 69 66.436 -4.683 28.008 1.00 60.97 MOTA 2889 OH2 TIP3 70 22.063 -20.641 4.804 1.00 42.25 TIP3 71 MOTA 2892 OH2 59.860 -7.407 4.859 1.00 56.78 ATOM 2895 OH2 TIP3 72 16.887 -13.832 -2.611 1.00 59.32 ATOM 2898 OH2 TIP3 73 -15.108 7.351 4.303 1.00 31.87 2.922 MOTA 2901 OH2 TIP3 74 13.663 1.00 32.901 37.89 MOTA 2904 OH2 TIP3 75 0.173 -2.666 11.035 1.00 39.12 MOTA 2907 OH2 TIP3 76 17.533 2.317 5.808 1.00 18.66 TIP3 77 6.349 MOTA 2910 OH2 27.183 3.730 1.00 29.04 MOTA 2913 OH2 TIP3 78 -8.812 5.887 9.703 1.00 30.53 MOTA 2916 OH2 TIP3 79 -2.195 8.694 1.00 30.79 1.614 TIP3 80 MOTA 2919 OH2 -5.304 -3.157 6.846 1.00 47.38 MOTA 2922 OH2 TIP3 81 2.918 1.973 1.00 17.401 20.47 1.00 MOTA 2925 OH2 TIP3 82 20.333 3.188 3.159 24.44 OH2 TIP3 83 22.276 1.00 MOTA 2928 0.408 -2.516 31.11 MOTA OH2 TIP3 84 -6.123 1.00 2931 20.095 -1.372 17.62 OH2 ATOM 2934 TIP3 85 11.018 -15.627 7.421 1.00 60.29 ATOM 2937 OH2 TIP3 86 4.089 -12.037 11.797 1.00 39.47

ATOM 2940	OH2 TIP3 8	7 -			
ATOM 2943	OH2 TIP3 88	0.7		~ · ~ / O	1.00 30.31
ATOM 2946	OH2 TIP3 89	40.4	93 1.004	5.319	
ATOM 2949	OH2 TIP3 90	40.4		0.022	_
ATOM 2952	OH2	2.1.		4.052	
ATOM 2955	0770	-2./3	31 4.833	-4.212	
ATOM 2958	0110	07.32	27.812	2.191	
ATOM 2961		~4.03	1 -12.871	0.285	1.00 37.47
ATOM 2964	OTTO	60.30	1 -4.459	33.927	1.00 44.73
3 50 0 1 1	0170	10.48	8 5,951	3.205	1.00 40.13
3 m	0***0	-9.70	8 -4.233	4.439	1.00 41.53
A MONG	0770	72.95	0 -1.768	10.144	1.00 29.77
7 MON	2772	-3.28	7 5.612	30.618	1.00 39.69
N/IIOM		36.658	3 1.007	11.717	1.00 34.65
A TOM			6.459		1.00 35.43
7 TOM 0	5 101	5.833	8.726		1.00 20.70
7.004	OH2 TIP3 102	-13.529	7.868		1.00 47.13
. Amora	OH2 TIP3 103	26.795	-10.682		1.00 31.95
A TOM	H2 TIP3 104	23.711			1.00 28.65
7,000	H2 TIP3 105	-2.187			1.00 28.29
Amore and	H2 TIP3 106	59.483	12.232	3.920	1.00 44.98
7 MOM Dec	H2 TIP3 107	4.439	-10.915	33.535	L.00 39.58
ATTOM Asset	H2 TIP3 108	8.041		1.996 1	00 43.77
ATOM Sees	H2 TIP3 109	75.836	2.687	C.648 1	00 45.32
7/TOM DATE	H2 TIP3 110	48.604		25.476 ₁	.00 41.65
ATOM	T.I.	2.396		14.349 1	.00 36.36
ATOM 3015 OF	[2 TIP3 112	82.927		9.259 1	.00 34.21
ATOM 3018 OH	13	8.983		12.807 1	.00 36.54
ATOM 3021 OH	2 TIP3 114	-8.690	-6.631 -	-3.299 1	.00 47.01
ATOM 3024 OH	2 TIP3 115	7.941	4.367	4.504 1	.00 41.25
ATOM 3027 OH	2 TIP3 116	51.295	-13.921		00 36.12
ATOM 3030 OH		20.432	6.440 1		00 28.37
ATOM 3033 OH:			3.771 1		00 31.22
ATOM 3036 OH2	2 TIP3 119	72.882	3.887 2		00 30.22
ATOM 3039 OH2		5.187	-11.863 2		00 47.49
ATOM 3042 OH2		33.889	2.571 1	6.293 1.	
ATOM 3045 OH2	TIP3 122	9.504	-12.183 ·	7.160 1.	
ATOM 3048 OH2	TIP3 123	8.397	3.827 -	1.647 1.	•
ATOM 3051 OH2		7.281	7.321 2	2.391 1.0	
ATOM 3054 OH2		35.682	-1.725 c).534 1.0	
ATOM 3057 OH2	TIP3 126	44.465		.089 1.0	
ATOM 3060 OH2	TIP3 127	45.247	11.893 21	.405 1.0	~
ATOM 3063 OH2	TIP3 128	57.386	-10.506 <u>14</u>	.020 1.0	
ATOM 3066 OH2		-3.033	15.103 16	.644 1.0	2
ATOM 3069 OH2		85.621		.814 1.0	
ATOM 3072 OH2		13.040			
ATOM 3075 OH2		75.607			
ATOM 3078 OH2	TIP3 132	13.080			
ATOM 3081 OH2	TIP3 133	11.308			
ATOM 3084 OH2	TIP3 134	13.716 -	16		
A TOM	TIP3 135	_	_	848 1.00 178 1.00	
7.0014	TIP3 136	25.841 -			
7 TOM	TIP3 137			950 1.00	
AMON	T1P3 138	_		585 1.00	
ATTOM THE	TIP3 139			477 1.00	36.37
ATOM 3099 OH2	TIP3 140	44.936		224 1.00	28.35
SSSD/55145 . 04			7.528 11.9	961 1.00	46.60

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MOTA	3102	OH2	TIP3	141	80.781	12.162	16.353	1.00	41.46
MOTA	3105	OH2	TIP3	142	2.547	-7.532	-1.453	1.00	41.42
ATOM	3108	OH2	TIP3	143	31.850	-5.907	21.194	1.00	54.70
ATOM	3111	OH2	TIP3	144	74.524	-2.663	12.264	1.00	40.35
ATOM	3114	OH2	TIP3	145	7.592	6.769	-0.931	1.00	58.34
MOTA	3117	OH2	TIP3	146	71.168	5.735	21.648	1.00	27.86
ATOM	3120	OH2	TIP3	147	67.876	-4.900	8.725	1.00	33.58
ATOM	3123	OH2	TIP3	148	0.554	-10.181	6.605	1.00	75.65
MOTA	3126	OH2	TIP3	149	67.965	18.266	10.874	1.00	30.42
MOTA	3129	OH2	TIP3	150	3.509	8.125	4.021	1.00	40.77
MOTA	3132	OH2	TIP3	151	52.216	12.175	18.131	1.00	47.63
ATOM	3135	OH2	TIP3	152	-10.336	6.394	5.014	1.00	48.53
ATOM	3138	OH2	TIP3	153	76.427	1.384	-1.196	1.00	47.21
ATOM	3141	OH2	TIP3	154	10.116	-12.199	17.089	1.00	70.16
ATOM	3144	OH2	TIP3	155	34.043	14.595	18.314	1.00	40.56
MOTA	3147	OH2	TIP3	156	2.488	-8.304	16.835	1.00	64.47
ATOM	3150	OH2	TIP3	157	29.610	1.954	6.685	1.00	48.74
ATOM	3153	OH2	TIP3	158	32.578	-17.270	12.109	1.00	37.35
ATOM	3156	OH2	TIP3	159	42.013	18.106	11.196	1.00	68.33
ATOM	3159	OH2	TIP3	160	87.646	10.346	5.465	1.00	75.39
ATOM	3162	OH2	TIP3	161	69.931	-3.739	24.921	1.00	70.42
ATOM	3165	OH2	TIP3	162	77.277	5.700	23.531	1.00	53.26
ATOM	3168	OH2	TIP3	163	34.172	15.704	1.865	1.00	44.88
MOTA	3171	OH2	TIP3	164	-9.871	7.514	7.751	1.00	39.18
ATOM	3174	OH2	TIP3	165	11.814	5.604	7.443	1.00	46.70
MOTA	3177	OH2	TIP3	166	-8.861	13.912	13.532	1.00	52.89
MOTA	3180	OH2	TIP3	167	32.195	3.409	18.336	1.00	32.33
MOTA	3183	OH2	TIP3	168	-8.858	9.696	24.279	1.00	38.90
MOTA	3186	OH2	TIP3	169	-1.135	-6.924	15.691	1.00	43.05
ATOM	3189	OH2	TIP3	170	79.806	0.323	15.371	1.00	36.91
ATOM	3192	OH2	TIP3	171	67.181	20.622	-1.545	1.00	44.72
MOTA	3195	OH2	TIP3	172	-0.823	3.732	1.065	1.00	52.11
MOTA	3198	OH2	TIP3	173	-0.130	6.021	2.491	1.00	40.87
MOTA	3201	OH2	TIP3	174	-1.027	8.941	1.064	1.00	60.72
MOTA	3204	OH2	TIP3	175	-5.566	8.867	2.163	1.00	47.25
MOTA	3207	OH2	TIP3	176	-7.259	10.294	4.033	1.00	53.61
MOTA	3210	OH2	TIP3	177	2.664	7.247	1.058	1.00	46.41
MOTA	3213	OH2	TIP3	178	5.295	10.728	8.257	1.00	39.84
MOTA	3216	OH2	TIP3	179	63.743	12.726	22.713	1.00	49.55
MOTA	3219	OH2	TIP3	180	79.165	1.016	17.948	1.00	51.41
ATOM	3222	OH2	TIP3	181	13.823	-1.538	-3.942	1.00	39.85
MOTA	3225	OH2	TIP3	182	59.255	3.213	32.873	1.00	76.77
MOTA	3228	OH2	TIP3	183	32.210	13.612	20.027	1.00	60.41
ATOM	3231	OH2	TIP3	184	72.606	16.267	22.574	1.00	60.78
MOTA	3234	OH2	TIP3	185	-0.147	5.713	30.877	1.00	50.19
ATOM	3237	OH2	TIP3	186	-1.207	-4.507	27.969	1.00	65.19
ATOM	3240	OH2	TIP3	187	81.340	15.584	16.808	1.00	64.48
ATOM	3243	OH2	TIP3	188	-17.535	3.884	23.785	1.00	57.17
ATOM	3246	OH2	TIP3	189	27.503	10.697	14.669	1.00	36.11
MOTA	3249	OH2	TIP3	190	34.585	4.535	27.618	1.00	61.68
ATOM	3252	OH2	TIP3	191	-3.701	-4.982	9.069	1.00	43.66
ATOM	3255	OH2	TIP3	192	42.524	7.811	22.390	1.00	34.53
ATOM	3258	OH2	TIP3		52.937	11.764	21.790	1.00	36.19
ATOM	3261	OH2	TIP3		-7.665	8.600	6.358	1.00	59.08
		~ 			,.005	0.000	3.330		55.00

ATOM 3	264 OH2 TIP3 1			
7.000	267 0***			6 F70 -
	270 0772	96 55.377		6.579 1.00 55.88
	272 0770	⁹⁷ 51.394		0.540 1.00 48.25
	76 077	⁹⁸ 20.021		2.988 1.00 46.81
	I	99 28.959	- -	/·226 1.00 52 98
		26.533		3.219 1.00 40 50
3	82 OH2 TIP3 20	36.739		4.295 1.00 54 24
70000	85 OH2 TIP3 20	16.968	3.003 18	3.397 1.00 42 12
3		13 28 177	-20.752 14	1.00 54 54
	OH2 TIP3 20	4 31.488	-14.418 6	.134 1.00 61 36
ATOM 32	94 OH2 TIP3 20			.796 1.00 47 40
ATOM 329	9/ OH2 TIP3 20	005	-16.494 15	.731 1.00 41.42
ATOM 330	00 OH2 TIP3 20		-12.200 6	.160 1.00 61.94
ATOM 330)3 OH2 TIP3 201	055	14.357 10	- 01.94
ATOM 330	6 OH2 TIP3 209	2/4	9.662 -1	500
ATOM 330	9 OH2 TIP3 210	251	12.484 -1.	- 10.43
ATOM 331	2 0170	/		
ATOM 331	2 211		10	000
ATOM 331	8 0112 ===	,	·	071
ATOM 3321		01.024	13.599 26.	- +2.63
ATOM 3324	1 0770	36.528	5.933 14.	055
ATOM 3327	7 215	90.599		740
ATOM 3330	216	_		342 1.00 54.08
ATOM 3333	1123 217	66.523	_	J4.04
ATOM 3336	0110	74.880		33.47
ATOM 3339	1123 219	-3.095		91 1.00 41.84
7.000	1123 220	5.601		42 1.00 52 25
	OH2 TIP3 221	35.616	-3.682 25.0	22 1.00 29 30
- -	OH2 TIP3 222	_	6.407 12.4	55 1.00 44 40
0	OH2 TIP3 223		16.006 14.0	81 1.00 44 22
3.000	OH2 TIP3 224	<u> </u>	11.503 26.8	14 1.00 53 82
3.000	OH2 TIP3 225		-5.481 20.9	29 1.00 61 42
3	OH2 TIP3 226	~ -	-3.876 -0.40	02 1.00 58.60
ATOM 3360	OH2 TIP3 227	11 077	11.220 23.13	33 1.00 59.84
ATOM 3363	OH2 TIP3 228	11.011	7.959 5.65	
ATOM 3366	OH2 TIP3 229	64.610	8.031 20.40	2.00 03.07
ATOM 3369	OH2 TIP3 230	11.446 -1	7.829 13.43	40.11
ATOM 3372	OH2 TIP3 231	72.056	1.258 -1.83	
ATOM 3375	OH2 TIP3 232		9.732 11.74	4
ATOM 3378	OH2 TIP3 233	43.344 2	0.728 30.06	2
ATOM 3381	0110	66.723 ₁	6.772 15.66	, - 04.52
ATOM 3384	OH2 TIP3 234 OH2 TIP3 235	88.036 2	2.036 4.25	33.79
ATOM 3387	2	12.085	2.346 27.862	00 61.83
ΛTOM		64.898 -(10.29
ATOM 22		72.114 28	• •	00.00
ATIOM and	230	25.792 -8		55.01
ATOM 222	OH2 TIP3 239			33.19
T. Trans	OH2 TIP3 240			1.00 51.54
ATOM 2.45	OH2 TIP3 241			1.00 46.53
ATTOM 2	OH2 TIP3 242		.818 -2.226	1.00 47.29
777074	OH2 TIP3 243		.496 18.074	1.00 40.10
ATTOM S.	DH2 TIP3 244	~ a	.480 5.497	1.00 49.90
)H2 TIP3 245	• -	093 11.497	1.00 45.71
ATOM 3417 O	H2 TIP3 246		232 32.172	
	- 	66.196 6.	250 12.159	
				1.00 34.47



TABLE 3

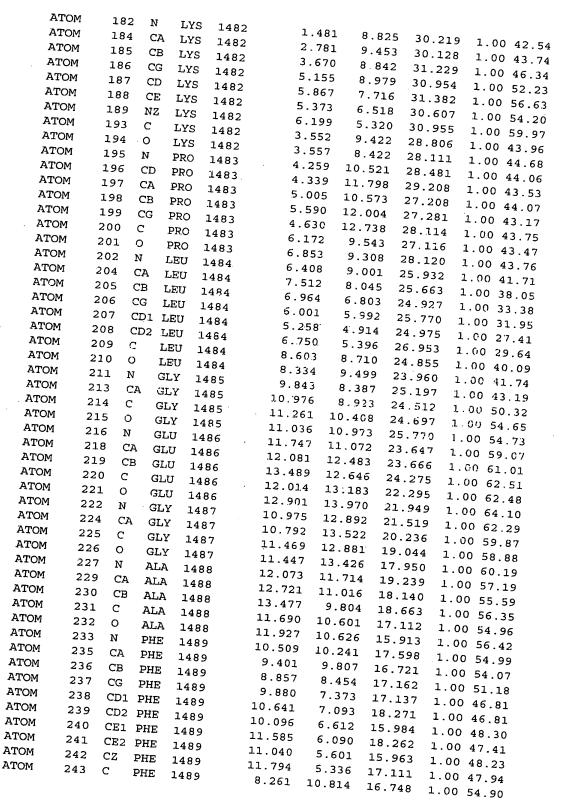
Atom		tom	. A.A	A.A	Х	Y	Z	occ	В	
No.		уре	Туре		 					
ATOM	. 1	N	GLU	1464	-13.712	16.996	8.424	1.00	61.15	
MOTA	3	CA	GLU	1464	-12.478	17.133	7.646		60.03	
MOTA	4	CB	GLU	1464	-11.465	18.020	8.378		62.43	
MOTA	5	C	GLU	1464	-11.865	15.766	7.319	1.00	57.36	
MOTA	6	0	GLU	1464	-11.765	15.402	6.145	1.00	60.80	
MOTA	7	N	LEU	1465	-11.466	15.003	8.333	1.00	50.25	
MOTA	9	CA	LEU	1465	-10.899	13.691	8.067	1.00	42.73	
ATOM	10	CB	LEU	1465	-10.097	13.171	9.258	1.00	41.34	
ATOM	11	CG	LEU	1465	-8.571	13.277	9.169	1.00	39.78	
MOTA	12	CD1	LEU	1465	-8.175	14.728	8.977	1.00	45.14	
MOTA	13	CD2	LEU	1465	-7.926	12.722	10.426	1.00	34.20	-
MOTA	14	С	LEU	1465	-12.009	12.706	7.748	1.00	39.42	
MOTA	15	0	LEU	1465	-13.070	12.719	8.375	1.00	36.63	
MOTA	1.6	N	PRO	1466	11.821	11.919	6.682	1.00	38.54	
ATOM	17	CD	PRO	1466	-10.682	12.019	5.751	1.00	37.04	
MOTA	18	CA	PRO	1466	-12.781	10.902	6.232	1.00	38.75	•
MOTA	1.9	CB	PRO	1466	-12.176	10.426	4.910	1.00	39.49	
MOTA	20	CG	PRO	1466	-10.681	10.667	5.109	100	40.64	
ATOM	21	C	PRO	1466	-12.859	9.756	7.246	1.00	39.08	
MOTA	22	0	PRO	1466	-11.834	9.283	7.748	1.00	41.23	
MOTA	23	N	GLU	1467	-14.064	9.278	7.513	1.00	37.11	
MOTA.	25	CA	GLU	1467	-14.247	8.213	8.482	1.00	35.96	
MOTA	26	CB	GLU	1467	-15.725	8.123	8.863	1.00	39.90	•
MOTA	27	CG	GLU	1467	-16.334	9.410	9.417	1.00	46.64	
MOTA	28	CD	GLU	1467	-17.823	9.280	9.694	1.00	51.50	
MOTA	° 59	OE1	GLU	1467	-18.294	8.135	9.854	1.00	54.17	
MOTA	30	OE2	GLU	1467	-18.529	10.315	9.756	1.00	53.39	
MOTA	31	С	GLU [.]	1467	-13.794	6.865	7.939	1.00	33.77	
ATOM	32	0	GLU	1467	-13.885	6.632	6.740	1.00	36.27	
MOTA	33	N	ASP	1468	-13.291	5.991	8.813	1.00	29.80	
MOTA	35	CA	ASP	1468	-12.869	4.649	8.409	1.00	28.19	
MOTA	36	CB	ASP	1468	-11.362	4.567	8.120	1.00	27.83	
MOTA	37	CG	ASP	1468	-10.942	3.223	7.507	1.00	27.78	
MOTA	38	OD1	ASP	1468	-11.689	2.225	7.592	1.00	25.64	
MOTA	39	OD2	ASP	1468	-9.836	3.165	6.935	1.00	27.59	
MOTA	40	С	ASP	1468	-13.244	3.672	9.512	1.00	28.05	
MOTA	41	0	ASP	1468	-12.462	3.404	10.437	1.00	25.89	
ATOM	42	N	PRO	1469	-14.446	3.089	9.403	1.00	29.07	
MOTA	43	CD	PRO	1469	-15.401	3.311	8.298	1.00	29.93	
ATOM	44	CA	PRO	1469	-14.981	2.124	10.365	1.00	28.65	
ATOM	45	CB	PRO	1469	-16.235	1.615	9.659	1.00	30.89	
ATOM	46	CG	PRO	1469	-16.690	2.811	8.879	1.00	28.99	
MOTA	47	С	PRO	1469	-14.029	0.974	10.687	1.00	27.63	
ATOM	48	0	PRO	1469	-14.136	0.364	11.748	1.00	26.94	
ATOM	49	N	ARG	1470	-13.128	0.666	9.758		26.37	
ATOM	51	CA	ARG	1470	-12.161	-0.414	9.947		26.64	



ATO)M -			
ATO			ARG 14	70 -11.363 -0.661 8.666
ATO			ARG 14	70 -13 150 5.00 1.00 27.12
			ARG 14	70 -11 100 1.014 7.424 1.00 29.72
ATO			ARG 147	70
ATO			ARG 147	70 0.044 5.971 1.00 32 56
ATO	50	NHl	ARG 147	4.948 1 00 37 60
OTA			ARG 147	0.784 4.091 1.00 44 25
ATON	0 1	C	ARG 147	0 4.778 1 00 34 70
ATOM		0	ARG 147	0 -11.129 -0.176 11.051 1.00 27.50
ATOM	1 66	N	TRP 147	10.504 -1.123 11 522 1 62
ATOM		CA	TRP 147	1.079 11 421 1 00
ATOM	69			1.362 12 408 1 00 00
ATOM	70			-8.661 1.938 11.686 1.00
ATOM	71			-8.010 0.051
ATOM				-7.100 .0.000
ATOM	73	CE3	_	-6 734 0 775
ATOM	74	CE3		-6.567 0.400 10.022 1.00 21.80
ATOM	75	CD1 7	_	-8 155 0 242
ATOM	77	NE1 T	_	-7.388 0.100 J.435 1.00 23.15
ATOM	78		RP 1471	-5.855 1 255 1.00 23.32
ATOM			RP 1471	-5 698 7 764
ATOM	79	CH2 T		-5.352 -2.235 1.00 21.72
ATOM	80	_	RP 1471	-10 224 2 272
ATOM	81		RP 1471	-9 497 2 222
ATOM	82		LU 1472	-11 217 2.334 14.546 1.00 29.29
	84	CA GI	U 1472	3.015 13.424 1.00 29.49
MOTA	85	CB GI	υ 1472	-12 020 14.453 1.00 29.97
ATOM		CG GI	Ψ 1472	13.961 1.00 33.80
ATOM		CD GL		12 475 0.030 14.731 1.00 33 27
ATOM	88	DE1 GL	U 1472	7.249 14.195 1.00 34.26
ATOM		DE2 GL		7.191 13.055 1 00 38 00
ATOM	90 (GL		0.203 14.910 1 00 24 01
ATOM	91 () GL		3.366 15.826 1 00 27 20
ATOM	92 N	LE		2.309 15.945 1 00 20 20
ATOM	94 C	A LE		-11.619 4.069 16.866 1 00 35.01
ATOM	95 C	B LEU	,5	3.652 18 220 1
ATOM	96 C	G LEU		3.210 18 948 1 00 01
ATOM	97 C	D1 LEU		-10.766 2.923 20 454 7 3
ATOM	98 C	D2 LEU	1473	-11.498 1.613 20 701 1 02
ATOM	99 C	LEU		-9.385 2.872 21 Apr 1
ATOM	100 O	LEU	5	-12.426 4.907 18 882 7 ac
ATOM	101 N	PRO	1473	-11.968 6.016 18 507
ATOM	102 CI		1474	-13.479 4.766 19 706 1
ATOM	103 CA		1474	-14 290 2 553
ATOM	104 CE		1474	-14 088 5 005
ATOM			1474	-15.197 5.204 20.411 1.00 30.61
ATOM			1474	-15.613 4 330 21.226 1.00 28.15
ATOM		PRO	1474	-13 036 6 545
3	107 0	PRO	1474	-12 253 5 020 21.312 1.00 32.98
3.550	108 N	ARG	1475	-13 035 7 075
T MOSS	110 CA	ARG	1475	-12 060 9 605 21.366 1.00 32.75
	111 CB	ARG	1475	12 250 22.168 1.00 34 22
70000	112 CG	ARG	1475	12 150 10.116 21.997 1.00 34 21
ATOM	113 CD	ARG	1475	11 055 10.349 20.559 1.00 42 48
				-11.956 12.056 20.364 1.00 45.16

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MOTA	114	NE	ARG	1475	-11.655	12.317	18.954	1.00 45.65
ATOM	116	CZ	ARG	1475	-10.447	12.599	18.484	1.00 41.31
ATOM	117		ARG	1475	-9.420	12.686	19.318	1.00 35.94
ATOM	120		ARG	1475	-10.253	12.673	17.172	1.00 42.37
MOTA	123	С	ARG	1475	-12.114	8.232	23.641	1.00 35.29
ATOM	124	0	ARG	1475	-11.094	8.178	24.318	1.00 37.28
ATOM	125	N	ASP	1476	-13.304	7.931	24.129	1.00 35.37
ATOM	127	CA	ASP	1476	-13.468	7.570	25.526	1.00 36.97
ATOM	128	CB	ASP	1476	-14.952	7.586	25.896	1.00 39.47
ATOM	129	CG	ASP	1476	-15.748	6.501	25.205	1.00 40.02
MOTA	130		ASP	1476	-15.221	5.809	24.320	1.00 41.08
ATOM	131		ASP	1476	-16.926	6.327	25.571	1.00 47.00
ATOM	132	C	ASP	1476	-12.850	6.225	25.894	1.00 36.07
MOTA	133	0	ASP	1476	-12 830	5.842	27.066	1.00 36.26
ATOM	134	N	ARG	1477	-12.382	5.495	24.888	1.00 36.94
ATOM	136	CA	ARG	1477	-11.766	4.189	25.104	1.00 35.22
ATOM	137	CB	ARG	1477	-12.081	3.268	23.925	1.00 34.29
MOTA	138	CG	ARG	1477	-13.546	3.056	23.675	1.00 32.23
ATOM	139	CD	ARG	1477	-14.206	2.434	24.879	1.00 30.56
ATOM	140	NE	ARG	1477	-14.426	3.419	25.925	1.00 31.86
ATOM	142	CZ	ARG	1477	-14.730	3.126	27.182	1.00 33.09
ATOM	1.43		ARG	1477	-14.855	1.858	27.563	1.00 35.00
MOTA	146		ARG		-14.904	4.101	28.053	1.00 29.62
MOTA	149	C	ARG	1477	-10.262	4.270	25.271	1.00 35.51
ATOM	150	0	ARG	1477	-9.621	3.290	25.637	1.00 35.44
ATOM	151	Ŋ	LEU	1478	-9.704	5.444	25.023	1.00 34.59
MOTA	153	CA	LEU	1478	-8.270	5.630	25.129	1.00 36.35
MOTA	154	CB	LEU	1.478	-7.750	6.254	23.840	1.00 36.41
MOTA	155	CG	LEU	1478	-6.250	6.185	23.556	1.00 37.19
MOTA	156		LEU	1478	-5.791	4.728	23.479	1.00 34.63
ATOM	157		LEU	1478	-5.959	6.914	22.251	1 00 34.88
ATOM	158	C	LEU	1478	-7.901	6.517	26.325	1.00 38.74
ATOM	159	0	LEU	1478	-8.146	7.733	26.309	1.00 41.20
ATOM	160	N	VAL	1479	-7.311	5.907	27.355	1.00 36.92
MOTA	162	CA	VAL	1479	-6.885	6.622	28.560	1.00 35.79
MOTA	163	CB	VAL	1479	-6.929	5.693	29.780	1.00 35.81
ATOM	164		VAL	1479	-6.579	6.453	31.032	1.00 40.11
MOTA	165		VAL	1479	-8.302	5.056	29.907	1.00 35.59
ATOM	166	C	VAL	1479	-5.438	7.118	28.362	1.00 36.60
ATOM	167	0	VAL	1479	-4.479	6.369	28.583	1.00 33.48
ATOM	168	N	LEU	1480	-5.282	8.372	27.938	1.00 39.09
MOTA	170	CA	LEU	1480	~3.949	8.932	27.675	1.00 42.05
ATOM	171	CB	LEU	1480	-4.040	10.277	26.952	1.00 41.08
MOTA	172	CG	LEU	1480	-4.633	10.286	25.529	1.00 39.28
MOTA	173		LEU	1480	-4.766	11.720	25.051	1.00 40.04
MOTA	174		LEU	1480	-3.758	9.489	24.582	1.00 39.66
ATOM	175	C	LEU	1480	-3.001	9.027	28.867	1.00 41.51
ATOM	176	0	LEU	1480	-3.312	9.637	29.886	1.00 41.73
ATOM	177	N	GLY	1481	-1.817	8.444	28.697	1.00 40.68
ATOM	179	CA	GLY	1481	-0.849	8.439	29.775	1.00 41.28
ATOM	180	C	GLY	1481	0.412	9.225	29.529	1.00 43.08
ATOM	181	0	GLY	1481	0.474	10.147	28.701	1.00 45.65



	10 565 16.184 1.00 59.10
244 O PHE 1489	7.199 10.565 25.
ATOM 244	8.431 11.908 17.504 1.00 50 20
ATOM 245 N GHI 1190	7.432 12.958 17.611 1.00 49.82
ATOM 247 CIL	6.745 12.844 18.942 1.00 50 95
ATOM 248 C GL1 1490	7.266 12.161 19.837 1.00 49 53
ATOM 249 O GLY 1490	5 614 13.514 19.124 1.00 251
ATOM 250 N GLN 1491	4 022 13.441 20.395 1.00 43.20
ATOM 252 CA GLIN 1432	2 927 14.590 20.564 1.00 51.71
ATOM 253 CB GLIN 1131	2 429 14.796 21.994 1.00 04.00
ATOM 254 CG GLIN 1451	2 545 16.039 22.180 1.00 /1.55
ATOM 255 CD GLN 1451	2 524 16.922 21.352 1.00 //.54
ATOM 256 OEL GLIN 1432	1.024 16.083 23.289 1.00 76.32
ATOM 257 NE2 GLN 1491	4 207 12.083 20.505 1.00 43.31
ATOM 260 C GLN 1431	2 151 11.869 19.919 1.00 40.02
261 O GLN 1491	4 949 11.129 21.184 1.00 41.00
NUOM 262 N VAL 1432	4 293 9.810 21.421 1.00 37.44
ATOM 264 CA VAL 1492	5 235 8 665 21 025 1.00 34 74
265 CB VAL 1492	4 593 7.325 21.285 1.00 28.57
266 CG1 VAL 1492	- 760 19 553 1.00 33.70
267 CG2 VAL 1492	4 014 9.621 22.901 1.00 38.67
268 C VAL 1492	4 907 9.769 23.735 1.00 38.02
ATOM 269 O VAL 1492	2 776 9.276 23.250 1.00 39.30
ATTOM 270 N VAL 1493	2 423 9.062 24.653 1.00 37.75
ATOM 272 CA VAL 1493	1 257 9.970 25.093 1.00 37.30
ATOM 273 CB VAL 1493	1.237 13 403 24.689 1.00 39.11
274 CG1 VAL 1493	0.074 9.480 24.555 1.00 38.99
275 CG2 VAL 1493	7 503 24 877 1.00 36.38
ATOM 276 C VAL 1493	2.032
277 O VAL 1493	26 123 1.00 35.42
278 N LEU 1494	1 718 5.817 26.483 1.00 33.03
280 CA LEU 1494	2 536 5.291 27.670 1.00 29.88
- TON 281 CB LEU 1494	2 117 3 945 28.279 1.00 30.32
ATOM 282 CG LEU 1494	2 103 2.844 27.244 1.00 30.83
ATOM 283 CD1 LEU 1494	2 049 3.574 29.400 1.00 32.12
ATOM 284 CD2 LEU 1494	0.260 5.934 26.870 1.00 34.27
285 C LEU 1494	0.168 6.994 27.348 1.00 34.03
286 O LEU 1494	2 527 4.898 26.608 1.00 32.20
NTOM 287 N ALA 1495	1 930 4.954 26.980 1.00 29.71
289 CA ALA 1495	= 1.930 = 723 25 930 1.00 25.48
290 CB ALA 1495	2.409 3.567 27.183 1.00 28.03
ATOM 291 C ALA 1495	1 936 2,563 26.998 1.00 27.20
ATOM 292 O ALA 1495	2 510 27 615 1.00 32.20
- TOM 293 N GLU 1496	27 824 1.00 33.31
295 CA GLU 1496	2 063 29 301 1.00 35.05
296 CB GLU 1496	1 962 30.198 1.00 39.14
ATOM 297 CG GLU 1496	-3.521 -31 663 1.00 42.5/
298 CD GLU 1496	3 083 32.061 1.00 42.59
ATOM 299 OE1 GLU 1496	-4.469
300 OE2 GLU 1496	3 274 26.994 1.00 33.40
ATOM 300 C GLU 1490	3 261 27 017 1.00 34.36
ATOM 302 O GLU 149	5 -6.433 26 177 1.00 31.6/
ATOM 303 N ALA 149	7 -5.873 1 168 25.351 1.00 31.23
ATOM SOE CA ALA 149	7 -7.051 1.168 23.331 2.44
ATOM 305 CA	

ATOM	W 305	
ATOM	. CD ALA 1497	-6.671 0.750 23 052
	ALA 1497	23.953 1.00 28.13
ATOM	308 O ALA 1497	7.500 0.168 25.974 1.00 32 02
ATOM	309 N ILE 1498	26.261 1.00 33 45
ATOM	311 CA ILE 1400	0.602 26.282 1 00 24 15
ATOM	312 CB TLF 1400	-10.222 -0.294 26 954
ATOM	313 CG2 TLF 1400	0.453 27 670 7
ATOM	314 001 1436	-12.267 -0.551 28 300 3 3
ATOM	215 00-	-10.663 1.316 28 770
ATOM	316 0	-11.656 2 262 1.00 35.29
ATOM	217 2	-10.953 -0.920 1.00 31.69
ATOM	318 M CT	-11.571 -0.337
ATOM	320 02 000	-10.859 -2.245
ATOM	221 2	~11.544 -2.010
ATOM	200 - 011 1499	-10.673 -2.202 -1.00 46.90
ATOM	322 O GLY 1499	-9 001 J.299 23.298 1.00 49 69
ATOM	323 N LEU 1500	710 720 - 1.209 23.387 1.00 51 47
ATOM	325 CA LEU 1500	710 003 22.223 1.00 49 92
ATOM	326 CB LEU 1500	2.765 20.973 1.00 49.62
ATOM	327 CG LEU 1500	2.898 21.185 1.00 49 96
	328 CD1 LEU 1500	-5 0C2 21.167 1.00 49 26
ATOM	329 CD2 LEU 1500	
ATOM	330 C LEU 1500	10-1.638 -0.883 19.899 1.00 47 00
ATOM	331 O LEU 1500	-10.535 -4.027 20.275 1 00 40 40
ATOM	332 N PRO 1505	-10.480 -5.145 20.806 1 00 47 00
ATOM	333 CD PRO 1505	-13.253 -5.837 25.284 1 00 50 50
ATOM	334 CA PRO 1505	13.8// -7.173 25 220 1 45
ATOM	335 CB PRO 1505	-14.19/ -4.825 25 770
. ATOM	336 CG PRO 1505	-15.548 -5.521 25 627
ATOM	777 ~	-15.216 -6.944 25 940
ATOM	339 0	-13.904 -4.396 27 227
ATOM	220	-13.883 -3.202 27 531
ATOM	244 1506	-13.640 -5.363 28 102 H
ATOM	240	-13.337 - 5.053 4.00 42.10
ATOM	242 00 1506	-14.202 -5.893 30 434
ATOM	344 T206	-15.657 -5.493 30 205
ATOM	245	-15.999 -4.300 T.00 48.72
ATOM	240	-16.529 -6.470
ATOM	240 0	-11.863 -5 251
_	350 N	-11.487 -5 343
3.000	353 ~-	-11.029 -5 394 33 1.00 46.50
3 moss	14 14G 15U/	-9.594 -5.466
3.000	353 CB ARG 1507	-9.111 -6.650 -1.00 47.52
3	354 CG ARG 1507	-9.327 7.000 28.142 1.00 54.20
7.000	355 CD ARG 1507	7.993 28.781 1.00 64.52
B. Change	356 NE ARG 1507	29.963 1.00 71 17
3.50	358 CZ ARG 1507	30.556 1.00 76 52
7 (7)	59 NH1 ARG 1507	-7 210 31.689 1.00 81 64
*	62 NH2 ARG 1507	32.375 1.00 83 30
3	65 C ARG 1507	32.174 1 00 84 44
3	66 O ARG 1507	-8.8/1 -4.234 28.485 1 00 42 44
	67 N VAL 1508	-9.227 -3.695 27.440 1 00 43 73
	69 CA VAL 1508	-7.912 -3.749 29.265 1 00 40 04
ATOM 37		7.143 -2.598 28.830 1 00 38 37
	- ~506	-6.786 -1.604 29.961 1.00 34.90
\$\$\$D/\$\$145		- 2.00 34.90

ATOM	371	CG1	VAL	1508	-8.038	-1.124	30.646	1.00 41.81
ATOM	372	CG2	VAL	1508	~5.850	-2.226	30.944	1.00 35.89
ATOM	373	С	VAL	1508	-5.874	-3.147	28.211	1.00 36.81
ATOM	374	0	VAL	1508	-5.371	-4.191	28.637	1.00 35.13
ATOM	375	N	THR	1509	-5.393	-2.465	27.180	1.00 36.04
ATOM	377	CA	THR	1509	-4.184	-2.854	26.485	1.00 33.31
ATOM	378	CB	THR	1509	-4.503	-3.254	25.025	1.00 33.79
MOTA	379	OG1	THR	1509	-5.511	-4.275	25.014	1.00 33.98
ATOM	381	CG2	THR	1509	-3.259	-3.774	24.321	1.00 32.78
MOTA	382	C	THR	1509	-3.268	-1.627	26.453	1.00 32.37
ATOM	383	0	THR	1509	-3.718	-0.533	26.113	1.00 31.97
ATOM	384	N	LYS	1510	-2.015	-1.786	26.884	1.00 32.96
ATOM	386	CA	LYS	1510	-1.071	-0.673	26.828	1.00 33.25
MOTA	387	CB	LYS	1510	0.157	-0.902	27.699	1.00 34.65
ATOM	388	CG	LYS	1510	-0.093	-0.909	29.197	1.00 39.64
ATOM	389	CD	LYS	1510	1.237	-1.105	29.913	1.00 43.51
ATOM	390	CE	LYS	1510	1.110	-1.949	31.173	1.00 48.42
ATOM	391	NZ	LYS	1510	0.399	-1.256	32.287	1.00 53.03
ATOM	395	С	LYS	1510	-0.646	-0.550	25.370	1.00 32.26
ATOM.	396	0	LYS	1510	-0.240	-1.533	24.736	1.00 30.20
ATOM	397	N	VAL	1511	-0.760	0.665	24.849	1.00 32.28
ATOM	399	CA	VAL	1511	.0.436	0.980	23.472	1.00 30.73
ATOM	400	CB	VAL	1511	-1.738	1.140	22.666	1.00 32.25
ATOM	401	CG1	VAL	1511	-2.566	0.147	22.723	1.00 29.00
ATOM	402	CG2	VAL	1511	-2.549	2.347	23.193	1.00 29.17
ATOM	403	C	VAL	1511	0.329	2.307	23.423	1.00 30.91
ATOM	404	0	VAL	1511	0.445	3.008	24.433	1.00 31.94
ATOM	405	N	ALA	1512	0.842	2.658	22.250	1.00 27.30
ATOM	407	CA	ALA	1512	1.550	3.914	22.094	1.00 24.22
ATOM	408	СВ	ALA	1512	2.921	3.694	21.493	1.00 23.39
ATOM	409	C	ALA	1512	0.698	4.769	21.181	1.00 23.62
ATOM	410	0	ALA	1512	0.116	4.271	20.228	1.00 22.69
ATOM	411	N	VAL	1513	0.605	6.054	21.484	1.00 27.51
ATOM	413	CA	VAL	1513	-0.192	6.984	20.688	1.00 30.03
ATOM	414	CB	VAL	1513	-1.359	7.613	21.522	1.00 28.31
ATOM	415	CG1	VAL	1513	-2.218	8.522	20.650	1.00 28.93
ATOM	416	CG2	VAL	1513	-2.214	6.542	22.159	1.00 26.00
ATOM	417	C	VAL	1513	0.674	8.108	20.107	1.00 31.21
ATOM	418	0	VAL	1513	1.370	8.816	20.834	1.00 29.73
ATOM	419	N	LYS	1514	0.631	8.225	18.784	1.00 33.99
ATOM	421	CA	LYS	1514	1.342	9.258	18.037	1.00 35.44
ATOM	422	CB	LYS	1514	1.831	8.692	16.707	1.00 34.55
ATOM	423	CG	LYS.	1514	2.835	7.586	16.872	1.00 35.38
ATOM	424	CD	LYS	1514	3.025	6.807	15.599	1.00 36.87
ATOM	425	CE	LYS	1514	3.457	7.710	14.438	1.00 45.19
ATOM	426	NZ	LYS	1514	4.598	8.622	14.755	1.00 44.31
ATOM	430	C	LYS	1514	0.304	10.345	17.761	1.00 35.97
ATOM	431	Ō	LYS	1514	-0.806	10.037	17.299	1.00 34.39
ATOM	432	N	MET	1515	0.673	11.596	18.028	1.00 38.17
ATOM	434	CA	MET	1515	-0.207	12.747	17.835	1.00 41.17
ATOM	435	СВ	MET	1515	-0.901	13.098	19.145	1.00 39.54
ATOM	436	CG	MET	1515	0.075	13.428	20.255	1.00 39.11
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	TOM 437 SD MET 1515	
	FOM 438 CE MET 1515	13.612 21.799 1 00 43 65
	10M 439 C MET 1515	11.937 22 007 7
	FOM 440 O MET 1515	0.612 13.939 17 391 1 22
AT	OM 441 N LEU 1516	1.834 13.905 17 445
	OM 443 CA LEU 1516	-0.053 14.962 16.872 1.00 45.72
ATO	OM 444 CB LEI 1516	0.640 16.175 16.448 1
ATO	OM 445 CG LETT 1536	-0.152 16.917 15 374
ATO	OM 446	-0.413 16.254 14 036 3 3
ATC	JM 447 CD2 LETT 1515	-1.418 17 104
ATC	OM 448 C 1516	0.884 16 100 48.16
ATO	JW 110 - 770 1216	0.810 17 170 1.00 42.80
ATO	M 450 N LVC 1516	0.217 16.927 18 703
ATO	M 452 CA 755	1.580 19 174
ATO	M 453 CD 733	1.823 19 103 17.402 1.00 60.97
ATO	M 454 CC THE	3.274 19 660 11.00 65.19
ATON	M 455 1517	4.294 10 550
ATOM	M 456 CD LYS 1517	5.646 18 035 1.00 72.86
ATOM	M 457 NZ	6.686 17 951
ATOM	1 161 - LIS 1517	8.010 18 241 13.19/ 1.00 74.38
ATOM	1 462 0	0.879 20 357
ATOM	1 462 1 1517	0.303 20 451
ATOM	165 N SER 1518	0.776 21 272
ATOM	166 OHK .1518	-0.107 22 422
ATOM	100 CB SER 1518	-0.002 23 222 18.972 1.00 71.92
ATOM	160 SER 1518	0 344 -3.322 20.202 1.00 69 89
ATOM	160 O SER 1518	17.718 1.00 74 68
ATOM	472 - ASP 1519	1 412 17.006 1 00 77 44
ATOM	470 CT ASP 1519	1 700 04 17.422 1.00 76 04
ATOM	472 ~ 1519	2 126 2 16.264 1.00 76 49
ATOM	474 6 ASP 1519	1 972 25.011 16.539 1.00 77 59
ATOM	475 - ASF 1519	2 274 2: 14.958 1.00 75.88
ATOM	1920	1.486 22 265
ATOM	470 CT ALIA 1520	1.574 21 420 14.956 1.00 74.39
ATOM	FUA 1520	0 930 20 22 13.758 1.00 72.83
ATOM	- ALA 1520	0 880 27 14.010 1.00 73 06
ATOM	401 TALLA 1520	10 006 22 12.598 1.00 71 47
ATOM	481 N THR 1521	1.440 33 015
ATOM	483 CA THR 1521	0.050 05 11.401 1.00 69 15
ATOM	484 CB THR 1521	1 950 22 715
ATOM	485 OG1 THR 1521	2 505 23.110 9.272 1.00 70.21
ATOM	487 CG2 THR 1521	2 052 8.607 1.00 72 71
ATOM	488 C THR 1521	-0.015 10.043 1.00 71 01
ATOM	489 O THR 1521	0.015 41.016 9.550 1.00 70 64
ATOM	490 N GLU 1522	20.443 9.932 1.00 72 38
	492 CA GLU 1522	8.542 1.00 69 70
ATOM	493 CB GLU 1522	7.815 1.00 67.41
ATOM	494 C GLU 1522	-0.710 21.800 6.761 1.00 70.01
ATOM	495 O GLU 1522	7.168 1 00 64 50
ATOM	496 N LYS 1523	7.006 1 00 63 76
ATOM	498 CA LYS 1523	0.512 20.419 6.827 1 00 60 75
ATOM	499 CB LYS 1523	1.483 19.502 6.240 1 00 50
ATOM	500 CG LYS 1523	2.782 20.230 5.883 1 00 60 63
		3.909 19.318 5.361 1.00 62.47
6000		00 02.4/

ATOM	501	CD	LYS	1523	3.459	18.461	4.168	1.00	63.35
ATOM	502	CE	LYS	1523	4.633	17.700	3.559	1.00	66.57
ATOM	503	NZ	LYS	1523	4.210	16.733	2.498	1.00	69.56
ATOM	507	С	LYS	1523 .	1.763	18.441	7.281	1.00	55.98
MOTA	508	0	LYS	1523	1.790	17.251	6.972	1.00	56.37
ATOM	509	N	ASP	1524	1.960	18.885	8.517	1.00	52.16
ATOM	511	CA	ASP	1524	2.211	17.980	9.630	1.00	48.91
ATOM	512	CB	ASP	1524	2.487	18.762	10.915	1.00	50.87
ATOM	513	CG	ASP	1524	3.865	19.401	10.928	1.00	53.00
ATOM	514	OD1	ASP	1524	4.004.	20.511	11.489	1.00	53.77
ATOM	515	OD2	ASP	1524	4.816	18.785	10.394	1.00	56.30
ATOM	516	С	ASP	1524	1.032	17.031	9.831	1.00	45.34
ATOM	517	0	ASP	1524	1.221	15.858	10.176	1.00	45.63
MOTA	518	N	LEU	1525	-0.176	17.530	9.593	1.00	40.15
ATOM	520	CA	LEU	1525	-1.368	16.715	9.711	1.00	39.38
ATOM	521	CB	LEU	1525	-2.624	17.588	9.633	1.00	41.66
ATOM	522	CG	LEU	1525	-4.020	16.937	9.585	1.00	42.75
ATOM	523	CD1	LEU	1525	-4.245	15.945	10.727	1.00	42.97
ATOM	524	CD2	LEU	1525	-5.058	18.026	9.644	1.00	42.24
ATOM	525	С	LEU	1525	-1.340	15.699	8.575	1.00	39.77
ATOM	526	0	LEU	1525	-1.509	14.506	8.813	1.00	39.11
ATOM	527	N .	SER	1526	-1.062	16,172	7.361	1.00	39.64
ATOM	529	CA	SER	1526	-0.998	15.320	6.181	1.00	40.65
ATOM	530	СВ	SER	1526	-0.541	16.105	4.947	1.00	43.32
ATOM	531	OG	SER	1526	-1.398	17.190	4.656	1.00	52.41
ATOM	533	C:	SER	1.526	-0.015	14.201	6.383	1.00	39.12
ATOM	534	O	SER	1526 .	-0.346	13.038	6.198	1.00	41.75
ATOM	535	N	ASP	1527	1.203	14.553	ö.769	1.00	38.30
ATOM	537	CA	ASP	1527	2 244	13.552	6.969	1.00	39.28
ATOM	538	CB	ASP	1527 .	3.531	14.208	7.47:	1.00	41.16
MOTA	539	CG	ASP	1527 ·	4.218	15.069	6.404	1.00	45.20
ATOM	540	OD1	ASP	1527	3.861	14.972	5.198	1.00	43.25
ATOM	541	OD2	ASP	1527	5.132	15.840	6.788	1.00	45.93
ATOM	542	С	ASP	1527	1.788	12.443	7.903	1.00	37.34
ATOM	543	0	ASP	1527	1.867	11.259	7.557	1.00	37.24
MOTA	544	N	LEU	1528	1.224	12.935	9.036	1.00	35.88
ATOM	546	CA	LEU	1528	0.728	11.874	10.009		35.07
ATOM	547	CB	LEU	1528	0.185	12.606	11.242	1.00	34.38
ATOM	548	CG	LEU	1528	-0.146	11.789	12.491	1.00	35.86
MOTA	549	CD1	LEU	1528	1.009	10.845	12.820	1.00	34.83
MOTA	550	CD2	LEU	1528	-0.435	12.711	13.642	1.00	29.98
MOTA	551	С	LEU	1528	-0.351	10.977	9.374	1.00	33.31
MOTA	552	0	LEU	1528	-0.342	9.756	9.552	1.00	34.55
ATOM	553	N	ILE	1529	-1.236	11.575	8.585	1.00	32.16
ATOM	555	CA	ILE	1529	-2.306	10.829	7.924		30.94
ATOM	556	CB	ILE	1529	-3.304	11.757	7.178		27.07
ATOM	557	CG2	ILE	1529	-4.388	10.926	6.521		26.06
A'TOM	558	CG1		1529	-3.953	12.723	8.169		23.67
ATOM	559	CD1	ILE	1529	-4.877	13.736	7.526		22.34
ATOM	560	C	ILE	1529	-1.684	9.856	6.947		31.34
ATOM	561	ō	ILE	1529	-2.058	8.683	6.912		33.57
ATOM	562	N	SER	1530	-0,703	10.331	6.191		30.74
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ATO		4 CA	SER 1	530	0 (
ATO		5 CB		530	0.0	_		.230	1.00	32.04
ATO		S OG		330	1.1			548	1.00	35.20
ATO		_	~	30	0.5 0.6		~	002	1.00	41.97
ATO		9 0		30	0.4			895		29.06
ATOM) N		31	1.2			377	1.00	26.64
ATOM	*		GLU 15		1.9			034.	1.00	23.86
ATOM		CB (GLU 15		2.7	`		759	1.00	23.86
ATOM	- · -	,	GLU 15		3.5			944		25.69
ATOM			GLU 15		4.34			701 :	1.00	23.65
ATOM	•	OE1 (LU 15:		4.92		319 10.		L.00	26.03
ATOM		OE2	LU 153	31	4.43		473 11.	572]	.00	25.92
ATOM		C G	LU 153		0.90		549 11.0	094 1	00	26.55
ATOM		O G	LU 153		1.20		325 8.2	222 1	.00	25.44
ATOM	580	N M	ET 153		-0.28			28 1	.00 :	23.67
ATOM	582	CA M	ET 153					00 1	.00.2	26.39
ATOM	583	CB M	ET 153		-1.36			48 1	.00 2	6.57
ATOM	584	CG M	ET 153		-2.47			14 1	.00 2	4.81
ATOM	585	SD M	ET 153		-3.64			91 1	.00 2	
ATOM	586	CE MI	ET 153		-4.96			60 1	.00 2	8.43
ATOM	587	C M			-5.17	_	-	76 1	.00 2	4.45
ATOM	588	O ME			-1.923	_		51 1.	00 2	8.30
ATOM	589	N GI			-2.048			331.	00 2	7.95
ATOM	591	CA GI			-2.221			521.	00 2	8.95
ATOM	592	CB GL			-2.732	-		5 î.	00 30	0.32
MOTA	593	CG GL			-2.983			'6 1.	00 25	5.40
ATOM	594	CD GL			-4.064				00 26	
ATOM	595	OE1 GL	-		-5.402 -5.012			91.	00 25	.89
ATOM	596	OE2 GL	U 1533		-5.913			0 1.	00 27	.24
ATOM		C GL			-5.964 -1.723	6.66		9 1.	00 30	.00
ATOM	598	O GL				4.08		3 1.0	00 31	.64
ATOM	599	N MET			-2.080	2.98		61.(00 33	
ATOM	601	CA MET			-0.455 0.664	4.47		5 1.(00 33	. 57
ATOM		CB MET			1.957	3.61		3 1.0	0 32	.86
ATOM	603 (CG MET			3.159	4.39		3 1.0	0 32	.89
ATOM		SD MET	1534		3.577	3.559		1.0	0 39	. 27
ATOM		CE MET	1534		5.153	3.513	-		0 51.	. 24
ATOM	606 (MET			0.670	4.319			0 44.	.97
ATOM	607 C) MET			0.816	2.373			0 31.	84
ATOM	608 V	MET	1535		0.509	1.250			0 33.	78
ATOM		A MET	1535		0.469	2.571		_	О 30.	36
ATOM		B MET	1535		0.419	1.453		1.0	0 28.	83
ATOM		G MET	1535		1.717	1.946		1.00	24.	75
ATOM	613 S	D MET	1535		1.722	2.540		1.00	21.	50
ATOM	614 C	E MET	1535		1.681	2.764	11.628	1.00	22.	97
ATOM	615 C	MET	1535			4.534	11.727	1.00	23.	90
ATOM	616 O	MET	1535		-0.725 -0.636	0.540	7.572	1.00	30.3	33
ATOM	617 N	LYS	1536		-0.636 -1.833	-0.694	7.706	1.00	33.3	31
ATOM	619 C		1536		-1.823	1.135	7.104	1.00	28.9	91
ATOM	620 CE		1536		-3.011	0.364	6.732	1.00	28.0	7
ATOM	621 CG		1536		-4.176	1.289	6.413	1.00	25.5	2
ATOM	622 CD		1536		-4.689	2.080	7.579	1.00	21.4	6
					-5.810	2.979	7.127	1.00	19.8	9
									. •	-



ATOM	623	CE	LYS	1536	-6.414	3.717	8.288	1.00 23.50
MOTA	624	NZ	LYS	1536	-7.469	4.668	7.850	1.00 23.53
MOTA	628	C	LYS	1536	-2.765	-0.542	5.530	1.00 29.09
MOTA	629	0	LYS	1536	-3.127	-1.708	5.550	1.00 34.02
MOTA	630	N	MET	1537	-2.141	-0.009	4.488	1.00 29.03
ATOM	632	CA	MET	1537	-1.869	-0.792	3.288	1.00 30.13
ATOM	633	CB	MET	1537	-1.315	0.111	2.177	1.00 31.96
ATOM	634	CG	MET	1537	-2.304	1.114	1.589	1.00 35.15
MOTA	635	SD	MET	1537	-3.757	0.380	0.787	1.00 41.18
MOTA	636	CE	MET	1537	-3.026	-0.360	-0.666	1.00 43.05
ATOM	637	C	MET	1537	-0.905	-1.946	3.531	1.00 30.22
MOTA	638	0	MET	1537	-1.118	-3.051	3.045	1.00 30.88
MOTA	639	N	ILE	1538	0.164	-1.686	4.275	1.00 30.91
ATOM	641	CA	ILE	1538	1.192	-2.701	4.536	1.00 30.29
ATOM	642	CB	ILE	1538	2.429	-2.082.	5.221	1.00 28.64
ATOM	643	CG2	ILE	1538	3.493	-3.142	5.453	1.00 29.84
ATOM	644	CG1	ILE	1538	3.025	-1.030	4.287	1.00 32.82
ATOM	645	CD1	ILE	1538	4.358	-0.446	4.763	1.00 38.38
ATOM	646	С	ILE	1538	0.759	-4.000	5.237	1.00 29.07
ATOM	647	0	ILE	1538	1.229	-5.078	4.876	1.00 28.30
ATOM	648	N	GLY	1539	-0.178	-3.925	6.174	1.00 27.61
ATOM	650	CA	GLY	1539	-0.592	-5.147	6.849	1.00 26.22
ATOM	651	С	GLY	1539	0.273	-5.484	8.055	1.00 25.67
ATOM	652	0	GLY	1.539	1.345	-4.906	8.241	1.00 28.05
ATOM	653	N	LYS	1540	-0.150	-6.483	8.819	1.00 23.80
ATOM	655	CA.	LYS	1540	0.532	-6.876	10.046	1.00 21.77
ATOM	656	СВ	LYS	1540	-0.491	-7.436	11.045	1.00 20.04
ATOM	657	CG	LYS	1540	-1.505	-6.435	11.480	1.00 24.45
ATOM	658	CD	LYS	1540		-6.997	12.488	1.00 32.57
ATOM	659	CE	LYS	1540	-3.516	-5.946	12.882	1.00 35.05
ATOM	660	NZ	LYS	1540	-2.959	-4.850	13.733	1.00 39.81
ATOM	664	С	LYS	1540	1.669	-7.862	9.958	1.00 20.19
ATOM	665	0	LYS	1.540	1.671	-8.738	9.099	1.00 21.80
ATOM	666	N	HIS	1541	2.626	-7.722	10.876	1.00 19.98
ATOM	668	CA	HIS	1541	3.770	-8.626	11.000	1.00 22.43
ATOM	669	СВ	HIS	1541	4.854	-8.374	9.965	1.00 22.34
ATOM	670	CG	HIS	1541	5.892	-9.455	9.923	1.00 20.68
ATOM	671	CD2	HIS	1541	5.906	-10.654	9.295	1.00 20.60
ATOM	672		HIS	1541	7.074	-9.382	10.633	1.00 23.67
ATOM	674		HIS	1541	7.771	-10.490	10.444	1.00 23.35
ATOM	675		HIS	1541		-11.278	9.634	1.00 22.04
ATOM	677	С	HIS	1541	4.385	-8.477	12.376	1.00 27.21
ATOM	678	0	HIS	1541	4.538	-7.367	12.885	1.00 31.33
ATOM	679	N	LYS	1542	4.726	-9.619	12.958	1.00 29.25
ATOM	681	CA	LYS	1542	5.319	-9.698	14.285	1.00 30.39
ATOM	682	CB	LYS	1542	5.660	-11.151	14.610	1.00 33.76
ATOM	683	CG	LYS	1542	6.232	-11.370	15.994	1.00 33.70
ATOM	684	CD	LYS	1542	6.400	-12.833	16.230	1.00 42.10
ATOM	685	CE	LYS	1542		-13.499	14.988	1.00 57.71
ATOM	686	NZ	LYS	1542		-14.904	15.237	1.00 57.71
ATOM	690	C	LYS	1542	6.515	-8.808	14.462	1.00 02.03
ATOM	691	0	LYS	1542	6.690	-8.232	15.522	1.00 27.21
111011		_			3.000	0.232	10.000	2.00 25.00

ATO		N A	ASN 1543	7 202
ATO			ASN 1543	7.293 -8.619 13.410 1.00 23.81
ATON			ASN 1543	0.4/2 -7.787 13.537 1.00 24.70
ATOM		_	SN 1543	3.697 -8.550 13.031 1.00 24.68
ATOM		OD1 A	SN 1543	0.734 -9.855 13.793 1.00 24.82
ATOM		ND2 A		10.055 10.942 13.239 1.00 27.33
ATOM		_	SN 1543	10.255 -9.758 15.078 1.00 16.75
ATOM	·	O A	SN 1543	8.444 -6.326 13.032 1.00 24.93 9.469 -5.781 12.623 1.00 25.93
ATOM		N I	LE 1544	7 276 5 5 5 1.00 26.76
ATOM		CA I	LE 1544	7 121 4 222
ATOM		CB I	LE 1544	6 536
ATOM	707	CG2 II	E 1544	0.026 -4.095 11.240 1.00 23.23
ATOM	708	CG1 II		5 192 4 503
ATOM	709	CD1 II		1.063 1.00 22.57
ATOM	710 (C II		9.659 1.00 17.59
ATOM	711 () II		5 336 56 13.696 1.00 21.64
ATOM	712 n	II.		5.399 -4.377 14.397 1.00 21.00
MOTA	714 (A IL		5.167 -2.340 13.856 1.00 21.59
ATOM	715 c	B IL		5.214 -1.687 14.746 1.00 24.05
ATOM	716 C	G2 IL		1.00 23.68
ATOM	717 C	G1 IL		0.500 15.831 1.00 21.90
ATOM	718 C	D1 IL		0.580 -0.284 16.050 1.00 21 94
ATOM	719 C			0.843 -0.808 17.446 1.00 9.18
ATOM	720 O			3.914 -1.641 13.955 1.00 25 08
ATOM	721 N			3.842 -1.001 12.897 1.00 26 68
ATOM	723 C			2.358 14.455 1.00 25.88
. ATOM	724 CI			1.002 -2.424 13.800 1.00 24 61
MOTA	725 CC			3.793 14.005 1.00 23.18
ATOM.	726 OI	1 ASN		1.739 -4.923 13.434 1.00 21.54
ATOM		2 ASN		1.884 -5.059 12.214 1.00 21.52
ATOM	730 C	ASN		2.319 -5.748 14.313 1.00 18 83
MOTA	731 0	ASN	1546	0.046 -1.368 14.292 1.00 23.02
ATOM	732 N	LEU	1547	0.739 ~0.911 15.429 1.00 25 66
ATOM	734 CA		1547	13.422 1.00 24 45
ATOM	735 CB		1547	1.336 -0.041 13.692 1.00 24.27
ATOM	736 CG		1547	0.553 12.360 1.00 18 04
ATOM	737 CD	1 LEU	1547	1.515 12.343 1.00 19 96
ATOM		2 LEU	1547	2.830 2.928 12.842 1.00 10.60
ATOM	739 C	LEU	1547	3.333 1.570 10.924 1.00 16.44
ATOM	740 0	LEU	1547	2.469 -0.826 14.384 1.00 26.95
ATOM	741 N	LEU	1548	2.033 -1.934 13.956 1.00 27.38
ATOM	743 CA	LEU	1548	2.338 -0.260 15.460 1.00 26.61
ATOM	744 CB	LEU	1548	16.222 1 00 26 25
ATOM	745 CG	LEU	1548	3.717 -0.951 17.721 1.00 22 48
ATOM		LEU		2.370 -1.553 18.117 1.00 20 24
ATOM		LEU	1548	-2.282 -1.656 19.616 1.00 19 27
ATOM	748 C	LEU	1548 1548	-2.175 -2.929 17.492 1.00 19.23
ATOM	749 0	LEU		-5.401 -0.198 16.017 1.00 26 75
ATOM	750 N	GLY	1548	-6.447 -0.837 16.036 7 00 35 56
ATOM	752 CA	GLY	1549	-5.367 1.115 15.823 1.00 25 78
ATOM	753 C	GLY	1549	-6.607 1.843 15.616 1.00 25 80
ATOM	754 0	GLY	1549	-6.319 3.324 15.490 1.00 27.76
		2111	1549	-5.148 3.716 15.405 1.00 28.05
				00 20.05



MOTA	755	N	ALA	1550	-7.369	4.143	15.530	1.00 27.34
MOTA	757	CA	ALA	1550	-7.212	5.582	15.414	1.00 25.85
MOTA	758	CB	ALA	1550	-6.925	5.947	13.978	1.00 23.09
MOTA	759	C	ALA	1550	-8.430	6.353	15.897	1.00 26.58
MOTA	760	0	ALA	1550	-9.562	5.866	15.797	1.00 28.26
MOTA	761	N	CYS	1551	-8.182	7.551	16.429	1.00 26.30
MOTA	763	CA	CYS	1551	-9.227	8.471	16.899	1.00 28.29
ATOM	764	CB	CYS	1551	-8.966	8.952	18.342	1.00 27.12
ATOM	7.65	SG	CYS	1551	-9.101	7.681	19.630	1.00 27.09
ATOM	766	С	CYS	1551	-9.092	9.646	15.934	1.00 28.57
ATOM	767	0	CYS	1551	-8.156	10.436	16.044	1.00 26.80
ATOM	768	N	THR	1552	~9.966	9.699	14.933	1.00 29.27
ATOM	770	CA	THR	1552	-9.889	10.736	13.921	1.00 29.30
ATOM	771	CB	THR	1552	- 9.779	10.110	12.495	1.00 27.19
MOTA	772	OG1	THR	1552	-10.978	9.393	12.191	1.00 26.68
ATOM	774	CG2	THR	1552	-8.629	9.133	12.414	1.00 27.00
MOTA	775	С	THR	1552	-11.045	11.716	13.905	1.00 29.86
ATOM	776	0	THR	1552.	-10.918	12.838	13.403	1.00 30.69
MOTA	777	N ·	GLN	1553	-12.201	11.268	14.369	1.00 31 21
ATOM	779	CA	GLN	1553	-13.374	12.124	14.329	1.00 34.31
ATOM	780	CB	GLN	1553	-14.641	11.279	14.147	1.00 33.00
ATOM	781	CG	GLN	1553	-14.714	10.530	12.820	1.00 34.68
ATOM	782	CD	GLN	1553	-14.584	11.453	11.617	1.00 39.26
ATOM	783	OE1		1553	-15.300	12.449	11.506	1.00 43.55
ATOM	784	NE2		1553		11.129	1.0.71.8	1.00 37.56
ATOM	787	C	GLN	1553	- 13.502	13.040	15.526	1.00 36.86
ATOM	788	0	GLN	1553	-13.030	12.714	16.613	1.00 34.88
АТОМ	789	N	ASP	1554	-14,122	14.195	15.290	1.00 40.73
MOTA	791	CA	ASP	1554	-14.369	15.202	16.313	1.00 42.49
ATOM	792	CB	ASP	1554	-15.693	14.913	17.028	1.00 46.26
MOTA	793	CG	ASP	1554	-16.907	15.174	16.153	1.00 51.14
ATOM	794		ASP	1554	-17.686	16.097	16.488	1.00 57.62
ATOM	795		ASP	1554	-17.092	14.463	15.146	1.00 55.72
ATOM	796	C	ASP	1554	-13.249	15.299	17.336	1.00 42.31
ATOM	797	0	ASP	1554	-13.443	14.955	18.501	1.00 43.61
ATOM	798	N	GLY	1555	-12.077	15.753	16.902	1.00 41.03
ATOM	800	CA	GLY	1555	-10.960	15.864	17.823	1.00 37.98
ATOM	801	C	GLY	1555	-9.605	15.674	17.167	1.00 38.30
ATOM	802	0	GLY	1555	-9.533	15.478	15.953	1.00 37.28
ATOM	803	N	PRO	1556	-8.511	15.693	17.961	1.00 37.62
ATOM	804	CD	PRO	1556	-8.575	15.755	19.429	1.00 37.23
ATOM	805	CA	PRO	1556	-7.123	15.533	17.500	1.00 33.79
ATOM	806	CB	PRO	1556	-6.296	15.748	18.773	1.00 33.33
ATOM	807	CG	PRO	1556	-7.254	16.353	19.770	1.00 36.99
ATOM	808	C	PRO	1556	-6.891	14.134	16.990	1.00 33.57
ATOM	809	0	PRO	1556	-7.378	13.175	17.568	1.00 33.37
		N	LEU	1557	-6.168	14.031	15.884	1.00 32.10
ATOM	810 812		LEU		-5.859	12.745	15.300	1.00 33.23
ATOM		CA		1557 1557				1.00 34.20
ATOM	813	CB	LEU	1557	-5.173 -4.674	12.950	13.944	
MOTA	814	CG	LEU	1557	-4.674	11.716	13.183	1.00 29.78
MOTA	815		LEU	1557	-5.810	10.730	12.943	1.00 29.22
MOTA	816	CD2	LEU	1557	-4.085	12.161	11.880	1.00 28.17

T TO LA									
ATOM	817			_		-4.95	0 11.92	7 16.22	5 1.00 36.29
ATOM	818					-3.84			
ATOM	819					-5.42	7 10.76		
ATOM	821					-4.61	9 9.89		
MOTA	822		_	R 1558		-5.32			
ATOM	823		G TY	R 1558		-5.36			
ATOM	824		D1 TY	R 1558		-6.364			
ATOM	825		E1 TY	R 1558		-6.438			
ATOM	826		D2 TY			-4.426			
ATOM	827	CI	E2 TY	R 1558		-4.488			
ATOM	828	CZ	Z TY	R 1558		-5.494	– -		
ATOM	829	OF	TYI			-5.561	-		
ATOM	831	C	TY	₹ 1558		-4.379			
ATOM	832	0	TYF			-5.329			
ATOM	833	N	VAI			-3.109			
ATOM	835	CA				-2.727			1.00 29.60
ATOM	836	СВ							1.00 27.08
ATOM	837		1 VAL			-1.647			1.00 24.96
ATOM	838		2 VAL			-1281			1.00 24 36
. ATOM	839	C	VAL			-2.147		13.765	1.00 19.21
ATOM	840	0	VAL			-2.238	6.102	16.794	1.00 25.65
ATOM	841	N	ILE			-1.169	6.257	17.389	1.00 24.97
ATOM	843	CA	ILE			-3.067	5.095	17.046	1.00 25.91
ATOM	844	CB	ILE			-2.777	4.062	18.042	1.00 26.94
ATOM	845	CG				-4.081	3.53.0	18.637	1.00 24.89
ATOM	846	CG:				3.785	2.744	19.900	1.00 17.89
ATOM	847		L ILE		•	-5.028	4.707	18.907	1.00 22.84
ATOM	848	CD		1560		-6.450	4.304	19.163	1.00 22.51
ATOM	849	0	ILE	1560		-1.955	2.896	17.467	1.00 30.61
ATOM	850	N	ILE	1560		-2.445	2.111	16.636	1.00 31.41
ATOM	852	CA	VAL	1561		-0.698	2.811	17.890	1.00 30.26
ATOM	853		VAL	1561		0.222	1.779	17.429	1.00 29.39
ATOM	854	CB	VAL	1561		1.466	2.437	16.730	1.00 30.18
ATOM			VAL	J.561		1.030	3.188	15.475	1.00 20.60
ATOM	855	CG2		1561		2.148	3.415	17.675	1.00 32.91
ATOM	856	C	VAL	1561		0.662	0.870	18.588	1.00 27.40
	857	0	VAL	1561		0.323	1.128	19.742	1.00 29.33
ATOM	858	N	GLU	1562		1.381	-0.209	18.279	1.00 24.75
ATOM ATOM	860	CA	GLU	1562		1.852	-1.142	19.308	1.00 22.64
	861	CB	GLU	1562		2.426	-2.410	18.676	1.00 17.97
ATOM	862	CG	GLU	1562		1.365	-3.282	18.029	1.00 24.33
ATOM	863	CD	GLU	1562		1.909	-4.552	17.383	1.00 26.80
ATOM			GLU	1562		1.247	-5.592	17.507	1.00 33.32
ATOM			GLU	1562		2.974	-4.538	16.722	1.00 35.32
ATOM		C	GLU	1562		2.885	-0.534	20.259	1.00 25.02
ATOM		0	GLU	1562		3.638	0.355		
ATOM	868	N	TYR	1563		2.897	-1.023		1.00 23.82
ATOM	870	CA	TYR	1563		3.805	-0.539		1.00 28.01
ATOM	871	CB	TYR	1563		3.045	-0.428		1.00 26.93
ATOM	872	CG	TYR	1563		3.868	0.008		1.00 27.19
ATOM	873	CD1		1563		4.581			1.00 27.72
ATOM			TYR	1563		5.303	1.196		1.00 30.61
ATOM		CD2		1563		3.908	1.620		1.00 33.05
				_		2.200	-0.753	26.176	1.00 25.77

MOTA	876	CE2	TYR	1563	4.626	-0.344	27.267	1.00 26.81
ATOM	877	CZ	TYR	1563	5.329	0.845	27.210	1.00 32.81
MOTA	878	OH	TYR	1563	6.091	1.271	28.276	1.00 40.16
ATOM	880	C	TYR	1563	4.989	-1.487	22.675	1.00 28.73
MOTA	881	0	TYR	1563	4.815	-2.704	22.735	1.00 27.05
MOTA	882	N	ALA	1564	6.189	-0.908	22.743	1.00 29.89
ATOM	884	CA	ALA	1564	7.453	-1.634	22.916	1.00 28.50
ATOM	885	CB	ALA	1564	8.392	-1.349	21.721	1.00 27.54
ATOM	886	C	ALA	1564	8.036	-1.092	24.229	1.00 27.05
ATOM	887	0	ALA	1564	8.790	-0.129	24.249	1.00 31.20
ATOM	888	N	SER	1565	7.650	-1.706	25.333	1.00 27.11
ATOM	890	CA	SER	1565	8.062	-1.251	26.652	1.00 28.91
ATOM	891	СВ	SER	1565	7.501	-2.152	27.729	1.00 27.33
ATOM	892	OG	SER	1565	8.108.	-3.419	27.650	1.00 26.58
MOTA	894	С	SER	1565	9.530	-1.085	26.915	1.00 30.19
ATOM	895	0	SER	1565	9.897	-0.330	27.810	1.00 33.44
ATOM	896	N	LYS	1566	10.368	-1.801	26.178	1.00 30.99
ATOM	898	CA	LYS	1566	11.798	-1.708	26.410	1.00 30.50
ATOM	899	СВ	LYS	1566	12.452	-3.082	26.335	1.00 30.38
ATOM	900	CG	LYS	1566	12.037.	-3.943	27.507	1.00 27.83
ATOM	901	CD	LYS	1566	12.605	-5.339	27.457	1.00 32.36
ATOM	902	CE	LYS	1566	12.345	-6.024	28.784	1.00 30.57
ATOM	903	NZ	LYS	1566	12.651	-7.460	28.722	1.00 34.82
ATOM	907	C	LYS	1566	12.526	-0.678	25.573	1.00 30.39
ATOM	908	ō	LYS	1566		-0.567	25.640	1.00 32.53
ATOM	909	N	GLY	1567	11.753	0.127	24.851	1.00 29.45
ATOM	911	CA	GLY	1567	12.319	1.184	24.035	1.00 29.17
ATOM	912	C	GLY	1567	13.079	0.742	22.806	1.00 28.14
ATOM	913	Ö	GLY	1567	12.875	.0.364	22.324	1.00 27.70
ATOM	914	N	ASN	1568	13.975	1.601	22.320	1.00 29.48
ATOM	916	CA	ASN	1568	14.754	1.308	21.121	1.00 30.06
ATOM	917	CB	ASN	1568	15.271	2.591	20.464	1.00 28.53
ATOM	918	CG	ASN	1568	16.342	3.285	21.281	1.00 30.13
ATOM	919		ASN	1568	17.305	2.670	21.730	1.00 31.50
ATOM	920		ASN	1568	16.212	4.591	21.420	1.00 30.91
ATOM	923	C	ASN	1568	15.892	0.333	21.352	1.00 28.83
ATOM	924	ō	ASN	1568	16.371	0.333	22.472	1.00 29.87
ATOM	925	N	LEU	1569	16.346	-0.300	20.274	1.00 27.43
ATOM	927	CA	LEU	1569	17.417	-1.291	20.323	1.00 29.95
ATOM	928	CB	LEU	1569	17.511	-2.022	18.972	1.00 28.96
ATOM	929	CG	LEU	1569	18.508	-3.173	18.797	1.00 20.30
ATOM	930		LEU	1569	18.431	-4.211	19.939	1.00 30.32
ATOM	931		LEU	1569	18.244	-3.819	17.461	1.00 25.70
ATOM	932	CD2	LEU	1569	18.805	-0.779	20.754	1.00 29.74
ATOM	933	N O	LEU	1569	19.530	-1.484	21.447	1.00 28.35
MOTA	934		ARG	1570	19.179	0.427	20.341	1.00 31.42
MOTA	936	CA	ARG	1570	20.485	0.985	20.703	1.00 32.81
MOTA	937	CB	ARG	1570	20.639	2.395	20.115	1.00 31.01
ATOM	938	CG	ARG	1570	21.922	3.091	20.543	1.00 35.33
MOTA	939	CD	ARG	1570	21.918	4.581	20.212	1.00 38.30
ATOM	940	NE	ARG	1570	20.700	5.272	20.649	1.00 47.77
ATOM	942	CZ	ARG	1570	20.393	5.595	21.912	1.00 53.56

ATO)M	943	ATLI 1	N D C									
ATC	-	946	NH1 I		1570	21.2	12	5.3	04 22.	931	1.0	0 51	30
ATC		949			1570	19.2		6.2	23 22.	161		0 51	
ATO	_	950	-	IRG IRG	1570	20.6		1.0	34 22.			0 35	
ATO		51			1570	21.5		0.45	55 22.8	314		0 34.	
ATO	_	53	-	LU	1571	19.6		1.72				0 36.	
ATO	_			LU	1571	19.63		1.85				0 37.	
ATO	_		_	LU	1571	18.40		2.66	2 24.7	725		0 41.	
ATO	_		_	LU	1571	18.40		4.11				3 49.	
ATO	-		OE1 G	LU	1571	17.04		4.82	3 24.4	59		59.	
ATO					1571	15.99		4.13				59.	
ATO			_	LU	1571	17.04		6.08				59.	
ATON	_			LU	1571	19.59		0.45				37.	
ATON		_		LU	1571	20.32		0.17	2 25.8			37.	
ATOM				YR	1572	18.75		-0.40			1.00	35.0	70 10 '
ATOM				/R	1572	18.59		-1.76				32.	
ATOM		-		/R	1572	17.57	1	-2.49				31.6	
ATOM			G TY		1572	17.37	6	-3.97	3 24.3			25.6	
ATOM			D1 TY		1572	16.392	2	-4.378				27.8	
ATOM			E1 TY		1572	16.180	כ	~5.713				28.5	
ATOM			D2 TY		1572	18.151		-4.941				22.1	
ATOM	- "		E2 TY		1572	17.948	3	-6.284			1 00	25.0	6
ATOM					1572	16.954	Į	-6.659	24.85			25.6	
ATOM					1572	16.732	?	-7.985				25.2	
ATOM	97				1572	19.904	:	-2.525				34.5	
ATOM	97		TY		1572	20.186		-3.309					
	97.		LE.		1573	20.692		-2.338	23.81			35.0	
MOTA	97	_		IJ	1573	21.970		-3.033	23.31			33.3	
MOTA	978				1573	22.487		-3.018	22.27			33.0	
ATOM	979				1573	21.833		-3.888	21.19			29.86	
MOTA	980		1 LET		1573	22.339		-3.448	19.84			23.3	
ATOM	981	_	2 LEC		1573	22.129		-5.354	21.42			16.57	
ATOM	982	_	LEU		L573.	22.997		-2.417	24.65			20.31	
ATOM	983		LEU		L 57 3	23.752		3.134	25.31			36.57	
ATOM	984		GLN		.574	23.003		1.090	24.735			39.00	
ATOM	986				.574	23.942		0.399	25.608			37.26	
ATOM	987			1	574	23.844		1.110	25.394			37.50	
ATOM	988	CG			574	24.526		1.582	24.113			36.96	
ATOM	989	CD	GLN		574	24.289		3.054	23.801			39.10	
ATOM	990		1 GLN		574	23.697		3.796	24.595			10.63	
ATOM	991		2 GLN	1	574	24.736		3.480	22.625		00 3	8.68	
ATOM	994	C	GLN	1	574	23.687		0.759	27.073			8.62	
ATOM	995	0	GLN	1	574	24.600		1.144			00 3	8.27	
ATOM	996	N	ALA	1	575	22.422		0.731	27.801		00 3	9.43	
ATOM	998	CA	ALA	1	575	22.021		1.044	27.469	1.	00 3	8.80	
ATOM	999	CB	ALA	19	575	20.551		0.714	28.831		00 3		
ATOM	1000	С	ALA	1.5	575	22.304			29.024		00 3		
ATOM	1001	0	ALA		575	22.006		2.484	29.275		00 4		
ATOM	1002	N	ARG		76	2.857		2.842	30.417		00 4		
ATOM	1004	CA	ARG		76	3.148		3.317	28.395		00 3		
ATOM	1005	CB	ARG		76	2.234		703	28.768		00 38		
ATOM	1006	CG	ARG		76	0.794		6.669	28.019		00 38		
ATOM	1007	CD	ARG		76	9.838		.518	28.472		00 39		
					· -	 J.038	-6	.352	27.687	1.0	0 37	1.87	

ATOM	1008	NE	ARG	1576	18.489	-6.260	28.235	1.00	41.03
MOTA	1010	CZ	ARG	1576	17.830	-5.123	28.436	1.00	43.27
MOTA	1011	NH1	ARG	1576	18.399	-3.961	28.143	1.00	42.64
MOTA	1014	NH2	ARG	1576	16.573	-5.152	28.877	1.00	46.13
MOTA	1017	C	ARG	1576	24.604	-5.076	28.612	1.00	39.77
ATOM	1018	0	ARG	1576	24.978	-6.256	28.623	1.00	40.25
ATOM	1019	N	ARG	1577	25.428	-4.042	28.501	1.00	40.39
MOTA	1021	CA	ARG	1577	26.866	-4.194	28.388	1.00	40.42
MOTA	1022	CB	ARG	1577	27.485	-2.871	27.952	1.00	37.67
MOTA	1023	CG	ARG	1577	27.247	-2.477	26.526	1.00	36.22
MOTA	1024	CD	ARG	1577	27.857	-1.113	26.287	1.00	35.55
ATOM	1025	NE	ARG	1577	27.971	-0.797	24.866	1.00	38.72
MOTA	1027	CZ	ARG	1577	28.395	0.369	24.384	1.00	37.57
MOTA	1028	NHl	ARG	1577	28.754	1.352	25.205	1.00	37.49
ATOM	1031	NH2	ARG	1577	28.449	0.562	23.074	1.00	39.58
MOTA	1034	C	ARG	1577	27.449	-4.548	29.760	1.00	42.45
MOTA	1035	0	ARG	1577	26.878	-4.180	30.801	1.00	42.57
MOTA	1036	N	PRO	1578	28.564	-5.296	29.797	1.00	43.36
ATOM	1037	CD	PRO	1578	29.270	-5.985	28.692	1.00	42.43
ATOM	1038	CA	PRO	1578	29.159	-5.648	31.082	1.00	43.08
MOTA	1039	CB.	PRO	1578	30.225	-6.676	30.709	1.00	40.33
ATOM	1040	CG	PRO	1578	30.600	-6.300	29.331	1.00	40.71
ATOM	1041	C	PRO	1578	29.768	-4.373	31.666	1.00	42.44
MOTA	1042	0	PRO	1578	30.261	-3.525	30.922	1.00	41.24
MOTA	1043	N	PRO	1579	29.705	-4.205	32.993	1.00	44.57
MOTA	1044	CD	PRO	1579	29.169	-5.143	33.994	1.00	46.68
MOTA	1045	CA	PRO	1579	30.251	-3.017	33.654	1.00	44.89
ATOM	1046	CB	PRO	1579	30.088.	-3.356	35.134	1.00	45.31
ATOM	1047	CG	PRO	1579	28.865	-4.224	35.142	1.00	44.45
ATOM	1048	C	PRO	1579	31.711	-2.767	33.289	1.00	45.17
MOTA	1049	0	PRO	1579	32.620	-3.257	33.953	1.00	47.72
MOTA	1050	N	ALA	1592	19.075	-5.384	32.475	1.00	49.23
MOTA	1052	CA	ALA	1592	20.500	-5.078	32.354	1.00	50.33
MOTA	1053	CB	ALA	1592	20.954	-4.184	33.503	1.00	51.83
MOTA	1054	С	ALA	1592	21.412	-6.308	32.251	1.00	50.65
MOTA	1055	0	ALA	1592	22.621	-6.166	32.044	1.00	51.55
MOTA	1056	N	ALA	1593	20.849	-7.505	32.409	1.00	49.06
ATOM	1058	CA	ALA	1593	21.638	-8.735	32.294	1.00	48.07
ATOM	1059	CB	ALA	1593	20.773	-9.953	32.579	1.00	47.87
ATOM	1060	С	ALA	1593	22.258	-8.840	30.891	1.00	47.59
ATOM	1061	0	ALA	1593	21.664	-8.426	29.894	1.00	49.09
MOTA	1062	N	GLN	1594	23.465	-9.388	30.830	1.00	47.30
MOTA	1064	CA	GLN	1594	24.186	-9.553	29.569	1.00	45.32
MOTA	1065	CB	GLN	1594	25.576	-10.118	29.837	1.00	44.82
ATOM	1066	CG	GLN	1594	26.523	-9.166	30.542	1.00	49.34
MOTA	1067	CD	GLN	1594	27.751	-9.877	31.111		52.40
MOTA	1068		GLN	1594		-10.847	30.537		51.16
MOTA	1069		GLN	1594	28.209	-9.408	32.265		54.00
MOTA	1072	С	GLN	1594		-10.432	28.539		45.00
ATOM	1073	0	GLN	1594		-11.393	28.876		45.28
MOTA	1074	N	LEU	1595		-10.104	27.273		45.08
MOTA	1076	CA	LEU	1595		-10.828	26.169		44.65

WO 98/07835

7.07	DONA .					
		1077	CB	LEU 159	95	22.758 -9.864 25.023 1.00.43.00
		L078	CG	LEU 159	95	21 619 0 000
		1079	CD1		95	21 855 7 562 - 1.00 43.22
		.080	CD2	LEU 159	5	20 276 0 570 - 1.00 41.25
AT		081	C	LEU 159	5	24.918 1.00 41.96
AT	_	082	0	LEU 159		25.044 -11.885 25.685 1.00 44.58
AT		083	N	SER 159		23.232 211.661 25.632 1.00 44.62
ATO		085	CA .	SER 159		24 225 25.376 1.00 45.71
ATO	OM 1	086		SER 159		21.323 -14.151 24.868 1 00 45 20
ATO	OM 1	087		SER 159		25.000 -15.495 25.124 1 00 46
ATC	OM 1	089	_	SER 1596		22.401 -15.605 24.432 1 00 44 00
ATC)M 1(090		ER 1596		24.557 -13.968 23.366 1 00 45 00
ATO)M 1(91				23.891 -13.156 22.707 1 00 45 03
ATO			_	,		25.475 -14.756 22.823 1.00 44.55
ATO:		_				25.782 -14.690 21.407 1 00 45 00
ATO		_		ER 1597		26 92115 642
ATO			_	ER 1597		27 976 15 536
ATO				ER 1597		24 526 15 055
ATON			_	ER 1597		24 233 14 400
ATON				KS 1598		23 767 -16 025 - 1.00 43.51
ATOM		'	CA LY			22 551 16 454
ATOM			R L'			21 979 -7 325
ATOM			G LY			21 374 70 615
ATOM			D LY			20 450 10 555
			E LY	S 1598		20 054 20 300
ATOM			Z LY	S 1598		21 210 21 5-
ATOM		_	LY	S 1598		21 521 95 222
ATOM			LY	S 1598		20.552 1.00 36.21
ATOM			AS:	P 1599		21.447
ATOM	111		A AS	P 1599		21.447 -14.624 21.681 1.00 33.57
ATOM	111	5 CI	3 ASI	1599		20.525 -3.508 21.841 1.00 31.94
ATOM	111		ASI	1599		20.743 -12.898 23.238 1.00 33.82
ATOM	111	7 or	l Asi	1599		20.143 -13.838 24.339 1.00 38.08
ATOM	1118	3 OI	2 ASE	1599		10.055 -13.717 25.475 1.00 37.52
ATOM	1119		ASF			20.77
ATOM	1120) 0	ASP			10.777 -12.430 20.802 1.00 30.89
ATOM	1121	N	LEU			20.153 7 00 20 00
ATOM	1123	CA				20.636 7 00 27 22
ATOM	1124	CB	LEU			-21.435 -11.050 19.666 1 00 31 6-
ATOM	1125	CG	LEU	1600		19.845 1 00 20 4
ATOM	1126		LEU	1600		24.341 -10.072 21 190 1 00 00
ATOM	1127	CD	E LEU			25.857 -9.923 21 226 1 00 20 77
ATOM	1128	C.	LEU	1600		23.666 -8.731 21.404 1.00 24.75
ATOM	1129	ō	LEU	1600		22.136 -11.478 18.212 1 00 21 22
ATOM	1130	N		1600		21.620 -10.686 17.418 1 00 37 00
ATOM	1132	CA	VAL	1601		22.439 -12.729 17.863 1.00 32.00
ATOM	1133		VAL	1601		22 161 12 22
ATOM	1134	CB	VAL	1601		22 827 34 600
ATOM	1134	CGI	VAL	1601		22 467 35 300
ATOM			VAL	1601		24 326 34 45
ATOM	1136	C	VAL	1601		20 642 13 345
ATOM	1137	0	VAL	1601		20 152 12 155
	1138	N	SER	1602		19 904 13 635
ATOM	1140	CA	SER	1602		18 450 13 705
						18.450 -13.726 17.318 1.00 27.07

MOTA	1141	CB	SER	1602	17.899	-14.362	18.584	1.00	29.97	
MOTA	1142	OG	SER	1602	16.488	-14.202	18.673	1.00	38.86	
ATOM	1144	C	SER	1602	17.864	-12.327	17.093	1.00	27.45	
ATOM	1145	0	SER	1602		-12.181	16.438	1.00	29.38	
MOTA	1146	N	CYS	1603	18.504	-11.306	17.663	1.00	25.31	
MOTA	1148	CA	CYS	1603	18.087	-9.909	17.461	1.00	24.49	
ATOM	1149	CB	CYS	1603	19.074	-8.965	18.143	1.00	21.15	
MOTA	1150	SG	CYS	1603	18.716	-7.213	18.030	0.50	11.83	PRT1
MOTA	1151	С	CYS	1603	18.155	-9.628	15.961	1.00	26.92	
MOTA	1152	0	CYS	1603	17.175	-9.238	15.329	1.00	30.04	
MOTA	1153	N	ALA	1604	19.340	-9.833	15.398	1.00	28.35	
MOTA	1155	CA	ALA	1604	19.573	-9.611	13.979	1.00	28.00	
MOTA	1156	CB	ALA	1604	20.970	-10.098	13.588	1.00	25.49	
MOTA	1157	C	ALA	1604	18.517	-10.295	13.132	1.00	26.69	
ATOM	1158	0	ALA	1604	17.892	-9.646	12.310	1.00	31.40	
ATOM	1159	N	TYR	1605	18.270	-11.577	13.399	1.00	26.33	
MOTA	1161	CA	TYR	1605	17.286	-12.384	12.666	1.00	24.79	
ATOM	1162	CB	TYR	1605	17.209	-13.771	13.300	1.00	23.42	
MOTA	1163	CG	TYR	1605	16.132	-14,663	12.742	1.00	29.93	
MOTA	1164	CD1	TYR	1605	16.281	-15.298	11.510	1.00	30.00	
MOTA	1165	CE1	TYR	1605	15.270	-16.097	10.989	1.00	32.29	
MOTA	1166	CD2	TYR	1605	14.949	-14.859	13.441	1.00	32.69	
ATOM	1167	CE2	TYR	1605	13.935	-15.650	12.934	1.00	33.02	
MOTA	1168	CZ	TYR '	1605	14.091	-16.266	11.713	1.00	34.40	
A'TOM	1169	OH	TYR	1605	13.037	-17.023	11.225	1.00	34.18	
ATOM	1171	С	TYR	1605	15.885	-11.750	12.572	1.00	26.08	
MOTA	1172	О	TYR	1605	15.327	-11.587	11.475	1.00	25.43	
MOTA	1173	N	GLN	1606	15.337	-11.366	13.717	1.00	25.38	
MOTA	1175	CA	GLN	1606	14.018	-10.737	13.776	1.00	25.47	
MOTA	1176	CB	GLN	1606	13.662	-10.424	15.227	1.00	24.21	
ATOM	1177	CG	GLN	1606	13.642	-11.636	16.127	1.00	24.37	
ATOM	1178	CD	GLN	1606	13.237	-11.279	17.540	1.00	27.16	*
MOTA	1179	OE1	GLN	1606	12.227	-10.603	17.758	1.00	29.64	
ATOM	1180	NE2	GLN	1606	14.033	-11.705	18.507	1.00	30.69	
ATOM	1183	С	GLN	1606	13.953	-9.449	12.949	1.00	26.89	
ATOM	1184	0	GLN	1606	12.936	-9.136	12.319	1.00	26.40	
MOTA	1185	N	VAL	1607	15.030	-8.674	13.000	1.00	27.79	
ATOM	1187	CA	VAL	1607	15.120	-7.430	12.255	1.00	26.35	
MOTA	1188	CB	VAL	1607	16.408	-6.667	12.625	1.00	24.87	
MOTA	1189	CG1		1607	16.556	-5.433	11.752	1.00	25.90	
MOTA	1190	CG2	VAL	1607	16.382	-6.282	14.094	1.00	17.95	
MOTA	1191	C	VAL	1607	15.121	-7.743	10.757	1.00	27.69	
ATOM	1192	0	VAL	1607	14.406	-7.093	9.979	1.00	30.85	
MOTA	1193	N	ALA	1608	15.902	-8.749	10.355	1.00	24.59	
MOTA	1195	CA	ALA	1608	15.965	-9.135	8.950	1.00	23.22	
MOTA	1196	CB	ALA	1608	16.971	-10.227	8.750	1.00	17.65	
MOTA	1197	С	ALA	1608	14.579	-9.589	8.492	1.00	24.58	
MOTA	1198	0	ALA	1608	14.201	-9.372	7.337	1.00	26.22	
MOTA	1199	N	ARG	1609	13.819	-10.191	9.409	1.00	25.65	
MOTA	1201	CA	ARG	1609	12.453	-10.648	9.124	1.00	24.86	
MOTA	1202	CB	ARG	1609	11.998	-11.660	10.160	1.00	28.15	
MOTA	1203	CG	ARG	1609	12.451	-13.050	9.863	1.00	30.10	



	MOT	1204	CD	ARG 160	9
	TOM	1205	NE	ARG 160	±1.083 =13.980 10 722 1 00 =
A	MOT	1207	CZ	ARG 160	10.942 -14.941 9 927 1 22
A ^c	TOM	1208	NH1	ARG 160	10.058 -15.792 10.437 1 00 35.58
		1211	NH2	ARG 1609	9.800 -15.790 11.740 1 00 33
A	rom	1214	C		9.468 -16.678 9.645 1.00 32.47
Αĵ	rom	1215	0		11.421 -9.518 9.000 1.00
AT		1216	N		10.522 -9.582 8 155 7 22.96
AT		1218	CA		11.501 -8.522 9 888 1 20
AT		1219	C	0	10.591 7.300 20.88
AT		220	_	0	10 822 6 745
AT		221		GLY 1610	9.872
ATC		223	~	MET 1611	12.097 -6 550
ATO		224		MET 1611	12.488 -5 255
ATO		225	~ ~	MET 1611	13.991 5.00
ATO		226		MET 1611	14 391 4 472
ATC				MET 1611	13.362 2.000
ATO		227		MET 1611	13.665 2.735 7.330 1.00 22.57
ATO		228		IET 1611	13 000 5.612 1.00 21 91
ATO		229		ET 1611	11 700 5.590 1.00 26 57
ATO		30		LU 1612	12 212 4.553 1.00 24.98
ATO		32		LU 1612	11 836 5.710 1.00 27.89
			CB G	LU 1612	12 120 12 4.632 1.00 26.91
ATO			CG G	LU 1612	11 602 15 5.024 1.00 26.70
ATON				LU 1612	11.443 4 026 1 00
ATOM			DE1 G	JU 1612	12.0/2 4 477 1 00 -
ATOM		37 (DE2 GI	U 1612	+3.443 5 600 1 00 -
ATOM			GI GI		3.617 1 00 22 0
ATOM	-	-	GI		4.305 1 00 27 55
ATOM			TY		9.9/4 -8.697 3.130 1.00 30 04
ATOM		2 C	A TY		5.337 1.00 2= 13
ATOM	124	3 C	B TY		5.133 1 00 21 02
ATOM	124	4 C	G TY		7.341 -8.625 6.462 1.00 21.00
ATOM	124	5 C	D1 TY		5.867 -8.318 6.335 1 00 17 45
ATOM	124	6 C;	El TY	₹ 1613	4.969 -9.307 5.968 1.00 10 24
ATOM	124	7 CI	D2 TYP		3.610 -9.049 5.872 1.00 18.03
ATOM	1248	G CI			5.373 -7.041 6.600 1 00 74 40
ATOM	1249	9 C2			4.017 -6.761 6.502 1.00
MOTA	1250	OF			3.137 -7.776 6.135 1.00 50
ATOM	1252		TYR		1.//9 -7 540
ATOM	1253		TYR		7.870 -7.170 4.504 1.00 21.91
MOTA	1254		LEU	-	7.125 -7.034 3.540 3.00 22.06
ATOM	1256				8.541 -6.154 5 045 1 00
ATOM	1257	CB	LEU		8.400 -4 704
ATOM	1258	CG		1614	9.219 3.020
ATOM	1259		LEU	1614	8.548 -3 413
ATOM	1260	CD	LEU	1614	9.509 2.55
ATOM	1261		LEU	1614	7 255 2 615 7.518 1.00 15.70
ATOM	1262	C	LEU	1614	8.793 -4 677
ATOM		0	LEU	1614	8 156 3 070
ATOM	1263	N	ALA	1615	9.840 = 5.307 2.294 1.00 24.91
ATOM	1265	CA	ALA	1615	10.333 -5.400 2.684 1.00 24.55
ATOM	1266	CB	ALA	1615	11 685 6 000 1.317 1.00 21.18
	1267	C	ALA	1615	9 334 6 705 1.254 1.00 18.35
					9.334 -6.107 0.404 1.00 21.97
SSSD/FF.					

MOTA	1268	0	ALA	1615	9.089	-5.642	-0.705	1.00	23.80
ATOM	1269	N	SER	1616	8.704	-7.173	0.893	1.00	22.49
ATOM	1271	CA	SER	1616	7.722	-7.919	0.097	1.00	21.81
MOTA	1272	CB	SER	1616	7.305	-9.179	0.831	1.00	19.78
ATOM	1273	OG	SER	1616	6.382	-8.862	1.851	1.00	23.88
ATOM	1275	C	SER	1616	6.475	-7.071	-0.149	1.00	23.60
ATOM	1276	0	SER	1616	5.733	-7.277	-1.117	1.00	21.74
ATOM	1277	N	LYS	1617	6.217	-6.169	0.789	1.00	25.84
ATOM	1279	CA	LYS	1617	5.078	-5.280	0.705	1.00	23.96
ATOM	1280	CB	LYS	1617	4.555	-4.951	2.099	1.00	20.74
ATOM	1281	ÇG	LYS	1617	3.843	-6.124	2.750	1.00	23.40
MOTA	1282	CD	LYS	1617	2.509	-6.395	2.081	1.00	28.70
ATOM	1283	CE	LYS	1617	1.714	-7.442	2.809	1.00	31.16
ATOM	1284	NZ	LYS	1617	2.339	-8.767	2.616	1.00	41.91
ATOM	1288	С	LYS	1617	5.409	-4.019	-0.061	1.00	24.25
MOTA	1289	Э	LYS	1617	4.640	-3.053	-0.022	1.00	25.22
ATOM	1290	N	LYS	1618	6.557	-4.028	-0.748		24.20
ATOM	1292	CA	LYS	1618	7.014	-2.904	-1.582		25.15
ATOM	1293	CB	LYS	1618	5.906	-2.507	-2.571		27.00
ATOM	1294	CG	LYS	1618	5.735	-3.411	-3.790		29.09
ATOM	1295	CD	LYS	1618	5.506.	-4.864	-3.432		31.82
MOTA	1296	CE	LYS	1618	5.533	-5.752	-4.663		30.21
ATOM	1297	ΝZ	LYS	1618	4.231	-5.707	-5.369		26.34
ATOM	1301	С	LYS	1618	7.466	-1.658	-0.816		23.50
ATOM	1302	0	LYS	1618	7.537	-0.576	-1.385		22.10
ATOM	0.303	N	CYS	1619	7.827	-1.821	0.449		23.72
ATOM	1305	CA	CYS	1619	8.213	-0.693	1.276		20.89
ATOM	1306	CB	CYS	1619	7.535	-0814	2.647	1.00	18.41
ATOM	1307	SG	CYS	1619	8.019	0.405	3.894	1.00	26.34
ATOM	1308	С	CYS	1619	9.717	-0.529	1.451		22.94
ATOM	1309	0	CYS	1619	10.419	-1.487	1.790	1.00	23.20
ATOM	1310	M	ILE	1620	10.197	0.690	1.211		21.17
ATOM	1312	CA	ILE	1620	11.610	1.039	1.388	1.00	22.35
ATOM	1313	CB	ILE	1620	12.151	1.823	0.172	1.00	17.30
ATOM	1314	CG2	ILE	1620	13.607	2.215	0.393	1.00	8.27
ATOM	1315	CG1	ILE	1620	11.966	0.997	-1.111	1.00	18.27
ATOM	1316	CD1	ILE	1620	12.127	1.803	-2.401	1.00	17.57
ATOM	1317	С	ILE	1620	11.631	1.926	2.652	1.00	25.20
ATOM	1318	0	ILE	1620	10.912	2.932	2.715	1.00	29.69
ATOM	1319	N	HIS	1621	12.398	1.526	3.665	1.00	22.66
ATOM	1321	CA	HIS	1621	12.463	2.254		1.00	22.78
ATOM	1322	CB	HIS	1621	13.214	1.425		1.00	22.65
ATOM	1323	CG	HIS	1621	13.024	1.897	7.398		22.07
MOTA	1324	CD2	HIS	1621	12.485	1.280	8.475		20.50
ATOM	1325		HIS	1621	13.449	3.134	7.842		23.11
ATOM	1327		HIS	1621	13.182	3.253	9.131		23.92
ATOM	1328		HIS	1621	12.596	2.144	9.543		24.44
ATOM	1330	C	HIS	1621	13.110	3.616	4.831		24.07
ATOM	1331	o	HIS	1621	12.561	4.597	5.306		24.37
ATOM	1332	N	ARG	1622	14.327	3.639			26.42
ATOM	1334	CA	ARG	1622	15.129				24.59
ATOM	1335	CB	ARG	1622	14.289	6.018	3.581		17.58
								~	



3 00	O. 4	_									
ATO		336	CG	ARG	1622	13.8	10 5	767 2.			
ATO		337	CD	ARG	1622	1.2.92					13.88
ATO		338	NE	ARG	1622	12.5		~ .		0.50	4.97
ATO		340	CZ	ARG	1622	11.53				0.50	6.49
ATC		341	NH1	ARG	1622	10.71		352 ~0.		0.50	3.84
ATC		344	NH2	ARG	1622	11.35).50	2.25
OTA		347		ARG	1622					.50	2.48
ATO		48	0 2	ARG	1622	15.91			388 1	.00	24.72
ATO		49	N A	ASP	1623	16.76		-	337 1	.00	26.90
ATO	M 13	51		ASP	1623	15.68	_		05 1	.00	25.61
ATO	M 13	52		ASP	1623	16.43			03 1	.00	28.41
IOTA	M 13	53		SP	1623	15.92			49 1	.00	30.38
ATO	M 13.	54	OD1 A		1623	16.89		72 9.3	73 1	. 00	33.47
ATON	M 13			SP.		16.42		38 10.3	82 1	.00	43.35
ATON				SP	1623	18.12					31.88
ATOM				SP	1623	16.498		97 8.7		00	28.86
ATOM				SP EU	1623	16.148					28.31
ATOM					1624	16.956		8.2		00 2	20.31 27.81
ATOM				EU	1624	17.087	1.48			00 2	27.8T
ATOM					1624	17.149	0.22			00 2	27.28
ATOM					1624	17.118					27.53
ATOM			D1 LE		1624	15.850	-1.34			00 2	7.69
ATOM			D2 LE		1624	17.228				00 2	3.77
ATOM					1624	18.340				00 2	9.15
ATOM					1624	19.464	1.77			00 2	6.27
ATOM	136				1625	18.116	1.59			30 2	5.89
ATOM	1369				1625	19.164	1.75)0, 5;	3.29
	1370		B AL	A .	L625 ·	19.520	3.23			00 1	9.68
ATOM ATOM	137		AL.	A 1	625	18.575	1.214)O 18	3.85
	1372	_	AL	I A	625	17.352	1.077			0 20	0.79
MOTA	1373		AL_{i}	A 1	.626	19.429	0.942			0 20).75
ATOM	1375		ALA	1. A	626	18.969				0 22	2.03
ATOM	1376		3 AL	A 1	626	20.139	0.408 -0.048			0 23	
ATOM	1377		ALA	1	626	18.111				0 22	
ATOM	1378	0	ALA		626	17.333	1.397		_	0 25	
ATOM	1379	N	ARG	1	627	18.303	1.006			0 29	.51
ATOM	1381	CA	ARG		627	17.503	2.685	16.407		0 26	. 92
MOTA	1382	CB	ARG		527	18.017	3.722	17.048	1.00	27	.30
ATOM	1383	CG			527		5.107	16.627	1.00	28	.29
ATOM	1384	CD	ARG		527	18.086	5.287		1.00	36.	. 26
ATOM	1385	NE	ARG		527	18.255	6.756	14.688		41.	
ATOM	1387	cz	ARG		27	18.548	6.928	13.261	1.00	39.	94
ATOM	1388	NH:	L ARG		27	19.779	6.904	12.749	1.00	42.	33
ATOM	1391		ARG		27	20.826	6.721	13.539	1.00	44.	75
ATOM	1394	C	ARG			19.976	7.059	11.450	1.00	41	50
ATOM	1395	0	ARG		27	16.029	3.567	16.591	1.00	27	42
ATOM	1396	N	ASN	16		15.092	3.897	17.333	1.00	26	52
ATOM	1398	CA	ASN	16:		15.850	3.039	15.375	1.00	26	82
ATOM	1399	CB	ASN	16:		14.534	2.849	14.758	1.00	24	02 00
ATOM	1400	CG		16:		14.569	3.308	13.301	1.00	26	20
ATOM	1401		ASN	162		14.709	4.823	13.167	1.00	20	3 U
ATOM	1402		ASN	162		14.018	5.567	13.844	1.00	20	- 0 T A
ATOM	1405		ASN	162		15.599	5.277	12.297	1 00	20.5	9
- • •	~ 403	С	ASN	162	28	13.945	1.440	14.862	1.00	24.3	52
								502	1.00	24.3	55

31.1

MOTA	1406	0	ASN	1628	13.026	1.084	14.105	1.00	24.66
MOTA	1407	N	VAL	1629	14.473	0.637	15.785	1.00	22.35
MOTA	1409	CA	VAL	1629	13.988	-0.718	16.055	1.00	20.65
MOTA	1410	CB	VAL	1629	15.077	-1.813	15.822	1.00	18.07
ATOM	1411	CG1	VAL	1629	14.612	-3.142	16.398	1.00	11.84
ATOM	1412	CG2	VAL	1629	15.378	-1.977	14.346	1.00	12.65
ATOM	1413	С	VAL	1629	13.625	-0.670	17.536	1.00	24.27
MOTA	1414	0	VAL	1629	14.427	-0.237	18.361	1.00	25.94
ATOM	1415	N	LEU	1630	12.393	-1.031	17.866	1.00	24.99
ATOM	1417	CA	LEU	1630	11.936	-1.010	19.247	1.00	25.50
ATOM	1418	CB	LEU	1630	10.609	-0.252	19.339	1.00	22.79
ATOM	1419	CG	LEU	1630	10.634	1.179	18.789	1.00	17.86
A'TOM	1420	CD1	LEU	1630	9.240	1.680	18.654	1.00	18.49
MOTA.	1421	CD2	LEU	1630	11.409	2.100	19.668	1.00	17.63
ATOM	1422	C	LEU	1630	11.833	-2.434	19.829	1.00	28.29
MOTA	1423	0	LEU	1630	11.666	-3.412	19.092	1.00	28.56
ATOM	1424	N	VAL	1631	11.933	-2.542	21.150	1.00	29.46
ATOM	1426	CA	VAL	1631	11.883	-3.831	21.833	1.00	29.40
ATOM	1427	CB	VAL	1631	13.222	-4.105	22.553	1.00	27.48
MOTA	1428	CG1	VAL	1631	13210	-5.477	23.233	1.00	24.53
MOTA	1429	CG2	VAL	1631	14.376	-3.976	21.576	1.00	22.55
ATOM	1430	С	VAL	1631	10.730	3.918	22.853	1.00	31.94
MOTA	1431	0	VAL	1631	10.630	-3.102	23.787	1.00	33.13
MOTA	1432	N	THR	1632	9.866	··4.911	22.659	1.00	32.21
ATOM	1434	CA	THR	1632	8.728	-5.149	23.540	1.00	31.77
ATOM	1435	CB	THR	1632	7.674	-6.061	22.874	1.00	32.38
ATOM	1436	OG1	THR	1632	8.169	-7.406	22.792	1.00	32.38
ATOM	1438	CG2	THR	1632	7.330	5.554	21.480	1.00	28.05
MOTA	1439	C	THR	1632	9.157	-5.810	24.842	1.00	30.39
.ATOM	1440	Ο.	THR	1632	10.256	-6.320	24.947	1.00	30.28
MOTA	1441	N	GLU	1633	8.260	-5.823	25.822	1.00	32.43
ATOM	1443	CA	GLU	1633	8.513	-6.424	27.122	1.00	32.84
ATOM	1.444	CB	GLU	1633	7.259	-6.310	27.991	1.00	35.28
MOTA	1.445	CG	GLU	1633	7.386	-6.881	29.399	1.00	46.57
ATOM	1446	CD	GLU	1633	8.463	-6.192	30.260	1.00	54.03
ATOM	1447	OE1	GLU	1633	8.519	-4.939	30.297	1.00	58.68
MOTA	1448	OE2	GLU	1633	9.249	-6.916	30.918	1.00	56.84
ATOM	1449	C	GLU	1633	8.914	-7.889	26.986	1.00	35.14
ATOM	1450	0	GLU	1633	9.632	-8.435	27.826	1.00	33.92
ATOM	1451	N	ASP	1634	8.456	-8.526	25.910	1.00	38.25
ATOM	1453	CA	ASP	1634	8.768	-9.941	25.677	1.00	39.22
ATOM	1454	CB	ASP	1634	7.588	-10.639	24.990	1.00	44.88
ATOM	1455	CG	ASP	1634	6.258	-10.420	25.725	1.00	54.17
MOTA	1456	OD1	ASP	1634	6.064	-11.042	26.799	1.00	56.33
ATOM	1457	OD2	ASP	1634	5.412	-9.622	25.236	1.00	54.47
ATOM	1458	С	ASP	1634	10.035	-10.109	24.849	1.00	37.53
MOTA	1459	0	ASP	1634	10.395	-11.225	24.495	1.00	36.33
ATOM	1460	N	ASN	1635	10.730	-8.998	24.589		39.12
ATOM	1462	CA	ASN	1635	11.974	-8.948	23.792		37.21
ATOM	1463	CB	ASN	1635	13.042	-9.891	24.361	1.00	37.83
ATOM	1464	CG	ASN	1635	13.576	-9.426	25.677		38.65
ATOM	1465	OD1	ASN	1635	13.795	-8.236	25.880	1.00	43.82



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	TOM 1466	ND2 ASN 1635				
	TOM 1469	C ASN 1635	± J ,	768 -10	353 26.	596 1.00 39 49
A.	TOM 1470	0 3.000	~ . .	807 -9.		
A	FOM 1471	1035		649 -9.	834 21.	
Al	TOM 1473	1036	10.			
AT	OM 1474	CD 1775	10.			- 44.30
	OM 1475	CB VAL 1636		895 -9.		
	- · · -	CG1 VAL 1636		_		- 04.04
AT	014	CG2 VAL 1636				584 1.00 29 16
		C VAL 1636	10.9	384 -10.2		38 1.00 34 29
AT		O VAL 1636				29 1.00 29.28
AT	_	N MET 1637	10.5			37 1.00 27.08
ATO		CA MET 1637	11.7		755 18.6	23 1.00 27.82
ATC		CD	12.3	18 -6.6	34 17.8	7 . 0 2
ATC	DM 1483	00 100	13.5	78 -7.0		7.09
ATO		103/	14.6	48 -7.6		~,,
ATO	24	CB 145	15.2			
ATO	Μ	103/	15.10			
ATO	M 7.45-	C MET 1637	11.27			28 1.00 26.00
ATO	, M	O MET 1637	10.75		- +	8 1.00 26.01
ATO	M 2400 1	N LYS 1638	10.98			1 1.00 26 05
		CA LYS 1638	9.98	-		3 1.00 25.44
ATON		CB LYS 1638				6 1.00 22.01
ATOM	-152 (CG LYS 1638	8.69			8 1.00 19.65
ATOM		D LYS 1638	7.88		4 17.03	1.00 21.22
ATOM		E LYS 1638	6.66		4 17.869	
ATOM			5.77		3 18.076	/ .)
ATOM	1499 C		4.97	6.52	2 16.869	
ATOM		1038	10.477	7 -3.106		
ATOM		710 1038	10.896			
ATOM		1039	10.371			
ATOM		1039	10.803			/
ATOM	1504 CE	1039	11.090		- , 4	1.00 24.90
ATOM	1505 CG	1039	11.413			1.00 22.12
ATOM	1506 CG	2033	12.256	-1.275		1.00 17.41
	1507 CD	1 ILE 1639		-3.423	11.664	1.00 18.67
ATOM	1508 C	ILE 1639	12.309	-4.308	10.492	1.00 26.15
ATOM	1509 O	ILE 1639	9.772	-0.856	13.117	1.00 28.52
ATOM	1510 N	ALA 1640	8.557	~1.094	12.964	1.00 27.86
ATOM	1512 CA	ALA 1640	10.267	0.363	13.358	1 00 27.86
ATOM	1513 CB		9.444	1.564	13.445	1.00 30.06
ATOM	1514 C	-010	9.627	2.211	14.812	1.00 29.37
ATOM	1515 0	-010	9.782	2.566		1.00 28.25
ATOM	1505	ALA 1640	10.808	2.453	12.344	1.00 29.68
ATOM	1500	ASP 1641	8.892	3.536	11.660	1.00 30.81
ATOM		ASP 1641	9.067		12.154	1.00 30.35
ATOM	1519 CB	ASP 1641	10.309	4.608	11.154	1.00 30.40
	1520 CG	ASP 1641	10.018	5.454	11.454	1.00 32.89
ATOM	1521 OD1	ASP 1641		6.678	12.321	1.00 34.68
ATOM	1522 OD2	ASP 1641	10.952	7.497	12.469	1.00 35.84
ATOM	1523 C	ASP 1641	8.897	6.824		1.00 38.22
ATOM	1524 O		9.102	4.162		7 00 38.22
ATOM	1505		9.484	4.941	_	1.00 28.91
7000	1500	~~~	8.650	2.941	_	1.00 29.26
	1500	PHE 1642	8.648	2.435		1.00 27.21
		PHE 1642	8.432	0.909	8.072	.00 25.07
	1529 CG	PHE 1642	7.135	0.451	8.043 1	00 19.64
				A - 45T	8.639 1	.00 16.47
SSSD/EE14						•



	·
	5.974 0.400 7.878 1.00 21.72
1530 CD1 PHE 1012	945 1.00 17.02
ATOM 1531 CD2 PHE 1642	4 701 -0.082 8.422 1.00 20.57
ATOM 1532 CE1 PHE 1642	10 496 1.00 10.12
ATOM 1533 CE2 PHE 1642	4 743 -0.515 9.739 1.00 20.52
770M 1534 CZ PHE 1642	7 157 1.00 23.37
1535 C PHE 1642	5 971 1.00 20.10
7536 O PHE 1642	7 707 1.00 23.03
- 17 CLV 1643	6 866 1.00 24.02
1530 CA GLY 1643	- 6 893 1.00 24.01
ATOM 1555 G GLY 1643	5.786 3.524 6.436 1.00 19.20
ATOM 1510 GLY 1643	4.922 7 376 1.00 29.50
ATOM 1512 N LEU 1644	6.930 7.491 1.00 34.24
ATOM 1542 CA LEU 1644	7.169
ATOM 1544 CB LEU 1644	8.490
ATOM 1545 CD - 777 1644	8.473
ATOM 1546 CC - 1811 1644	7.320 9.442 1.00 35.23
ATOM 1547 CD2 LEU 1644	9.854 9.773 6 179 1.00 37.54
ATOM 1548 CD2 121 1644	7.213 8.576 5.176 1.00 37.48
ATOM 1549 C - 1644	7.759 8.123 5.00 41.66
ATOM 1550 0 1645	6.577 9.744 5.067 1.00 43.66
ATOM 1551 N 1645	6.524 10.652 5 202 1.00 38.13
ATOM 1553 CA ALA 1645	5 309 11.565
ATOM 1554 CB ALL:	7.819 11.473 3.00 47.17
ATOM 1555 C 213 1645	8.105 12.082 1.00 45.69
ATOM 1556 0 1221	8 622 11.402
ATOM 155/ N 1646	9.871 12.222 4.054 1.00.49.50
ATOM 1559 CA ALA 1016	10.971 11.405 4.776 1 00 50 98
ATOM 1560 55	10.338 12.661 2.712 1.00 52 84
ATOM 1561 C ALA 1646	10.319 11.880 1.755 1.00 53 09
ATOM 1562	10.755 13.919 2.330 1.00 55 06
ATOM 1563 N ASP 1617	11.253 14.419 1.322 1.00 56 05
ATOM 1565 CA ASP 1647	10.868 15.887 1.092 1.00 59.31
ATOM 1566 CB ASP 1047	11.084 16.342 -0.332 - 1.00 59 51
ATOM 1567 CG ASP 1047	12.070 15.928 -1.005 - 1.00 63 48
ATOM 1568 OD1 ASP 1047	10.265 17.150 -0.837 - 1.00.55.26
ATOM 1569 OD2 ASP 1047	12.770 14.264 1.332 1.00.53.18
ATOM 1570 C ASP 1047	13.487 15.075 1.320
ATOM 1571 O ASP 1510	13.235 13.198 0.001 1 00 57 79
ATOM 1572 N 1LE 1040	14.652 12.877 0.535 1.00 53 86
ATOM 1574 CA 111 1515	14 890 11.624 -0.271 1.00 5314
7 TOM 1575 CB 1LE 1040	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
NEOM 1576 CG2 ILE 1648	14 454 11.886 -1.718 1.00 48.22
NTOM 1577 CG1 ILE 1648	15 108 11.083 -2.751 1.00 43.2
7578 CD1 ILE 1648	15 439 14.044 0.014 1.00 62.32
1579 C ILE 1648	16 591 14.271 0.380 1.00 04.72
NEOM 1580 O ILE 1648	14 905 14.791 -0.884 1.00 0311
1581 N HIS 1049	25 450 15.941 -1.500 1.00 05.05
ATOM 1583 CA HIS 1649	15.430 16.285 -2.844 1.00 70.35
ATOM 1584 CB HIS 1649	15.123 15.332 -3.944 1.00 73.90
ATOM 1585 CG HIS 1649	15.123 13.628 -4.208 1.00 75.13
ATOM 1303 CD2 HTS 1649	16.237
A10th - 1649	14.23
ATOM 1500 CE1 HIS 1649	14.798 14.148 -5.773 -24
ATOM 1589 CEI HIS 1015	



ATOM 1590 NE2 HIS 1649	
ATOM 1592 C HTC 151	13.905 - 5 340 -
ATOM 1502 6 1049	15.419 17.150 -0.576
ATOM 1504 3	15.517 18 394
ATOM 1500 00 1115 1650	15.218 16 912 1.041 1.00 72.83
ATOM 1507 CA HIS 1650	15 190 77 - 0.718 1.00 71.28
ATOM 1500 - 1550	13 776 70 1.710 1.00 72 52
7 HIS 1650	13 272 10 1.956 1.00 75 67
770M 1599 CD2 HIS 1650	0.882 1.00 00
ATOM 1600 ND1 HIS 1650	13.451 20.734 0.691 1.00.96 17
ATOM 1602 CE1 HIS 1650	12.529 18.955 -0.185 1 00 86 3-
ATOM 1603 NE2 HTS 1650	12.262 19.972 -0.993
ATOM 1605 C HTC 1650	12.814 21.058 -0 491
ATOM 1606 O HTC 1650	15.856 17.593 3 000
ATOM 1607 37 1650	15.783 19 224
ATOM 1600 CD 1651	16.543 16.451 4.010 1.00 69.56
ATOM 1610 CD 1651	17.221 15 930 3.033 1.00 70.84
ATOM 1611 1651	17 622 14.222 1.00 70.50
ATOM 1651	18 499 33 4.031 1.00 71.73
1612 CG1 ILE 1651	3,194 1 00 71 1-
7 CD1 ILE 1651	3.890 1 00 72 70
1614 C ILE 1651	3.593 1 00 75 10
1100 1615 O ILE 1617	16.472 16.734 4.569 1 00 65
1110M 1616 N ASP 1653	19.3/5 .16.882 3 745
ATOM 1618 CA ASP 1652	18.543 17.222 5 802 11.50 70.30
ATOM 1619 CB ASD 1672	19.707 17.987 6 340
ATOM 1620 CG ASD 11632	19.344 18.923 7 300
ATOM 1631 07-	20.512 19 700 - 1.00 /0.53
ATOM 1632 000	21.306 20 242
ATOM 1632 ~ 1652	20.646 20 034
ATOM 1624 0 255	20.802 17 023 9.060 1.00 76.01
ATOM 1625 37 ASP 1652	20 746 26 5.673 1.00 66.08
ATOM 1637	21 802 15 7.762 1.00 64 92
ATOM 2500	22 926 15 5.814 1.00 64.14
ATOM 1653	0.089 1 00 62 65
Amore 11R 1653	4,875 1 00 61 61
ATOM 1630 CD1 TYR 1653	23.362 14.971 3.795 1 00 52 25
1031 CE1 TVD 1572	24.153 14.679 2.684 1.00 62.37
ATOM 1632 CD2 TVD 1674	23.725 13.773 1 717
ATOM 1633 CE2 TVP 1655	22.121 14.335 2 230 -
ATOM 1634 CZ TYR 1653	21.685 13.429 2 252
ATOM 1635 OH TVD 1655	22.487 13.148 1 950 7
ATOM 1637 ** 1653	22.044 12 222
ATOM 1638 0 7777	23.733 16.313 7 245
ATOM 1630 3	24.403 15 453 1.00 63.49
ATOM 1641 67	23.644 17.564 1.00 63.39
ATOM 1654	24 270 7.789 1.00 64 37
ATOM 1642	24 047 10.013 8.963 1.00 63 95
Amov. 1654	26 038 8.741 1.00 60 86
ATTOM 1644 CD1 TYR 1654	7,691 7 00 57
ATOM 1645 CE1 TYR 1654	23.736 19.698 6.353 1 00 50 22
ATOM 1646 CD2 TYR 1654	26.734 19.708 5.383 1.00 50.03
ATOM 1647 CE2 TYR 1654	27.364 19.252 8.035 1 00 56 50
ATOM 1648 CZ TVP 365.	28.366 19.261 7.079 1.00 50.79
ATOM 1649 OH TYR 1654	20.04/ 19.488 5 754
ATOM 1651 C TYR 1654	29.048 19.485 4 806 60.88
1054	23.560 17 000 4.23
660-	17.980 10.239 1.00 65.89
SSSD/5514501	

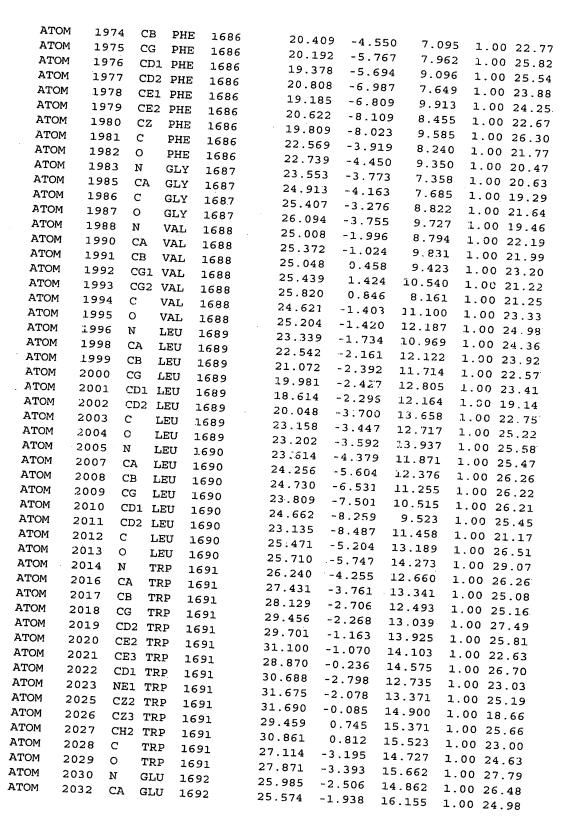
MOTA	1652	0	TYR	1654	24.074	18.283	11.316	1.00	67.56
MOTA	1653	N	LYS	1655	22.297	17.586	10.135	1.00	67.36
ATOM	1655	CA	LYS	1655	21.443	17.527	11.315	1.00	69.11
MOTA	1656	CB	LYS	1655	19.972	17.611	10.915	1.00	69.86
MOTA	1657	CG	LYS	1655	19.019	17.651	12.090	1.00	71.45
ATOM	1658	CD	LYS	1655	17.607	17.867	11.603	1.00	75.40
MOTA	1659	CE	LYS	1655	16.595	17.393	12.627	1.00	78.22
MOTA	1660	NZ	LYS	1655	15.204	17.553	12.110	1.00	80.61
MOTA	1664	C	LYS	1655	21.714	16.242	12.093	1.00	69.65
MOTA	1665	0	LYS	1655	21.872	15.169	11.497	1.00	70.67
MOTA	1666	N	LYS	1656	21.766	16.358	13.419	1.00	68.19
MOTA	1668	CA	LYS	1656	22.035	15.212	14.275	1.00	68.00
MOTA	1669	CB	LYS	1656	22.983	15.618	15.403	1.00	65.53
MOTA	1670	CG	LYS	1656	24.395	15.895	14.946	1.00	62.71
MOTA	1671	CD	LYS	1656	25.280	16.221	16.138	1.00	64.38
ATOM	1672	CE	LYS	1656	26.764	16.031	15.832	1.00	63.23
ATOM	1673	NZ	LYS	1.656	27.592	16.186	17.062	1.00	61.72
MOTA	1677	С	LYS	1656	20.777	14.560	14.855	1.00	
ATOM	1678	0	LYS	1656	19.695	15.148	14.837	1.00	69.20
ATOM	1679	N	THR	1657	20.928	13.337	15.359	1.00	68.48
MOTA	1681	CA	THR	1657	1.9.821	12.607	15.960	1.00	
ATOM	1682	CB	THR	1657	20.109	11.078	16.021	1.00	
ATOM	1683	OG1	THR	1657	21.295	10.823	16.787	1.00	68.72
MOTA	1685	CG2	THR	1657	20.289	10.500	14.637	1.00	
MOTA	1686	C	THR	1657	19.682	13.131	17.383		67.80
ATOM	1687	0	THR	1657	20.424	14.022	17.790		67.87
ATOM	1688	N	ALA	1658	18753	12.569	18.148		68.95
ATOM	1690	CA	ALA	1658	18.580	12.992	19.537	1.00	70.64
ATOM	1691	СВ	ALA	1658	17.391	12.254	20.173		71.19
MOTA	1692	C	ALA	1658	19.880	12.709	20.313	1.00	69.64
ATOM	1693	0	ALA	1658	20.394	13.566	21.042	1.00	70.13
.ATOM	1694	N	ASN	1659	20.440	11.526	20.080		68.02
ATOM	1696	CA	ASN	1659	21.663	11.092	20.746	1.00	66.10
ATOM	1697	CB	ASN	1659	21.835	9.583	20.557	1.00	70.23
ATOM	1698	CG	ASN	1659	22.632	8.937	21.679	1.00	74.09
ATOM	1699	OD1	ASN	1659	22.525	9.331	22.840	1.00	75.21
MOTA	1700		ASN	1659	23.402	7.907	21.342	1.00	75.03
ATOM	1703	С	ASN	1659	22.910	11.816	20.249	1.00	63.30
MOTA	1704	0	ASN	1659	24.004	11.585	20.762	1.00	61.12
ATOM	1705	N	GLY	1660	22.744	12.678	19.246	1.00	61.61
ATOM	1707	CA	GLY	1660	23.867	13.421	18.689		59.06
ATOM	1708	С	GLY	1660	24.604	12.750	17.536		56.84
ATOM	1709	0	GLY	1660	25.726	13.132	17.196		55.69
ATOM	1710	N	ARG	1661	23.980	11.758	16.914		55.73
ATOM	1712	CA	ARG	1661	24.626	11.062	15.808		52.76
ATOM	1713	СВ	ARG	1661	24.387	9.549	15.883		52.39
ATOM	1714	CG	ARG	1661	24.977	8.874	17.111		54.08
ATOM	1715	CD	ARG	1661	24.776	7.376	17.045		58.37
ATOM	1716	NE	ARG	1661	25.178	6.665	18.260		59.27
MOTA	1718	CZ	ARG	1661	24.952	5.369	18.471		59.83
ATOM	1719		ARG	1661	24.319	4.643	17.550		57.04
ATOM	1722	NH2	ARG	1661	25.375	4.792	19.591		59.47

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	TOM	1725	C	ARG	1661	24	2.66				
		1726	0	ARG	1661	24.		.609 14	.468	1.00	49.58
		1727	N	LEU	1662	23.		.321 14	.375	1.00	47.38
		1729	CA	LEU	1662	24.9	_	.266 13	.430	1.00	46.26
		1730	CB	LEU	1662	24.6		717 12	.092	1.00	44.75
		1731	CG	LEU	1662	25.8		261 11	.425	1.00	43.49
		L732	CD1		1662	26.4		561 12	.020	1.00	43.49
	C MO'	.733			1662	27.9			727	1 00	42.40
AT	OM 1	734				25.6			507	1 00	40.19
AT		735	_		1662	23.9	99 10.		276	1 00	40.19
AT	OM 1	736			1662	24.7	04 9.		892	1.00	43.58
ATO		737			1663	22.6	BO 10.6		010	1.00	43.68
ATO	•••	738			1663	21.72	23 11.6		521	1.00	10.72
ATO		739	~-		1663	21.98	31 9. <i>6</i>			1.00	10.27
ATO	_	740	_		663	20.59				1.00	36.86
ATC		741	~		.663	20.37				1.00 3	6.67
ATO		742			663	22.64				1.00 3	6.84
ATO					663	22.44		-	907	1.00 3	3.34
ATO					664	23.42				1.00 3	3.65
ATO					664	24.09				1.00 з	1.26
ATO	- '			AL 1	664	24.88		_		1.00 3	0.43
ATO			CG1 V		564	23,94				1.00 2	7.09
ATO			CG2 V		564	25.894				1.00 2	3.98
ATON					664	25.044			_	00 26	5.06
ATOM) VI	AT 16	64	25.461				.00 28	3.18
ATOM			1 T?	'S 16	65	25.353			53 1	.00 38	3.30
			A Ly	S 16	65	26.243		, ,,,	39 1	.00 25	.52
ATOM		-	B LY	S 16	65	26.915		9.0.	L2 1	.00 25	.48
ATOM		_	G LY	S 16	65	27.910			79 1	.00 23	.52
ATOM			D LY			28.363			1	.00 23	.14
ATOM		7 C	E LY			29.430		-	0 1	.00 29	.84
ATOM	•		Z Ly				9.87		5 1.	.00 28	. 33
ATOM	176	2 C	LY			29.794	10.283		7 1.	00 30	. 88
ATOM	176	3 0	LYS			25.595	5.823		3 1.	00 25	. 26
ATOM	1764		TRI			26.261	4.798		2 1.	00 23	05
ATOM	1766	5 CZ				24.289	5.815		5 1.	00 27.	05
ATOM	1767	7 CE		-		23.543	4.588		1 1.	00 27.	17
ATOM	1768	CG				22.282	4.529	8.760		00 26.	90
ATOM	1769	CD				22.563	4.067	10.197		00 29.	62
ATOM	1770	CE				23.065	4.857	11.283		00 29.	61
ATOM	1771	CE		166		23.230	3.988	12.393		00 28.) E
ATOM	1772	CD	TRP	1666		23.406	6.208	11.430		0 29.	43 1 E
MOTA	1773		1 TRP	1666		22.436	2.793	10.690		0 26.4	10
ATOM	1775	CZ	2 TRP			22.834	2.737	11.997		0 24.8	18
ATOM	1776	CZ	TRP	1666		23.719	4.430	13.636		0 28.4	γ.
ATOM	1777	CHO	TRP	1666		23.894	6.647	12.670	1.0	0 28.4	<i>i</i> 0
ATOM	1778	C	TRP	1666		24.048	5.756	13.749	1.0	0 29.3	. B
ATOM	1779	Ö		1666		23.176	4.499	6.385	1.0	0 29.8	3
ATOM	1780	N	TRP	1666		22.745	3.451	5.900	1.0	0 27.7	1
ATOM	1782	CA	MET	1667		23.439	5.572	5.645	1.0	0 29.4	2
ATOM	1783		MET	1667		23.098	5.642	4 222	Τ.00	25.5	2
ATOM	1784	CB	MET	1667		22.972	7.095	4.232	⊥.00	25.2	4
ATOM	1785	CG	MET	1667		21.830	7.836	3.792	1.00	26.5	3
	1/05	SD	MET	1667		21.846	9.559	4.391	1.00	32.3	5
								3.877	1.00	40.32	2
CCC C In .											

MOTA	1786	CE	MET	1667	21.033	9.447	2.341	1.00 38.17
ATOM	1787	С	MET	1667	24.042	4.960	3.276	1.00 25.07
MOTA	1788	0	MET	1667	25.256	5.037	3.411	1.00 27.61
ATOM	1789	N	ALA	1668	23.473	4.302	2.282	1.00 24.92
MOTA	1791	CA	ALA	1668	24.272	3.647	1.271	1.00 26.92
ATOM	1792	CB	ALA	1668	23.397	2.720	0.425	1.00 25.09.
ATOM	1793	C	ALA	1668	24.866	4.759	0.410	1.00 27.82
ATOM	1794	0	ALA	1668	24.254	5.817	0.242	1.00 27.06
ATOM	1795	N	PRO	1669	26.050	4.530	-0.170	1.00 27.84
MOTA	1796	CD	PRO	166.9	26.912	3.339	-0.107	1.00 27.12
ATOM	1797	CA	PRO	1669	26.662	5.561	-1.005	1.00 28.04
MOTA	1798	CB	PRO	1669	27.868	4.835	-1.593	1.00 26.71
MOTA	1799	CG	PRO	1669	28.249	3.893	-0.498	1.00 27.49
ATOM	1800	C	PRO	1669	25.734	6.078	-2.108	1.00 28.51
ATOM	1801	0	PRO	1669	25.685	7.281	-2.371	1.00 30.64
ATOM	1802	N	GLU	1670	24.992	5.179	-2.746	1.00 28.25
ATOM	1804	CA	GLU	1670	24.095	5.584	-3.826	1.00 26.82
ATOM	1805	CB	GLU	1670	23.600	4.369	-4.620	1.00 29.32
ATOM	1806	CG	GLU	1670	22.604	3.486	-3.889	1.00 30.38
ATOM	1807	CD	GLU	1670	23.223	2.266	-3.229	1.00 32.52
MOTA	1808	OE1	GLU	1670	22.444	1.393	-2.794	1.00 28.06
MOTA	1809	OE2	GLU	1670	24.474	2.175	-3.130	1.00 28.67
ATOM	1810	C	GLU	1670	22924	6.440	-3.356	1.00 24.79
MOTA	1811	0	GLU	1670	22.410	7.236	-4.123	1.09 22.31
MOTA	1812	N	ALA	1671	22.512	6.265	-2.101	1.00 26.70
ATOM	1814	CA	ALA	1671	21.423	7.040	-1.490	1.00 25.67
MOTA	1815	CB	ALA	1671	20.813	6.292	-0.312	1.00 18.88
MOTA	1816	C	ALA	1671	21.984	8.365	-1.006	1.00 26 05
MOTA	1817	0	ALA	1671	21.400	9.414	-1.229	1.00 28.14
ATOM	1818	N	LEU	1672	23.138	8.300	-0.358	1.00 29.03
MOTA	1820	CA	LEU	1672	23.807	9.481	0.172	1.00 34.07
MOTA	1821	CB	LEU	1672	25.030	9.064	0.986	1.00 34.45
MOTA	1822	CG	LEU	1672	25.870	10.157	1.648	1.00 39.50
ATOM	1823	CD1	LEU	1672	25.081	10.853	2.740	1.00 41.71
ATOM	1824	CD2	LEU	1672	27.123	9.530	2.243	1.00 40.16
ATOM	1825	C	LEU	1672	24.248	10.431	-0.942	1.00 38.47
ATOM	1826	0	LEU	1672	23.958	11.625	-0.898	1.00 42.25
ATOM	1827	N	PHE	1673	24.924	9.901	-1.956	1.00 39.07
ATOM	1829	CA	PHE	1673	25.414	10.725	-3.053	1.00 38.00
ATOM	1830	CB	PHE	1673	26.699	10.110	-3.639	1.00 36.48
ATOM	1831	CG	PHE	1673	27.826	9.928	-2.637	1.00 33.36
ATOM	1832		PHE	1673	28.524	8.724	-2.580	1.00 29.55
ATOM	1833		PHE	1673	28.205	10.960	-1.779	1.00 31.85
ATOM	1834		PHE	1673	29.580	8.540	-1.692	1.00 26.33
MOTA	1835		PHE	1673	29.265	10.786	-0.880	1.00 30.95
MOTA	1836	CZ	PHE	1673	29.954	9.568	-0.838	1.00 28.99
MOTA	1837	C	PHE	1673	24.413	10.957	-4.194	1.00 39.64
ATOM	1838	0	PHE	1673	24.364	12.046	-4.760	1.00 37.72
ATOM	1839	N	ASP	1674	23.651	9.928	-4.554	1.00 41.35
MOTA	1841	CA	ASP	1674	22.716	10.027	-5.666	1.00 43.38
ATOM	1842	CB	ASP	1674	22.934	8.858	-6.625	1.00 47.84
ATOM	1843	CG	ASP	1674	24.359	8.765	-7.121	1.00 53.24

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ATO		CZ ARG		19.6				4
ATO	,	NH1 ARC		18.6				
ATON		NH2 ARG		20.1				
ATON	5	C ARG		18.64				2
ATOM		O ARG		17.46				
ATOM	_	N ILE		19.27				
ATOM	_	CA ILE	1676	18.54				;
ATOM		CB ILE	1676	19.32				
ATOM		CG2 ILE	1676	1.8.45			,5	
ATOM		CG1 ILE	1676	19.76		* * * * * * *		
ATOM		CD1 ILE	1676	20.65		_ -	1.00 32.68	
ATOM		C ILE	1676	18.32		2	1.00 35.75	
ATOM	•	O ILE	1676	19.26			1.00 31.08	
ATOM		N TYR	1677	17.10			1.00 28.77	
ATOM	1876	C'A TYR	1677	16.77			1.00 30.32	
ATOM	1877	CB TYR	1677	15.846			1.00 29.68	
ATOM	1878	CG TYR	1677	16.523			1.00 31.14	
ATOM	1879	CD1 TYR	1677	16.616			1 00 32.95	
ATOM	1880	CE1 TYR	1677	17.208			1.00 30.40	
ATOM		CD2 TYR	1677	17.048			1.00 27.57	
ATOM		CE2 TYR	1677	17.642	7.059		1.00 32.13	
ATOM		CZ TYR	1677	17.711	8.366		1.00 31.50	
ATOM		OH TYR	1677	18.235	9.326		1.00 31.12	
ATOM	100-	C TYR	1677	16.123	3.424		1.00 32.18	
ATOM	2000	O TYR	1677	15.268	3.537	-3.811	1.00 28.88	
ATOM			1678	16.556	2.253	-2.481	1.00 32.20	
ATOM		7m	1678	16.023	0.988	-2.971	1.00 26.34 1.00 25.55	
ATOM	-		1678	16.917	0.394	-4.043	1.00 28.81	
ATOM	_		1678	18.221	0.179	-3.483	1.00 28.81	
ATOM	1895 C		1678	17.010	1.320		1.00 27.25	
ATOM	1896 O		1678	16.037	0.007		1.00 27.25	
ATOM	1897 N		1678	16.505	0.312		1.00 21.78	
ATOM			L679	15.559	-1.198		1.00 20.86	
ATOM			1679	15.580	-2.216	·		
ATOM			1679	14.816	-3.453		1.00 20.30	
ATOM	_		.679	13.367	-3.196		1.00 17.22	
ATOM			.679	12.662	-3.275		1.00 19.02	
ATOM		-	679	12.459	-2.830		1.00 14.89	
ATOM			679	11.260	-2.697		.00 18.98	
ATOM			679	11.359	-2.961		.00 16.10	
ATOM			679	17.050	-2.535		.00 15.18	
	1909 0	HIS 1	679	17.428	-2.901		.00 20.44	
						550 I	.00 22.58	

ATOM	1910	N	GLN	1680	17.874	-2.310	-1.781	1.00	20.58
MOTA	1912	CA	GLN	1680	19.303	-2.539	-1.721	1.00	22.70
ATOM	1913	CB	GLN	1680	19.935	-2.427	-3.106	1.00	26.26
ATOM	1914	CG	GLN	1680	19.934	-3.711	-3.889	1.00	31.86
MOTA	1915	CD	GLN	1680	18.949	-3.687	-5.026	1.00	37.54
ATOM	1916	OE1	GLN	1680	17.931	-3.000	-4.961	1.00	42.70
ATOM	1917	NE2	GLN	1680	19.256	-4.409	-6.091	1.00	37.42
ATOM	1920	С	GLN	1680	19.985	-1.559	-0.797	1.00	24.93
ATOM	1921	0	GLN	1680	20.875	-1.943	-0.039	1.00	26.39
ATOM	1922	N	SER	1681	19.605	-0.286	-0.867	1.00	24.70
ATOM	1924	CA	SER	1681	20.239	0.678	0.030	1.00	23.24
ATOM	1925	CB	SER	1681	19.923	2.128	-0.346	1.00	19.33
ATOM	1926	OG	SER	1681	18.544	2.326	-0.545	1.00	18.55
ATOM	1928	С	SER	1681	19.852	0.364	1.464	1.00	21.77
ATOM	1929	0	SER	1681	20.645	0.609	2.366	1.00	24.14
ATOM	1930	N	ASP	1682	18.659	-0.210	1.670	1.00	21.80
ATOM	1932	CA	ASP	1682	18.180	-0.604	3.003	1.00	22.45
ATOM	1933	CB	ASP	1682	16.730	-1.111	2.963		25.27
ATOM	1934	CG	ASP	1682	15.678	0.004	3.132	1.00	28.21
ATOM	1935	OD1	ASP	1682	14.500	-0.245	2.786	1.00	25.41
ATOM	1936	OD2	ASP	1682	15.992	1.102	3.639		30.19
ATOM	1937	С	ASP	1682	19.076	-1.736	3.517		23.69
ATOM	1.938	O	ASP	1682	19.385	-1.799	4.709	1.00	24.74
ATOM	1939	N	VAL	1683	19.474	-2.635	2.620		23.49
ATOM	1941	CA	VAL	1683	20.354	-3.737	3.003		21.77
ATOM	1942	СВ	VAL	1683	20.543	-4.741	1.837	1.00	20.49
ATOM	1943	CG1	VAL	1683	21.770	5.613	2.039		19.82
ATOM	1944	CG2	VAL	1683	19.320	-5.618	1.736	1.00	19.29
ATOM	1945	C	LIAV	1683	21.674	-3.153	3.523		21.93
ATOM	1946	Ö	VAL	1683	22.161	-3.570	4.573	1.00	21.06
ATOM	1947	N	TRP	1684	22.207	-2.143	2.837	1.00	20.64
ATOM	1949	CA	TRP	1684	23.424	-1.482	3.295	1.00	20.98
.ATOM	1950	CB	TRP	1684	23.711	-0.224	2.463	1.00	19.56
MOTA	1951	CG	TRP	1684	24.859	0.609	2.970	1.00	23.22
ATOM	1952	CD2	TRP	1684	26.182	0.686	2.421		24.64
ATOM	1953	CE2	TRP	1684	26.929	1.559	3.249	1.00	24.69
ATOM	1954	CE3	TRP	1684	26.813	0.102	1.315	1.00	26.41
A'TOM	1955	CD1	TRP	1684	24.857	1.430	4.075	1.00	23.64
ATOM	1956	NE1	TRP	1684	26.097	1.994	4.246	1.00	23.28
ATOM	1958	CZ2	TRP	1684	28.275	1.859	3.000		20.55
ATOM	1959	CZ3	TRP	1684	28.165	0.409	1.072	1.00	22.82
ATOM	1960	CH2		1684	28.872	1.274	1.908		19.24
ATOM	1961	С	TRP	1684	23.201	-1.112	4.771	1.00	21.12
ATOM	1962	0	TRP	1684	23.931	-1.560	5.652		22.08
ATOM	1963	N	SER	1685	22.150	-0.342	5.032		23.27
ATOM	1965	CA	SER	1685	21.787	0.086	6.386		22.54
ATOM	1966	СВ	SER	1685	20.429	0.768	6.356		21.98
ATOM	1967	OG	SER	1685	20.318	1.626	5.220		25.48
ATOM	1969	C	SER	1685	21.747	-1.068	7.389		21.33
ATOM	1970	0	SER	1685	22.145	-0.902	8.545		19.52
ATOM	1971	N	PHE	1686	21.260	-2.228	6.946		23.10
ATOM	1973	CA	PHE	1686	21.174	-3.424	7.800		23.09
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ATOM	2033	CB	GLU	1692	24.335	-1.060	15.994	1.00	22.29
ATOM	2034	CG	GLU	1692	24.507	0.107	15.056	1.00	18.31
MOTA	2035	CD	GLU	1692	23.255	0.933	14.978	1.00	25.10
MOTA	2036	OE1	GLU	1692	22.433	0.704	14.066	1.00	26.95
MOTA	2037	OE2	GLU	1692	23.067	1.815	15.840	1.00	27.05
MOTA	2038	C	GLU	1692	25.260	-3.036	17.163	1.00	25.18
ATOM	2039	0	GLU	1692	25.602	-2.927	18.341	1.00	26.12
ATOM	2040	N	ILE	1693	24.593	-4.087	16.698	1.00	27.16
ATOM	2042	CA	ILE	1693	24.231	-5.214	17.555	1.00	25.91
MOTA	2043	CB	ILE	1693	23.373	-6.287	16.777	1.00	25.70
MOTA	2044	CG2	ILE	1693	23.171	-7.564	17.638	1.00	18.73
ATOM	2045	CG1	ILE	1693	22.005	-5.682	16.382	1.00	23.45
ATOM	2046	CD1	ILE	1693	21.208	-6.485	15.346	1.00	15.62
MOTA	2047	С	ILE	1693	25.496	-5.847	18.107	1.00	26.70
ATOM	2048	0	ILE	1693	25.672	-5.961	19.316	1.00	28.19
MOTA	2049	N	PHE	1694	26.442	-6.133	17.229	1.00	28.78
ATOM	2051	CA	PHE	16.94	27.664	-6.779	17.679	1.00	29.72
ATOM	2052	CB	PHE	1694	28.261	-7.598	16.542	1.00	27.18
ATOM	2053	CG	PHE	1694	27.315	-8.649	16.048	1.00	25.38
ATOM	2054	CD1	PHE	1694	26.793	-8.599	14.770	1.00	26.16
MOTA	2055	CD2	PHE	1694	26.844	-9.625	16.919	1.00	26.37
MOTA	2056	CE1	PHE	1694.	25.808	-9.505	14.370	1.00	31.37
ATOM	2057	CE2	PHE	1694	25.863	-10.533	16.536	1.00	25.23
MOTA	2058	CZ		1694		-10.478	15.268	1.00	29.46
MOTA	2059	С	PHE	1694	28.663	-5.906	18.438		30.92
ATOM	2060	0	PHE	1694	29.697	-6.403	18.902		32.23
ATOM	2061	N	THR	1695	28.344	-4.616	18.575		29.46.
ATOM	2063	CA	THR	1695	29.170	-3.698	19.348		27.17
ATOM	2064	CB	THR	1695	29.665	-2.474	18.535		23.32
ATOM	2065	OG1	THR	1695	28.553	-1.710	18.046		24.73
MOTA	2067	CG2	THR	1695	30.538	-2.914	17.395		21.34
ATOM	2068	С	THR	1695	28.307	-3.230	20.519		28.81
MOTA	2069	0	THR.	1695	28.707	-2.346	21.289	1.00	31.85
MOTA	2070	N	LEU	1696	27.130	-3.841	20.651		26.30
MOTA	2072	CA	LEU	1696	26.188	-3.523	21.720	1.00	25.99
ATOM	2073	СВ	LEU	1696	26.704	-4.043	23.060	1.00	24.51
ATOM	2074	CG	LEU	1696	26.974	-5.539	23.194		23.32
ATOM	2075	CD1	LEU	1696	27.447	-5.843	24.597		26.45
MOTA	2076	CD2	LEU	1696	25.726	-6.297	22.907		29.79
ATOM	2077	C	LEU	1696	25.892	-2.036	21.837		24.90
ATOM	2078	0	LEU	1696	26.083	-1.457	22.889		28.99
ATOM	2079	N	GLY	1697	25.386	-1.432	20.771		25.05
ATOM	2081	CA	GLY	1697	25.072	-0.016	20.811		24.31
ATOM	2082	C	GLY	1697	26.241	0.847	20.381		27.15
ATOM	2083	0	GLY	1697	26.297	2.035	20.701		29.57
ATOM	2083	N	GLY	1698	27.177	0.261	19.639		27.33
ATOM						1.023	19.178		27.04
	2086	CA	GLY	1698	28.319		18.173		
ATOM	2087	C	GLY	1698	27.966	2.109			29.78 32.03
MOTA	2088	O N	GLY	1698	27.115	1.929	17.301		
MOTA	2089	N	SER	1699	28.633	3.247	18.295		30.60
ATOM	2091	CA	SER	1699	28.413	4.385	17.414		31.48
MOTA	2092	CB	SER	1699	28.747	5.692	18.164	1.00	32.97



ATO		93	og s	ER 169	9	28.3	50	6.84	0 17 4			
ATO		95	C S	ER 169	9	29.3		4.23	- · · • ·			37.75
ATO		96	0 s	ER 169	9	30.5		4.03				32.74
ATO		97]	N P	RO 170				4.27	-			33.04
ATOM		98 (CD P	RO 170		27.2						31.40
ATON	4 209	99 (CA PI	RO 170	0	29.5		4.32				30.88
ATOM	1 210	00 (CB PI	RO 170	0	28.4		4.153				30.55
ATOM	1 210)1 (CG PI	20 170		27.2		4.024				30.13
ATOM	1 210)2 (PF			30.30		3.535				31.10
ATOM		3 () PF			29.76		5.427				31.19
ATOM	210	4 N	TY			31.57		6.522				35.48
ATOM		6 C	A TY			32.44		5.277				29.51
ATOM	210	7 C	В ту			32.08		6.412	-			30.10
ATOM	210	8 C	G TY			32.10		7.029				32.84
ATOM	210	9 C	D1 TY	R 1701		30.92		6.078				88.43
ATOM	211		E1 TY					5.795				0.14
ATOM	211		D2 TY			30.93		5.000	8.51		0 з	9.07
ATOM	211		E2 TY			33.29		5.522	9.890		0 3	8.19
ATOM	211					33.32		4.726	8.754			1.52
ATOM	2114					32.13		4.471	8.067			4.97
ATOM	2116		TY			32.15		3.700	6.919		5 0	4.77
ATOM	2117		TY			32.42		7.524	13.965			0.38
ATOM	2118		PRO			32.00		8.655	13.685			0.54
ATOM	2119					32.94		7.239	15.170	1.00		0.61
ATOM	2120			· · · - -		33.578		5.985	15.608	1.00		
ATOM	2121					32.97		8.239	16.248	1.00	28	3.48
ATOM	2122					33.554		7.463	17.429	1.00		3.43
ATOM	2123		PRO			33.320		6.025	17.085			0.63
ATOM	2124		PRO			33.897		9.385	15.981	1.00		
ATOM	2125					34.998		9.156	15.418	1.00		
ATOM	2127	CA	GLY			33.440		10.613	16.084	1.00		
AT'OM	2128	C				34.239		11.787	15.767	1.00		
ATOM	2129	0	GLY			34.374		12.143	14.296	1.00		
ATOM	2130	N	GLY			35.055		L3.104	13.962	1.00		.54
ATOM	2132	CA	VAL	1704		33.726		11.380	13.418	1.00		
ATOM	2133	CB	VAL	1704		33.798	1	1.616	11.975	1.00		
ATOM	2134		VAL	1704		33.806	-	.0.289	11.228	1.00		
ATOM	2135		L VAL	1704		34.074	1	.0.525	9.750	1.00		
ATOM	2135	CG2		1704		34.851		9.375	11.822	1.00		
ATOM		C	VAL	1704		32.620	1	2.466	11.477		33.	
ATOM	2137	0	VAL	1704		31.466		2.045	11.529	1.00		
ATOM	2138	N	PRO	1705		32.906		3.681	10.979	1.00		
	2139	CD	PRO	1705		34.217			11.008	1.00		
ATOM	2140	CA	PRO	170.5		31.868			10.474	1.00		
ATOM	2141	CB	PRO	1705		32.534		 .	10.627			
ATOM	2142	CG	PRO	1705		33.939			10.027	1.00		
ATOM	2143	C	PRO	1705		31.473		4.293		1.00		
ATOM	2144	0	PRO	1705		32.255		3.690	9.031	1.00		
ATOM	2145	N	VAL	1706		30.296		1.780	8.288	1.00		
ATOM	2147	CA	VAL	1706		29.743		1.582	8.624	1.00		
ATOM	2148	CB	VAL	1706		28.667		5.658	7.276	1.00		
ATOM	2149		VAL	1706		28.106		5.441	6.942	1.00		
ATOM	2150	CG2	VAL	1706		27.536		5.595	5.535	1.00 3		
									7.952	1.00 4	10.	79

ATOM	2151	C	VAL	1706	30.762	14.559	6.138	1.00	37.09
MOTA	2152	0	VAL	1706	30.927	13.543	5.461	1.00	38.75
ATOM	2153	N	GLU	1707	31.477	15.663	5.967	1.00	37.08
MOTA	2155	CA	GLU	1707	32.472	15.793	4.910	1.00	35.52
MOTA	2156	CB	GLU	1707	33.059	17.206	4.918	1.00	38.30
ATOM	2157	C	GLU	1707	33.588	14.762	4.945	1.00	34.20
MOTA	2158	0	GLU	1707	34.153	14.445	3.908	1.00	33.48
ATOM	2159	N	GLU	1708	33.936	14.273	6.132	1.00	34.20
ATOM	2161	CA	GLU	1708	34.981	13.256	6.241	1.00	36.08
ATOM	2162	CB	GLU	1708	35.555	13.178	7.660	1.00	40.39
ATOM	2163	CG	GLU	1708	36.212	14.464	8.179	1.00	45.41
ATOM	2164	CD	GLU	1708	37.471	14.871	7.430		50.66
MOTA	2165	OE1	GLU	1708	38.199	13.986	6.909	1.00	54.73
MOTA	2166	OE2	GLU	1708	37.747	16.092	7.392	1.00	52.85
MOTA	2167	C	GLU	1708	34.369	11.911	5.855		35.22
ATOM	2168	0	GLU	1708	35.035	11.045	5.260	1.00	34.04
ATOM	2169	N	LEU	1709	33.089	11.745	6.178		33.30
ATOM	2171	CA	LEU	1709	32.376	10.519	5.860		31.44
ATOM	2172	СВ	LEU	1709	30.975	10.531	6.474		26.89
ATOM	2173	CG	LEU	1709	30.065	9.366	6.073	1.00	
ATOM	2174	CD1		1709	30.652	8.036	6.503	1.00	22.75
ATOM	2175		LEU	1709	28.717	9.574	6.597		26.15
MOTA	2176	C	LEU	1709	32.291	10.325	4.350	1.00	31.18
ATOM	2177	0	LEU	1709	32.490	9.209	3.858	1.00	29.88
ATOM	2178	N	PHE	1710	32.011	11.408	3.623	1.00	30.16
ATOM	2180	CA	PHE	1710	31.915	11.333	2.169	1.00	31.64
ATOM	2181	СВ	PHE	1710	31.658	12.710	1.567	1.00	33.44
ATOM	2182	CG	PHE	1710	30.287	13.231	1.827	1.00	37.78
ATOM	2183	CD1		1710	29.287	12.395	2.303	1.00	41.46
ATOM	2184	CD2	PHE	1710	29.991	14.565	1.613	1.00	40.72
ATOM	2185	CE1		1710	28.012	12.882	2.566	1.00	41.30
ATOM	2186		PHE	1710	28.715	15.058	1.875		42.99
ATOM	2187	CZ	PHE	1710	27.725	14.208	2.354		40.95
ATOM	2188	C	PHE	1710	33.202	10.771	1.609		32.38
ATOM	2189	O	PHE	1710	33.183	9.815	0.825		32.26
ATOM	2190	N	LYS	1711	34.310	11.336	2.085	1.00	31.26
ATOM	2192	CA	LYS	1711	35.664	10.971	1.697	1.00	29.73
ATOM	2193	CB	LYS	1711	36.642	11.932	2.379	1.00	33.49
ATOM	2194	CG	LYS	1711	38.103	11.716	2.042		39.79
ATOM	2195	CD	LYS	1711	38.981	12.731	2.755		43.35
ATOM	2196	CE	LYS	1711	40.413	12.686	2.238		46.23
ATOM	2197	NZ	LYS	1711	41.116	11.422	2.600		53.67
ATOM	2201	C	LYS	1711	35.999	9.501	2.015		29.34
ATOM	2202	0	LYS	1711	36.670	8.836	1.231		28.77
ATOM	2202	N	LEU	1712	35.541	9.000	3.164		30.40
ATOM	2205	CA	LEU	1712	35.776	7.599	3.532		28.72
ATOM	2205	CB	LEU	1712	35.776	7.399	4.942		27.71
ATOM	2207	CG	LEU	1712	35.241	7.293	6.166		28.23
ATOM	2207		PEO						28.23
ATOM	2208		LEU	1712 1712	35.186	7.593 7.297	7.440 6.266		27.01
ATOM		CD2			37.389				
	2210		LEU	1712	35.022	6.738	2.530		30.03
MOTA	2211	0	LEU	1712	35.571	5.796	1.957	1.00	29.28



A MOV	
ATOM 2212 N LEU 1713	
ATOM 2214 CA LEU 1713	32 904 6 330 2.325 1.00 31.98
ATOM 2215 CB LEU 1713	31.467 6.339 1.403 1.00 34.30
ATOM 2216 CG LEU 1713	30.663 6.872 1.447 1.00 37.65
ATOM 2217 CD1 LEU 1713	0.450 2.686 1.00 37 06
ATOM 2218 CD2 LEI 1713	2.781 1.00 36 80
ATOM 2219 C LEU 1713	4.950 2.641 1.00 37 02
ATOM 2220 O LEU 1713	33.451 6.344 -0.011 1.00 35 45
ATOM 2221 N LYS 1714	33.468 5.298 -0.662 1.00 20 20
ATOM 2222 CD	33.920 7.498 -0.481 7.00 22 22
ATOM 2224 CD	34.487 7.590 -1.821 1.00 22
ATOM 2225 215 1.714	34.881 9.027 -2.158 1.00 21 75
ATOM 2226 00	33 724 0 000
ATOM 2227 OF	32 814 0 425
ATOM 2224 CB BIS 1714	31 612 10 264
ATOM 2222	30 674 0 041
ATOM 2222	35 706 6 677
ATOM 2224	35 990 6 17-
ATOM 2226	36 420 6 420
ATOM 2225	37 602 5 644
ATOM 2020	38 617 6 177
ATTOM	39 085 7 577
ATOM 2239 CD GLU 1715	39 654 0 370
ATOM 2240 OE1 GLU 1715	39 920 7 51.44
ATOM 2241 OE2 GLU 1715	2.003 1.00 51.40
ATOM 2242 C GLU 1715	37.000 9.573 0.726 1.00 54.23
ATOM 2243 O GLU 1715	30.104 4.183 -0.581 1.00 35.09
ATOM 2244 N GLY 1716	3.35/ -0.482 1.00 37 59
ATOM 2246 CA GLV 1716	3.866 -0.455 1.00 33 79
ATOM 2247 C GLY 1716	2.498 -0.197 1.00 30 96
ATOM 2248 O GLV 1716	1.9/6 1 198 7 00 00
ATOM 2249 N HIS 1717	0.766 1.416 1.00 29 20
ATOM 2251 CA HIS 1717	2.155 1.00 28 16
ATOM 2252 CB HTS 1717	36.282 2.489 3.532 1.00 29 80
ATOM 2252 GG ****	3./43 4.378 1.00 22
ATOM 2254 CD2 HIS 1717	3.469 5.826 1 00 36 00
ATOM 3355	37.955 3.375 6.516 1.00 35 55
ATOM 2257 CD1	35.782 3.279 6.746 1.00 27 25
ATOM 2250 XT2	36.309 3.080 7.942 7.00 35 07
ATOM 2260 G ****	37 624 2 72.
ATOM 2261 0	35.171 1.645 4 153 + 00 35.83
ATOM 2262 N	33 907 7 900
ATOM 2264 CD	35 571 0 664
7.TOM 2255	34 632 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
VALOW 2022	34 592 1 575
VIIIO74	34 050 7 553
ATOM 2267 CD ARG 1718	32 609 3 77
ATOM 2268 NE ARG 1718	32 032 1 75
ATOM 2270 CZ ARG 1718	32 147 2 2 2 1 1 1 2 2 4 9 6
ATOM 2271 NH1 ARG 1718	32 924 0 25 1.204 1.00 23.90
ATOM 2274 NH2 ARG 1718	31.512 0.912 1.454 1.00 20.04
ATOM 2277 C ARG 1718	35 001 -0.338 0.045 1.00 20.04
ATOM 2278 O ARG 1718	7.101 1.00 33 92
ATOM 2279 N MET 1719	7.377 1.00 36 49
	34.134 -0.355 8.028 1.00 33.22

ATOM	2281	CA	MET	1719	34.428	-0.459	9.448	1.00	32.33
ATOM	2282	CB	MET	1719 .	33.148	-0.285	10.277	1.00	34.72
MOTA	2283	CG	MET	1719	32.454	1.066	10.076	1.00	35.04
MOTA	2284	SD	MET	1719	31.025	1.447	11.141	1.00	34.06
ATOM	2285	CE	MET	1719	29.757	0.470	10.409	1.00	33.14
ATOM	2286	С	MET	1719	35.068	-1.797	9.747	1.00	35.53
ATOM.	2287	0	MET	1719 .	34.896	-2.756	8.991	1.00	35.48
MOTA	2288	N	ASP	1720	35.826	-1.843	10.840	1.00	38.65
ATOM	2290	CA	ASP	1720	36.521	-3.049	11.281	1.00	39.03
ATOM	2291	CB	ASP	1720	37.659	-2.678	12.237	1.00	43.11
ATOM	2292	CG	ASP	1720	38.743	-1.846	11.569	1.00	46.69
MOTA	2293	OD1	ASP	1720	38.587	-1.536	10.364	1.00	54.08
ATOM	2294	OD2	ASP	1720	39.750	-1.503	12.239	1.00	45.93
ATOM	2295	C	ASP	1720	35.580	-4.023	11.972	1.00	38.50
ATOM	2296	0	ASP	1720	34.554	-3.617	12.528	1.00	37.73
ATOM	2297	N	LYS	1721	35.961	5.298	11.981	1.00	38.10
MOTA	2299	CA	LYS	1721	35.151	-6.339	12.600	1.00	38.12
ATOM	2300	CB	LYS	1721	35.727	-7.733	12.323	1.00	38.20
ATOM	2301	CG	LYS	1721	34.825	-8.858	12.825	1.00	38.48
ATOM	2302	CD	LYS	1721	35.375	-19.238	12.543	1.00	37.49
ATOM	2303	CE	LYS	1721	36.320	-10.691	13.625	1.00	39 11
ATOM	2304	NZ	LYS	1721 .	36.448	-12.167	13.628	1.00	40.75
ATOM	2308	С	LYS	1721	35.092	-6.142	14.091	1.00	40.24
ATOM	2309	0	LYS	1721	36.136	-6.032	14:739	1.00	42.70
ATOM	2310	N	PRO	1722	33.875	-6.082	14.658	1.00	41.23
ATOM	2311	CD	PRO	1722	32.547	-6.153	14.019	1.00	38.63
MOTA	2312	CA	PRO	1722	33.743	~5.901	16.104		41.71
A'TOM	2313	CB	PRO	1722	32.223	-5.957	16.306	1.00	38.90
ATOM	2314	CG	PRO	1722	31.679	-5.442	15.016	1.00	34.19
ATOM	2315	C	PRO	1722	34.418	-7.079	16.819	1.00	43.96
ATOM	2316	o	PRO	1722	34.542	-8.174	16.250	1.00	43.02
ATOM	2317	N	SER	1723	34.915	-6.860	18.028	1.00	46.76
ATOM	2319	CA	SER	1723	35.493	-7.973	18.747	1.00	50.74
ATOM	2320	CB	SER	1723	36.265	-7.500	19.980	1.00	49.47
ATOM	2321	OG	SER	1723	35.400	-7.130	21.035	1.00	53.87
ATOM	2323	С	SER	1723	34.259	-8.782	19.143	1.00	53.24
ATOM	2324	0	SER	1723	33.136	-8.259	19.130	1.00	53.97
ATOM	2325	N	ASN	1724	34.443	-10.064	19.426	1.00	56.59
MOTA	2327	CA	ASN	1724	33.316	-10.899	19.825	1.00	59.55
MOTA	2328	CB	ASN	1724	32.739	-10.386	21.162	1.00	66.12
ATOM	2329	CG	ASN	1724		-10.128	22.213	1.00	71.34
ATOM	2330	OD1	ASN	1724	34.661	-10.990	22.485	1.00	73.38
ATOM	2331	ND2	ASN	1724	33.831	-8.926	22.779	1.00	74.19
ATOM	2334	С	ASN	1724	32.256	-10.900	18.711	1.00	57.31
ATOM	2335	0	ASN	1724		-10.662	18.940		59.27
ATOM	2336	N	CYS	1725		-11.132	17.493		54.50
MOTA	2338	CA	CYS	1725	31.881	-11.203	16.300		50.89
MOTA	2339	CB	CYS	1725	31.827	-9.848	15.576		50.09
ATOM	2340	SG	CYS	1725	30.893	-9.833	14.006		44.81
ATOM	2341	С	CYS	1725	32.596	-12.235	15.439		47.28
ATOM	2342	0	CYS	1725	33.820	-12.172	15.288		48.97
ATOM	2343	N	THR	1726	31.863	-13.229	14.950		42.60

Δ,	TOM 234			
			THR 172	6 32.472 -14.275 14.139 1.00 30 22
			THR 172	6 31 520 15 404
			1/2	30 290 75 005
			THR 1726	31 210 -16 004
	OM 2350	-	THR 1726	5 33 050 16.084 15.326 1.00 33.12
	OM 2351	0	THR 1726	
	'OM 2352	N .	ASN 1727	1 22.373 -12.704 12.357 1.00 39.57
AT		CA	ASN 1727	12 12 12 12 12 12 12 12 12 12 12 12 12 1
AT			ASN 1727	
AT			ASN 1727	35.290 -14.880 10 221 1 00 10
ATO		OD1 2		36.580 -14.593 10.953 1 00 44
ATO	OM 2358			37.188 -13.539 10.781 1.00 45
ATO	OM 2361	_		37.010 -15.536 11.778 1 00 40 55
ATC		_	,	32.958 -14.159 9.786 1.00 33 a-
ATC			SN 1727	32 883 -13 421
ATO			LU 1728	32 041 -15 055
ATO	-005		LU 1728	30 854 15 376
ATO	• •		LU 1728	30.109 -16 551
ATO	,		LU 1728	28 973 -17 000
ATO	2500	CD G	LՄ 1.728	28 329 -19 306 - 100 35.84
ATO		OE1 G		28 409 -19 622
		OE2 GI	່ວປີ ວັ.728	27 734 19 005
ATON	,-	C. GI	U 1728	29 925 14 364
ATON	,_	O GI	.Ŭ 1728	29 521 12 57
ATOM		N LE	U 1.729	39 632 8.272 1.00 39.58
ATOM	_	CA LE		28 747 10.527 1.00 32.09
ATOM		CB LE		12.530 10.710 1 00 20 1-
ATOM		CG LE		20.331 12.389 12.170 1.00 20
ATOM		CD1 LE		
ATOM		CD2 LE		27.131 -13.388 i4 089 7 00 30 to
ATOM	2380	C' LE		-0.000 -13.10/ 11.845 1 00 0n
ATOM	2381 (LET		29.359 -11.252 10.175 1 00 22
ATOM	2382 1	7 TYF	_ , 42,5	28.638 -10.367 9 693 1 02 25
ATOM	2384 ('A TYR		30.688 -11.143 10.251 1 00 21
ATOM	000-	B TYR		31.378 -9.959 9.734 1.00 22
ATOM		G TYR	- -	32.849 -9.940 10.154 1.00 37.22
ATOM	-	D1 TYR		33 591 0 702
ATOM				33 093 7 440
ATOM			• •	33 725 (20.
ATOM			1730	34 750 0 040
ATOM		E2 TYR	1730	35 400 7 70
ATOM			1730	34 882 6 462
ATOM	2392 O		1730	35 473 5 334 1.00 28.56
ATOM	2394 C	TYR	1730	31 297 2 25
	2395 O	TYR	1730	31 062 0 000
ATOM	2396 N	MET	1731	31 442 33 33 33 1.00 29.16
ATOM	2398 CZ	MET	1731	31 366 11 379 7.623 1.00 31.05
ATOM	2399 CE	MET	1731	31.506 -11.313 6.187 1.00 34.59
ATOM	2400 CG	MET	1731	31 335 5.840 1.00 41.42
ATOM	2401 SD		1731	12.343 -13.149 4 403 1 00 50 5
ATOM	2402 CE		1731	31.801 -14.840 3 994 7 00 64 7
ATOM	2403 C	MET	1731	32.926 -14.502 2.606 1.00 63
ATOM	2404 O	MET		^{29.992} -10.869 5.695 1.00 24 75
ATOM	2405 N	MET	1731	29.863 -10.268 4 619 1 00 27
		1	1732	78 071 11 1
				28.971 -11.153 6.501 1.00 33.32

ATOM	2407	CA	MET	1732	27.594	-10.770	6.194	1.00 31.78
ATOM	2408	CB	MET	1732	26.634	-11.346	7.236	1.00 30.42
MOTA	2409	CG	MET	1732	25.172	-11.071	6.938	1.00 30.28
MOTA	2410	SD	MET	1732	24.071	-11.709	8.183	1.00 27.41
ATOM	2411	CE	MET	1732	23.738	-13.369	7.471	1.00 22.35
MOTA	2412	C	MET	1732	27.484	-9.243	6.158	1.00 31.10
ATOM	2413	0	MET	1732	. 26.794	-8.680	5.303	1.00 31.08
MOTA	2414	N	MET	1733	28.139	-8.586	7.114	1.00 31.22
MOTA	2416	CA	MET	1733	28.161	-7.128	7.189	1.00 30.93
MOTA	2417	CB	MET	1733	29.001	-6.665	8.376	1.00 31.91
ATOM	2418	CG	MET	1733	28.368	-6.906	9.710	1.00 33.63
MOTA	2419	SD	MET	1733	29.375	-6.210	11.021	1.00 34.53
MOTA	2420	CE	MET	1733	29.106	-7395	12.280	1.00 34.12
MOTA	2421	C	MET	1733	28.830	-6.623	5.921	1.00 32.49
MOTA	2422	0	MET	1733	28.357	-5.682	5.281	1.00 33.61
MOTA	2423	N	ARG	1734	29.932	-7.269	5.551	1.00 32.11
ATOM	2425	CA	ARG	1734	30.673	-6.889	4.355	1.00 31.13
MOTA	2426	CB	ARG	1734	32.012	-7.623	4.308	1.00 28.68
MOTA	2427	CG	ARG	1734	32.953	-7.267	5.451	1.00 27.19
MOTA	2428	CD	ARG	1734	33.159	-5.766	5.558	1.00 26.80
MOTA	2429	NE	ARG	1734	33.864	-5.243	4.393	1.00 35.67
MOTA	2431	CZ.	ARG	1734	35.187	-5.305	4.223	1.00 38.03
MOTA	2432	NH1	ARG	1734	35.967	-5.861	5.148	1.00 38.07
MOTA	2435	NH2	ARG	1734	35.729	-4.850	3.094	1.00 38.87
MOTA	2438	C	ARG	1734	29.873	-7.098	3.065	1.00 29.53
MOTA	2439	Ο .	ARG	1734	30.029	-6.334	2.121	1.00 29.11
ATOM	2440	N	ASP	1735	29.036		3.925	1.00 29.48
MOTA	2442	CA	ASP	1735	. 28.193	-8.412	1.859	1.00 26.82
MOTA	2443	CB	ASP	1735	27.591		1.933	1.00 30.25
MOTA	2444	CG	ASP	1735	28.632	-10.895	1.773	1.00 35.13
MOTA	2445		ASP	1735	29.626	-10.645	1.052	1.00 35.19
MOTA	2446		ASP	1735	28.458	-11.990	2.366	1.00 39.35
MOTA	2447	C	ASP	1.735	27.082	-7.375	1.760	100 23.88
MOTA	2448	0	ASP	1735	26.692		0.656	1.00 24.83
MOTA	2449	N	CYS	1736	26.574		2.913	1.00 22.13
MOTA	2451	CA	CYS	1736	25.538		2.965	1.00 21.74
MOTA	2452	CB	CYS	1736	25.005		4.401	1.00 20.46
MOTA	2453	SG	CYS	1736	23.978		5.053	1.00 19.59
MOTA	2454	С	CYS	1736	26.104		2.456	1.00 20.51
ATOM	2455	0	CYS	1736	25.377		1.887	1.00 16.07
ATOM	2456	N	TRP	1737	27.401		2.670	1.00 21.58
ATOM	2458	CA	TRP	1737	28.080		2.248	1.00 20.57
MOTA	2459	CB	TRP	1737	29.107		3.291	1.00 17.02
ATOM	2460	CG	TRP	1737	28.558	-2.415	4.654	1.00 20.35
ATOM	2461		TRP	1737	29.254	-2.564	5.897	1.00 20.42
MOTA	2462		TRP	1737	28.387	-2.122	6.923	1.00 21.18
MOTA	2463	CE3	TRP	1737	30.538		6.243	1.00 21.60
MOTA	2464		TRP	1737	27.317		4.970	1.00 19.86
ATOM	2465		TRP	1737	27.210		6.328	1.00 21.03
MOTA	2467	CZ2		1737	28.760	-2.125	8.276	1.00 21.70
MOTA	2468	CZ3		1737	30.910	-3.031	7.594	1.00 21.73
ATOM	2469	CH2	TRP	1737	30.025	-2.584	8.588	1.00 23.06

ATO	4 247					
ATOM				RP 1737		. 98
ATOM				RP 1737	29.758 -2.607 0.610 1.00 25	
					28.269 -4.185 0.063 1.00 27.	
ATOM			'A H		28.885 -4.352 -1.243 1.00 25.	
ATOM			B HI		28.263 -5.522 -2.013 1 00 24	
ATOM			G HI		29.105 -6.005 -3.162 1.00 26.	
ATOM			D2 HI		20 500	
ATOM			D1 HI		20 553	
ATOM			E1 HI		20 220	
ATOM	2481	1 N	E2 HI	S 1738	20 250	
MOTA	2483	3 C	HI		1.00 23.	
MOTA	2484	1 0	HI		27 705	
ATOM	2485	5 N	AL		20 700	
ATOM	2487	7 C2			20 000	
ATOM	2488	C C			21 702	
ATOM	2489		AL		31.193 -1.285 -4.117 1.00 25.8	87
ATOM	2490		AL		28.765 -1.418 -4.617 1.00 26.6	57
ATOM	2491		VAI	- -	28.207 -0.367 -4.930 1.00 28.2	28
ATOM	2493				28.529 -2.573 -5.235 1.00 25.1	
ATOM	2494				27.526 -2.706 -6.292 1.00 24.1	
ATOM	2495		3 VAI 3 VAI		27.969 -3.737 -7.378 1.00 24.2	
ATOM	2496				26.979 -3.792 -8.503 1.00 20.0	
ATOM	2497		2 VAI		29.331 -3.375 -7.926 1.00 26 7	
ATOM		_	VAI		26.234 -3.196 -5.639 1.00 23.9	
	2498	0	VAL	_	26.173 -4.349 -5.175 1.00 26.3	
ATOM	2499	N	PRO	_ · · - _	25.173 -2.357 -5.653 1.00 24.5	
ATOM	2500	CD			25.096 -1.065 -6.369 1.00 17.7	
MOTA	2501	CA	PRO	1741	23.868 -2.686 -5.058 1.00 22.2	
ATOM	2502	CB	PRO		22.979 -1.536 -5.545 1.00 17.8	
ATOM	2503	CG	PRO	1741	23.925 -0.410 -5.710 1.00 13.2	
ATOM	2504	C	PRO	1741	23.275 -4.057 -5.418 1.00 24.0	
ATOM	2505	0	PRO	1741	22 725	
ATOM	2506	N	SER	1742	22 422	
ATOM	2508	CA	SER	1742	20:000	
MOTA	2509	CB	SER	1742	20 004	
MOTA	2510	OG	SER	1742	24 22	
MOTA	2512	C	SER	1742		
ATOM	2513	0	SER	1742	20 22.20	
ATOM	2514	N	GLN	1743	24 752	
MOTA	2516	CA	GLN	1743	25 501	
ATOM	2517	CB	GLN	1743	26 000	
ATOM	2518	CG	GLN	1743	26.993 -7.773 -5.807 1.00 24.02	
ATOM	2519	CD	GLN	1743	27.263 -7.768 -7.295 1.00 22.75	
ATOM	2520		GLN	1743	26.585 -8.938 -8.014 1.00 26.21	
ATOM	2521		GLN		26.999 -10.087 -7.864 1.00 28.67	
ATOM	2524	C	GLN	1743	25.535 -8.649 -8.787 1.00 21.57	
ATOM	2525	0		1743	25.270 -8.148 -4.007 1.00 24.86	
ATOM	2526		GLN	1743	25.685 -9.173 -3.456 1.00 25.24	
ATOM		N	ARG	1744	24.525 -7.244 -3.389 1.00 23.38	
ATOM	2528	CA	ARG	1744	24.230 -7.376 -1.976 1.00 22.41	
ATOM	2529	CB	ARG	1744	23.727 -6.055 -1.415 1.00 22.24	
ATOM	2530	CG	ARG	1744	24.718 -4.909 -1.523 1.00 22.53	
	2531	CD	ARG	1744	24.084 -3.577 -1.134 1.00 19.82	
ATOM	2532	NE	ARG	1744	24.963 -2.475 -1.517 1.00 22.51	

ATOM	2534	CZ	ARG	1744	24.592	-1.201	-1.663	1.00 22.92
MOTA	2535	NHl	ARG	1744	23.332	-0.814	-1.458	1.00 18.28
MOTA	2538	NH2	ARG	1744	25.491	-0.310	-2.060	1.00 22.15
MOTA	2541	С	ARG	1744	23.163	-8.458	-1.833	1.00 24.61
MOTA	2542	0	ARG	1744	22.428	-8.755	-2.786	1.00 26.94
MOTA	2543	N	PRO	1745	23.143	-9.155	-0.688	1.00 23.21
ATOM	2544	CD	PRO	1745	24.052	-9.107	0.470	1.00 22.38
MOTA	2545	CA	PRO	1745	22.129	-10.190	-0.522	1.00 22.24
MOTA	2546	CB	PRO	1745	22.623	-10.942	0.711	1.00 21.13
MOTA	2547	CG	PRO	1745	23.286	-9.864	1.504	1.00 20.24
ATOM	2548	С	PRO	1745	20.800	-9.506	-0.256	1.00 23.11
MOTA	2549	0	PRO	1745	20.743	-8.300	0.020	1.00 25.93
MOTA	2550	N	THR	1746	19.724	-10.256	-0.373	1.00 20.82
ATOM	2552	CA	THR	1746	18.420	-9.697	-0.112	1.00 20.47
ATOM	2553	CB	THR	1746	17386	-10.342	-1.041	1.00 18.61
MOTA	2554	OG1	THR	1746	17.382	-11.755	-0.822	1.00 21.86
ATOM	2556	CG2	THR	1746	17.746	-10.078	-2.487	1.00 21.13
ATOM	2557	C	THR	1746	18.060	-9.970	1.344	1.00 20.84
ATOM	2558	0	THR	1746	18.787	-10.674	2.055	1.00 22.08
ATOM	2559	N	PHE	1747	16.953	-9.406	1.810	1.00 21.58
ATOM	2561	CA	PHE	1747	16.536	-9.675	3.178	1.00 21.15
ATOM	2562	CB	PHE	1747	15.442	-8.710	3.613	1.00 20.34
ATOM	2563	CG	PHE	1747	15.961	-7.350	3.982	1.00 23.18
ATOM	2564	CD1		1747	16.729	-7.170	5.130	1.00 22.26
ATOM	2565	CD2	PHE	1747	15.668	-6.240	3.196	1.00 23.41
ATOM	2566	CE1	PHE	.1747	17.186	-5.909	5.484	1.00 17.31
ATOM	2567	CE2	PHE	1747	16.124	-4.967	3.548	1.00 17.93
ATOM	2568	CZ	PHE	1747	16.883	-4.809	4.696	1.00 19.06
ATOM	2569	C	PHE	1747	16.062	-11.124	3.217	1.00 21.61
ATOM	2570	0	PHE	1747		-11.823	4.212	1.00 22.19
ATOM	2571	74	LYS	1748	15.490	-11.588	2.111	1.00 22.00
ATOM	2573	CA	LYS	1748	15.048	-12.973	2.009	1.00 24.34
ATOM	2574	СВ	LYS	1748	14.471	-13.227	0.621	1.00 23.61
ATOM	2575	CG	LYS	1748	14.050	-14.663	0.416	1.00 27.45
ATOM MOTA	2576	CD	LYS	1748	13.633	-14.932	-0.998	1.00 28.97
ATOM	2577	CE	LYS	1748	13.244	-14.332	-1.163	1.00 28.97
ATOM	2578	NZ	LYS	1748	12.213	-16.795	-0.153	1.00 33.93
ATOM		C	LYS					
	2582 2583	0	LYS	1748		-13.907 -14.863	2.264	1.00 27.58
ATOM				1748			3.034	1.00 29.73
MOTA	2584	N	GLN	1749		-13.604	1.640	1.00 25.88
ATOM	2586	CA	GLN	1749		-14.394	1.804	1.00 23.72
ATOM	2587	CB	GLN	1749		-13.925	0.837	1.00 27.00
ATOM	2588	CG	GLN	1749		-13.954	-0.628	1.00 32.28
MOTA	2589	CD	GLN	1749		-13.331	-1.477	1.00 36.35
ATOM	2590		GLN	1749		-12.528	-2.368	1.00 37.63
MOTA	2591		GLN	1749		-13.702	-1.194	1.00 38.60
ATOM	2594	С	GLN	1749		-14.266	3.212	1.00 23.44
MOTA	2595	0	GLN	1749		-15.260	3.826	1.00 23.52
MOTA	2596	N	LEU	1750		-13.035	3.703	1.00 21.73
MOTA	2598	CA	LEU	1750		-12.796	5.054	1.00 20.90
MOTA	2599	CB	LEU	1750	19.752	-11.308	5.359	1.00 18.60
MOTA	2600	CG	LEU	1750	20.654	-10.439	4.485	1.00 16.53



7, 17(-),	4 260				·
AOTA			D1 LI		
AOTA			D2 LE		22.100 -10.612 4.939 1.00 14.74
ATOM				•	18.982 -13.548 6.108 1.00 21.25
ATOM					19.534 -14.056 7.084 1.00 21.26
ATOM				L 1751	17.671 -13.607 5.917 1.00 21.64
ATOM			A VA	L 1751	16.793 -14.289 6.845 1.00 21.21
ATOM	=	_	B VA		15.353 -14.072 6.432 1.00 19.03
ATOM			G1 VA		14.453 -14.970 7.220 1.00 23.34
ATOM			G2 VA	L 1751	14.978 -12.648 6.684 1.00 22.78
ATOM			VA	L 1751	17 107
ATOM		_	VA	L 1751	17 117
ATOM			GL	U 1752	3.5 4.5 25.01
ATOM	2619	5 C2	A GL	U 1752	77 77 77
ATOM			GL	U 1752	17 765 40
ATOM	2617	7 C	GLi	U 1752	16 300 55 50
ATOM	2618	CI	GLI	J 1752	16 304
MOTA	2619	O O	E1 GL	J 1752	15 205 10 10
ATOM	2620	OE	2 GL	J 1752	15 52.52
MOTA	2621		GLt		10 740 57 57
MOTA	2622	0	GL		10 220
MOTA	2623	N	ASI		20 050 17
. ATOM	2625	C'A	ASE		27 411
ATOM	2626	CB	ASI		0.54/ 1.00 35.13
MOTA	2627	CG	ASI		20 100
ATOM	2628	OD	1 ASP		22 222 1
ATOM	2629		2 ASP		22 000 43.01
ATOM	2630	C	ASP		22.250
ATOM.	2631	0	ASP		00 001
ATOM	2632	N	LEU	· -	21.971 -17.773 8.901 1.00 36.22
ATOM	2634	CA	LEU		20.652 -15.978 8.633 1.00 30.73
ATOM	2635	СВ	LEU		20.568 -15.730 10.070 1.00 28.51
ATOM	2636	CG	LEU		19.881 -14.394 10.355 1.00 25.20
ATOM	2637	CD:	L LEU		20.810 -13.225 10.016 1.00 26.72
ATOM	2638	CD		1754	20.045 -11.903 9.905 1.00 24.18
ATOM	2639	С	LEU	1754	21.932 -13.168 11.063 1.00 25.69
ATOM	2640	0	LEU	1754	19.860 -16.870 10.763 1.00 28.74
MOTA	2641	N	ASP	1755	20.270 -17.290 11.832 1.00 29.08
ATOM	2643	CA	ASP	1755	18.834 -17.419 10.130 1.00 29.97
ATOM	2644	СВ	ASP	1755	18.109 -18.519 10.732 1.00 31.58
ATOM	2645	CG		1755	16.944 -18.930 9.843 1.00 36.47
ATOM	2646		ASP	1755	16.100 -20.005 10.467 1.00 39.40
ATOM	2647		ASP	1755	15.731 -19.869 11.651 1.00 45.91
ATOM	2648	C	ASP		15.813 -20.995 9.774 1.00 45.68
ATOM	2649	0	ASP	1755	19.040 -19.703 10.952 1.00 32.29
ATOM	2650	N	ARG	1755	18.978 -20.380 11.979 1.00 31.66
ATOM	2652	CA	ARG	1756	19.926 -19.923 9.989 1.00 32.32
ATOM	2653	CB	ARG	1756	20.884 -21.015 10.059 1.00 32.73
ATOM	2654	CG	ARG	1756	21.598 -21.145 8.704 1.00 34.47
ATOM	2655	CD		1756	22.733 -22.157 8.645 1.00 37.78
ATOM	2656	NE	ARG	1756	23.299 -22.274 7.237 1.00 43.87
ATOM	2658	CZ	ARG	1756	23.791 -20.999 6.702 1.00 48.78
ATOM	2659		ARG ARG	1756	24.890 -20.380 7.122 1.00 52 92
011	2009	MUT	AKG	1756	25.630 -20.914 8.091 1.00 55.88
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ATOM	2662	NH2	ARG	1756	25.237	-19.214	6.593	1.00	52.53
MOTA	2665	С	ARG	1756	21.889	-20.761	11.186	1.00	33.76
MOTA	2666	0	ARG	1756	22.131	-21.619	12.049	1.00	34.53
ATOM	2667	N	ILE	1757	22.432	-19.553	11.204	1.00	33.49
MOTA	2669	CA	ILE	1757	23.405	-19.176	12.205	1.00	32.71
MOTA	2670	CB	ILE	1757	23.980	-17.764	11.919	1.00	31.86
MOTA	2671	CG2	ILE	1757	25.111	-17.454	12.869	1.00	31.71
ATOM	2672	CG1	ILE	1757 .	24.520	-17.704	10.488	1.00	31.41
MOTA	2673	CD1	ILE	1757	25.075	-16.366	10.096	1.00	27.68
MOTA	2674	С	ILE	1757	22.807	-19.236	13.604	1.00	34.20
MOTA	2675	0	ILE	1757	23.399	-19.833	14.495		35.83
MOTA	2676	N	VAL	1758	21.620	-18.667	13.792	1.00	35.40
MOTA	2678	C.A.	VAL	1758	20.981	-18.653	15.108	1.00	37.49
MOTA	2679	CB	VAL	1758	19.501	-18.160	15.061	1.00	34.42
MOTA	2680	CG1	VAL	1758	18.899	-18.199	16.456	1.00	37.37
ATOM	2681	CG2	VAL	1758	19.403	-16.742	14.519	1.00	30.02
MOTA	2682	С	VAL	1758	21.010	-20.050	15.715	1.00	41.64
ATOM	2683	0	VAL	1758	21.533	-20.246	16.817	1.00	43.69
MOTA	2684	N	ALA	1759	20.492	-21.01.5	14.961	1.00	44.52
MOTA	2686	CA	ALA	1759	20.434	-22.415	15.387	1.00	45.20
ATOM	2687	CB	ALA	1759	19.833	-23.268	14.277	1.00	43.44
MOTA	2688	C	ALA	1759	21.791	-22.968	15.795	1.00	45.91
MOTA	2689	0	ALA	1759	21.890	-23.780	16.710	1.00	47.41
ATOM	2690	N	LEU	1760	22.833	-22.511	15.120	1.00	47.70
ATOM	2692	CA	LEU	1760	24.190	-22.960	15.399	1.00	50.91
ATOM	2693	CB	LEU	1760 -	25.015	-22.912	14.109	1.00	52.93
ATOM	2694	CG	LEU	1760	24.448	-23.723	12.947	1.00	57.55
MO'LA	2695	CD1	LEU	1760 .	25.189	-23.390	11.660	1.00	60.76
MOTA	2696	CD2	LEU	1760	24.539	-25.208	13.273	1.00	58.66
MOTA	2697	С	LEU	1760	24.882	-22.111	16.472	1.00	52.07
ATOM	2698	O	LEU	1760	25.967	-22.459	16.953	1.00	51.95
ATOM	2699	N	THR	1761	24.267	-21.000	16.850	1.00	52.05
MOTA	2701	CA	THR	1761	24.868	-20.131	17.836	1.00	53.28
MOTA	2702	CB	THR	1761	24.362	-18.693	17.673	1.00	54.58
MOTA	2703	OG1	THR	1761	24.633	-18.259	16.339	1.00	53.68
MOTA	2705	CG2	THR	1761	25.090	-17.762	18.621	1.00	55.45
MOTA	2706	С	THR	1761	24.715	-20.619	19.272	1.00	53.31
ATOM	2707	0	THR	1761	23.629	-20.986	19.713	1.00	53.89
MOTA	2708	N	SER	1762	25.832	-20.617	19.993	1.00	53.51
ATOM	2710	CA	SER	1762	25.876	-21.045	21.383	1.00	53.15
MOTA	2711	CB	SER	1762	27.340	-21.131 c	21.830	1.00	57.27
ATOM	2712	OG	SER	1762	27.492	-21.872	23.028	1.00	61.22
MOTA	2714	C	SER	1762	25.110	-20.048	22.257	1.00	49.15
ATOM	2715	0	SER	1762	25.229	-18.831	22.071	1.00	46.61
MOTA	3466	N	ALA	461	79.636	26.047	14.493	1.00	61.05
ATOM	3468	CA	ALA	461	79.609	24.852	13.654	1.00	58.10
ATOM	3469	CB	ALA	461	78.335	24.024	13.935	1.00	60.39
MOTA	3470	C	ALA	461	79.694	25.239	12.179	1.00	54.65
MOTA	3471	0	ALA	461	79.653	24.382	11.297	1.00	54.05
ATOM	3472	N	ALA	462	79.867	26.537	11.935	1.00	51.68
MOTA	3474	CA	ALA	462	79.972	27.085	10.584	1.00	48.47
ATOM	3475	CB	ALA	462	80.099	28.619	10.633	1.00	46.99

ATO	N 2	476	_					
ATO		476		LA 462	81.123	26.489	9.766	7 00 44 05
ATO	_	477		LA 462	80.918			00 44.00
		178		YR 463	82.329			
ATC		180		YR 463	83.493		_	
ATO		81		YR 463	84.642			55.04
ATO		82		YR 463	84.354			1.00 39.01
ATO			CD1 Ty	(R 463	84.073			1.00 41.95
ATO		84	CE1 TY	TR 463	83.754			1.00 42.40
ATO	M 34	85	CD2 TY	TR 463	84.311			1.00 42.02
ATO	M 34	86	CE2 TY		83.992	28.009	7.345	1.00 40.70
ATO	M 34	87	CZ TY		83.716	29.099		1.00 37.09
ATO	M 34	88	ОН ТУ		83.401	30.320	7.134	1.00 39.19
ATO	4 34	90	C TY			31.406	6.360	1.00 40.66
ATON	1 34:	91 (Э ТҮ		84.011	24.554	10.050	1.00 37.78
ATOM	1 349	92 1	4 GL		84.627	23.863	9.237	1.00 38.35
ATOM	1 349	94 (CA GL		83.746	24.143	11.285	1.00 37.67
ATOM	349		B GL		84.212	22.841	11.747	1.00 38.57
ATOM			G GL		85.707	22.890	12.024	1.00 41.44
ATOM			D GL		86.093	23.870	13.108	1.00 47.87
ATOM		-	E1 GLU	-	87.583	24.135	13.169	1.00 53.44
ATOM			E2 GLU		87.998	24.983	13.990	1.00 56.72
ATOM					88.344	23.513	12.397	1.00 54.85
ATOM		-		· -	83.504	22.393	13.001	1.00 38.15
ATOM	350				83.291	23.187	13.905	1.00 39.59
ATOM	350				83.121	21.124	13.051	1.00 37.13
ATOM	350				82.457	20.608	14.236	1.00 37.13
ATOM	350	_			81.502	19.456		1.00 37.93
ATOM					80.455	19.609		1.00 33.43
ATOM	350		O1 LEU		79.415	18.500		
ATOM	3508		2 LEU		79.797	20.980		1.00 24.85
ATOM	3509	_	LEU	465	83.540			1.00 29.05
ATOM	3510		LEU	465	84.703			1.00 41.02
ATOM	3511		PRO	466				1.00 40.24
ATOM	3512			466				1.00 43.58
ATOM	3513			466	_			1.00 45.33
	3514			466				1.00 44.72
ATOM	3515		PRO	466				.00 46.18
ATOM	3516	C	PRO	466				.00 48.84
ATOM	3517	0	PRO	466				.00 44.52
ATOM	3518	N	GLU	467	_			.00 43.38
ATOM	3520	CA	GLU	467	a =		17.492 1	.00 47.75
ATOM	3521	CB	GLU	467			17.218 1	.00 51.03
ATOM	3522	CG	GLU	467			6.659 1	.00 56.11
ATOM	3523	CD	GLU	467				.00 62.27
ATOM	3524	OE1	GLU	467				.00 66.39
ATOM	3525		GLU	467				.00 69.85
ATOM	3526	C	GLU	467	A = -:			.00 66.09
ATOM	3527	Ò	GLU	467	A =		8.435 1	.00 49.62
ATOM	3528	N	ASP	468			9.578 1.	00 49.62
ATOM	3530	CA	ASP	468			8.166 1.	00 48.07
ATOM	3531	CB	ASP	468		_	9.198 1.	00 46.32
ATOM	3532	CG	ASP	468			9.587 1.	00 45.15
ATOM	3533		ASP			1.740 20		00 44.19
			TOF	468	82.544 1			00 42.04

ATOM	3534	OD2	ASP	468	84.629	11.033	21.188	1.00	38.14
MOTA	3535	С	ASP	468	85.877	11.556	18.580	1.00	45.54
ATOM	3536	0	ASP	468	85.141	10.815	17.928	1.00	45.94
ATOM	3537	N	PRO	469	87.181	11.308	18.732	1.00	45.89
MOTA	3538	CD	PRO	469	88.111	12.189	19.464	1.00	45.11
MOTA	3539	CA	PRO	469	87.885	10.130	18.215	1.00	45.91
MOTA	3540	CB	PRO	469	89.208	10.187	18.968	1.00	45.90
MOTA	3541	CG	PRO	469	89.456	11.662	19.042	1.00	45.73
ATOM	3542	C	PRO	469	87.170	8.806	18.473	1.00	45.48
MOTA	3543	0	PRO	469	87.188	7.905	17.629	1.00	46.83
MOTA	3544	N	ARG	470	86.495	8.717	19.613	1.00	42.12
MOTA	3546	CA	ARG	470	85.786	7.506	19.999	1.00	41.21
MOTA	3547	CB	ARG	470	85.083	7.704	21.331	1.00	43.14
MOTA	3548	CG	ARG	470	85.885	8.424	22.375	1.00	45.68
MOTA	3549	CD	ARG	470	85.014	8.705	23.564	1.00	45.98
MOTA	3550	NE	ARG	470	83.802	9.417	23.184	1.00	47.28
MOTA	3552	CZ	ARG	470	82.921	9.877	24.057	1.00	50.54
MOTA	3553	NH1	ARG	470	83.127	9.687	25.354	1.00	47.56
MOTA	3556	NH2	ARG	470	81.843	10.527	23 637	1.00	54.59
MOTA	3559	C	ARG	470	84.736	7.058	19.004	1.00	40.57
MOTA	3560	0	ARG	470	84.411	5.877	18.941	1.00	43.13
MOTA	3561	N	TRP	471	84.182	8.01.4	18.268	1.00	38.07
ATOM	3563	CA	TRP	471	83.124	7.736	17.314	1.00	35.09
ATOM	3564	CB	TRP	471	81.890	8.515	17.739	1.00	33.42
ATOM	3565	CG	TRP	471	81.259	7.958	18.952	1.00	31.71
MOTA	3566	CD2	TRP	471	80.512	6.740	19.026	1.00	34.81
MOTA	3567	CE2	TRP	471	80.061	6.610	20.355	1.00	33.17
ATOM	3568	CE3	TRP	471	80.174	5.744	18.092	1.00	37.60
ATOM	3569	CD1	TRP	471	81.246	8.503	20.199	1.00	25.70
ATOM	3570	NE1	TRP	471	80.525	7.697	21.051	1.00	28.79
ATOM	3572	CZ2	TRP	471	79.289	5.522	20.776	1.00	35.80
MOTA	3573	CZ3	TRP	471	79.409	4.660	18.509	1.00	35.52
MOTA	3574	CH2	TRP	471	78.973	4.560	19.839	1.00	34.51
MOTA	3575	C	TRP	471	83.432	8.065	15.872	1.00	35.77
MOTA	3576	0	TRP	471	82.690	7.670	14.968	1.00	37.45
ATOM	3577	N	GLU	472	84.533	8.770	15.651	1.00	34.76
MOTA	3579	CA	GLU	472	84.895	9.184	14.308	1.00	34.51
MOTA	3580	CB	GLU	472	86.065	10.174	14.365	1.00	32.30
MOTA	3581	CG	GLU	472	86.221	11.038	13.103	1.00	36.57
MOTA	3582	CD	GLU	472	85.082	12.035	12.872	1.00	36.34
ATOM	3583	OE1	GLU	472	84.515	12.558	13.857	1.00	36.01
MOTA	3584	OE2	GLU	472	84.777	12.318	11.694	1.00	31.95
ATOM	3585	C	GLU	472	85.219	8.034	13.364	1.00	33.90
MOTA	3586	0	GLU	472	85.896	7.082	13.745	1.00	33.77
MOTA	3587	N	LEU	473	84.667	8.094	12.158	1.00	33.58
MOTA	3589	CA	LEU	473	84.944	7.095	11.146	1.00	34.82
ATOM	3590	CB	LEU	473	83.714	6.234	10.847	1.00	32.59
ATOM	3591	CG	LEU	473	84.020	5.091	9.867		33.78
ATOM	3592	CD1	LEU	473	84.786	4.000	10.578		32.94
ATOM	3593	CD2	LEU	473	82.759	4.518	9.273		35.34
MOTA	3594	С	LEU	473	85.380	7.828	9.883		37.95
ATOM	3595	0	LEU	473	84.720	8.781	9.457		39.55

ATOM	ī 3596	N	PRO	474	. 86.522	7 40		
ATOM	3597	CD			87.455			00 30.33
ATOM	3598	CA		- · -	87.094			
ATOM	3599	CB	PRO	474	88.382			= ,
ATOM	3600	CG	PRO	474	88.767			10.10
ATOM	3601	C	PRO	474	86.165			
ATOM	3602	0	PRO	474				
ATOM	3603	N	ARG	475	85.865	6.653		
ATOM	3605	CA	ARG	475	85.762	8.886		1.00 40.66
ATOM	3606	CB	ARG	475	84.850	8.840		1.00 40.66
ATOM	3607	CG	ARG	475	84.776	10.216		1.00 37.94
ATOM	3608	CD	ARG	475	84.354	11.300		1.00 36.12
ATOM	3609	NE	ARG	475	84.340	12.697		1.00 35.92
ATOM	3611	CZ	ARG	475	83.932	13.677	5.801	1.00 30.14
ATOM	3612		ARG		82.671	13.878	6.170	1.00 28.45
ATOM	3615	NH2		475 475	81.688	13.197	5.599	1.00 28.41
ATOM	3618	C	ARG		82.410	14.666	7.197	1.00 27.85
ATOM	3619	0	ARG	475	85.141	7.766	4.046	1.00 41.44
ATOM	3620	N	ASP	475 .	84.223	7.189	3.470	1.00 41.40
ATOM	3622	CA	ASP	476	86.419	7.475	3.830	1.00 44.99
ATOM	3623	CB	ASP	476	86.836	6.477	2.849	1.00 50.62
ATOM	3624	CG		476	88.344	6.540	2.644	1.00 54.47
ATOM	3625		ASP ·	476	89.105	5.969	3.819	1.00 60.03
ATOM	3626		ASP	476	89.569	4.810	3.722	1.00 65.09
ATOM	3627	C C		476	89.216	6.669	4.846	1.00 62.62
ATOM	3628	0	ASP	476	86.436	5.054	3.263	1.00 51.16
ATOM	3629	Ŋ	ASP	476	86.678	4.091	2.530	1.00 53.06
ATOM	3631	CA	ARG	477	85.900	4.916	4.471	1.00 49.58
ATOM	3632	CB	ARG	477	85.443	3.623	4.968	1.00 47.34
ATOM	3633		ARG	477 .	86.040	3.359	6.341	1.00 48.85
ATOM	3634		ARG	477	87.481	2.924	6.265	1.00 52.11
ATOM	3635		ARG	477	88.169	3.079	7.591	1.00 53.63
ATOM	3635		ARG	477	87.515	2.345	8.665	1.00 54.86
ATOM			ARG	477	87.932	2.363	9.927	1.00 57.15
ATOM		NH1		477	89.000	3.076	10.264	1.00 55.98
ATOM		NH2		477	87.269	1.691	10.855	1.00 58.31
ATOM			ARG	477	83.915	3.563	5.020	1.00 44.70
ATOM			ARG	477	83.339	2.780	5.770	1.00 44.63
ATOM			LEU	478	83.274	4.366		1.00 41.95
ATOM			LEU	478	81.832	4.440		1.00 38.58
ATOM			LEU	478	81.374	5.609		1.00 33.17
			LEU	478	79.872	5.731		1.00 29.07
ATOM		CD1 I		478	79.393	4.592		1.00 28.25
ATOM		CD2 I		478	79.590	7.059		1.00 30.79
ATOM			-EU	478	81.432	4.710		1.00 38.93
ATOM			ĿΕU	478	81.938	5.647		1.00 41.75
MOTA			'AL	479	80.562	3.880		1.00 37.96
MOTA			AL	479	80.113	4.086		1.00 37.96
ATOM ATOM	3658	CB V	AL	479	80.468	_		L.00 36.47

3.145

4.299

3.366

80.001

81.972

78.609

77.846

2.882 -0.192 1.00 36.47

2.651 -0.187 1.00 34.33

-1.612 1.00 34.43

0.775 1.00 38.10

1.019 1.00 40.13

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3659 CG1 VAL

3660 CG2 VAL

VAL

VAL

3661 C

3662 0

ATOM

MOTA

MOTA

MOTA

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LEU MOTA 3663 N 480 78.184 5.537 0.552 1.00 38.05 LEU 480 76.766 0.606 MOTA 3665 CA 5.879 1.00 35.90 3666 LEU 480 76.568 0.475 MOTA CB 7.393 1.00 33.98 LEU 480 ATOM 3667 CG 77.276 8.257 1.536 1.00 32.84 ATOM 3668 CD1 LEU 480 77.003 9.749 1.273 1.00 29.68 MOTA 3669 CD2 LEU 480 76.828 7.861 2.943 1.00 26.03 MOTA 3670 C LEU 480 76.015 5.146 -0.476 1.00 34.99 LEU 480 MOTA 3671 0 76.573 4.864 -1.526 1.00 36.12 3672 N GLY 481 -0.223 MOTA 74.753 4.836 1.00 35.21 3674 CA. GLY 481 MOTA 73.965 4.120 -1.204 1.00 34.79 MOTA 3675 C GLY 481 72.544 4.608 -1.332 1.00 36.31 MOTA 3676 0 GLY 481 72.237 5.775 -1.046 1.00 38.30 ATOM 3677 N LYS 482 71.665 3.705 -1.761 1.00 35.59 LYS MOTA 3679 CA 482 70.257 4.007 -1.959 1.00 35.24 -2.207 MOTA 3680 CB LYS 482 69.488 2.698 1.00 35.69 69.585 -0.823 MOTA 3681 С LYS 482 4.763 1.00 36.31 MOTA 3682 0 LYS 482 69.752 0.352 4.421 1.00 34.90 ATOM. PRO 483 3683 N 68.787. 5.786 -1.157 1.00 38.08 MOTA 3684 CD PRO 483 -2.483 68.432 6.320 1.00 39.57 MOTA 3685 CA PRO 483 -0.135 68.097 6.566 1.00 41.08 PRO MOTA 3686 CB 483 67.300 7.560 -0.987 1.00 39.80 -2.157 MOTA 3687 CGPRO 483 68.268 7.819 1.00 37.87 PRO MOTA 3688 C 483 67.130 5.652 0.606 1.00 42.11 PRO MOTA 3689 0 483 66.306 4.994 -0.025 1.00 43 01 LEU 484 A.TOM 3690 N 67.199 5.624 1.937 1.00 41.06 3692 CA LEU 484 2.751 MOTA 66.293 4.823 1.00 38.47 ATOM 3693 CB LEU 484 3.990 67.040 4.307 1.00 32.45 CG LEU ATOM 3694 484 67.968 3.098 3.809 1.00 27.68 ATOM CD1 LEU 1.00 20.29 3695 484 68.569 2.710 5.147 MOTA 3696 CD2 LEU 484 67.181 1.964 3.225 1.00 23.20 ATOM 3697 C LEU 484 65.084 5.637 3.180 1.00 42.18 MOTA 3698 О LEU 484 6.699 3.814 65.227 1.00 44.50 MOTA 3699 N GLY 485 63.893 5.170 2.817 1.00 45.68 MOTA 3701 CA GLY 485 62.692 5.863 3.220 1.00 49.88 MOTA 3702 С GLY 485 1.00 53.01 62.216 7.008 2.337 GLY MOTA 3703 0 485 62.438 7.005 1.117 1.00 50.26 3704 N GLU 486 MOTA. 61.592 8.020 2.949 1.00 56.24 CA GLU 486 MOTA 3706 61.064 9.183 2.257 1.00 58.07 3707 CB GLU 486 1.682 MOTA 59.666 8.845 1.00 55.60 3708 C GLU 486 3.088 1.00 59.35 MOTA 60.995 10.477 3709 0 GLU 486 3.000 MOTA 60.019 11.226 1.00 61.44 MOTA 3710 N GLY 487 62.027 10.747 3.879 - 1.00 59.60 MOTA 3712 CA GLY487 62.066 11.964 4.652 1.00 59.75 MOTA 3713 C GLY 487 61.337 11.959 5.974 1.00 61.44 MOTA 3714 0 GLY 487 61.231 12.979 6.627 1.00 61.96 MOTA 3715 N ALA 488 60.820 10.800 6.377 1.00 59.69 MOTA 3717 CA ALA 488 60.134 10.709 7.657 1.00 57.27 CB ALA 488 7.825 MOTA 3718 59.489 9.337 1.00 58.05 3719 С ALA 488 MOTA 61.137 10.970 8.754 1.00 56.28 0 ALA 488 MOTA 3720 60.810 11.446 9.834 1.00 57.31 PHE 489 8.480 MOTA 3721 N 62.389 10.630 1.00 54.40 PHE 489 63.462 10.830 9.466 1.00 54.56 MOTA 3723 CA



7,000			_						
ATO			CB PH		64.16	51	9.500	9.7	70 1.00 49.88
ATO			CG PH		63.22		8.454	10.35	- 00 15.00
ATO			CD1 PH		62.50		7.585	9.51	10.11
ATO			CD2 PH		63.01		8.344	11.73	23.10
ATO			CE1 PHI		61.62		6.653	10.03	
ATO	_		CE2 PHI	E 489	62.13		7.411	12.25	00 30.05
ATON			ZZ PHI	E 489	61.43		5.558	11.40	
ATON			PHE	489	64.45		1.896	8.97	
ATON			PHE	489	65.37		2.276	9.69	
ATOM	_	33 V	GLY	490	64.28		2.375	7.73	
ATOM		35 C	A GLY	4.90	65.14		3.400	7.14	
ATOM			GLY	490	65.89		2.778	5.99	
ATOM			GLY	490	65.35		.854		
ATOM		8 N	GLN	491	67.07		.304	5.36	
ATOM	_	0 C	A GLN	491	67.829		.658	5.63	
ATOM		1 C	B GLN	491	68.760		.580	4.562	52.00
ATOM			G GLN	491	69.422		.818	3.77	
MOTA	374	3 C	D GLN	491	70.046		.696	2.629	
ATOM	374	4 O	E1 GLN	491	70.113		.893	1.548	02.00
ATOM	374	5 N	E2 GLN	491	70.453		.082	1.701	
MOTA	374	8 C	GLN	491	68.632		.518	0.441	
ATOM	374		GLN	491	69.669		.704	5.165	
ATOM	3750	N C	VAL	492	68.103		.318	5.805	1.5
. ATOM	3752	2 .ZA	VAL	492	68.705			4.984	/.55
MOTA	3753	GE CE	VAL	492	67.760		.093 .320	5.456	
MOTA	3754	1 CG	1 VAL	492	68.412		045	6.412	
ATOM	3755		2 VAL	492	67.361			6.932	
ATOM	3756		VAL	492	69.004		211	7.606	
MOTA	3757	7 O	VAL	492	68.181		200	4.253	1.00 45.23
MOTA	3758	N	VAL	493	70.210		044	3.349	1.00 45.17
ATOM	3760	CA	VAL	493	70.599		654	4.208	1.00 43.75
ATOM	3761	CB	VAL	493	71.608		780	3.109	1.00 44.71
ATOM	3762	CG	1 VAL	493	71.159		471	2.148	1.00 46.20
ATOM	3763			493	73.045		902	1.838	1.00 46.16
ATOM	3764	C	VAL	493	71.205		428	2.706	1.00 42.06
ATOM	3765	O	VAL	493	71.701		482	3.624	1.00 44.09
ATOM	3766	N	LEU	494	71.102		402	4.745	1.00 43.73
ATOM	3768	CA	LEU	494	71.682		448	2.809	1.00 43.38
ATOM	3769	CB	LEU	494	70.988		158	3.142	1.00 43.29
ATOM	3770	CG	LEU	494	71.563		030	2.366	1.00 43.38
ATOM	3771	CD1	LEU	494	71.809	0.6		2.431	1.00 39.77
ATOM	3772		LEU	494	70.600	0.2		3.850	1.00 36.38
ATOM	3773	С	LEU	494	73.139	-0.3		1.760	1.00 42.50
ATOM	3774	0	LEU	494	73.435	3.2		2.725	1.00 42.72
ATOM	3775	N	ALA	495	74.044	3.9	_	1.720	1.00 43.83
MOTA	3777	CA	ALA	495		2.6		3.499	1.00 40.80
ATOM	3778	CB	ALA	495	75.456	2.7	_	3.183	1.00 43.80
ATOM	3779	C	ALA	495	76.059	4.0		3.821	1.00 43.76
ATOM	3780	Ō	ALA	495	76.171	1.5		3.682	1.00 46.68
ATOM	3781	N	GLU	496	75.668	0.8		4.551	1.00 48.52
ATOM	3783	CA	GLU	496	77.330	1.2	_	3.104	1.00 49.13
ATOM	3784	СВ	GLU	496	78.112	0.1		3.519	1.00 49.79
			- -		78.524	-0.7	32 2	2.318	1.00 53.83

ATOM	3785	CG	GLU	496	77.350	-1.224	1.496	1.00 61.33
ATOM	3786	CD	GLU	496	77.623	-2.561	0.862	1.00 64.74
MOTA	3787	OE1	GLU	496	76.704	-3.411	0.883	1.00 70.08
MOTA	3788	OE2	GLU	496	78.751	-2.760	0.356	1.00 64.12
ATOM	3789	С	GLU	496	79.333	0.601	4.230	1.00 48.46
ATOM	3790	0	GLU	496	80.192	1.236	3.631	1.00 48.79
MOTA	3791	N	ALA	497	79.373	0.375	5.530	1.00 49.25
ATOM	3793	CA	ALA	497	80.503	0.810	6.334	1.00 49.99
MOTA	3794	CB	ALA	497	80.048	1.156	7.732	1.00 48.16
ATOM	3795	C	ALA	497	81.544	-0.301	6.373	1.00 51.53
ATOM	3796	0	ALA	497	81.191	-1.473	6.409	1.00 52.41
ATOM	3797	N	ILE	498	82.821	0.061	6.335	1.00 52.35
ATOM	3799	CA	ILE	498	83.892	-0.928	6.369	1.00 52.03
ATOM	3800	CB	ILE	498	84.843	-0.797	5.145	1.00 52.83
ATOM	3801	CG2	ILE	498	85.990	-1.795	5.253	1.00 51.43
ATOM	3802	CG1	ILE	498	84.077	-1.006	3.830	1.00 53.85
ATOM	3803	CD1	ILE	498	83.411	0.254	3.271	1.00 55.62
ATOM	3804	C	ILE	498	84.702	-0.802	7.654	1.00 52.74
ATOM	3805	0	ILE	498	85.133	0.293	8.026	1.00 52.14
ATOM	3806	N	GLY	499	84.835	-1.926	8.354	1.00 52.58
MOTA	3808	CA	GLY	499	85.600	-1.974	9.592	1.00 53.03
ATOM	3809	C	GLY	499	85.165	-1.113	10.771	1.00 53.67
MOTA	3810	0	GLY	499	86.012	-0.544	11.463	1.00 53.99
MOTA	3811	N	LEU	500	83.862	-1.045	11.034	1.00 53.60
ATOM	3813	CA	LEU	500	83.337	-0.245	12.141	1.00 51.00
ATOM	3814	CB	LEU	500 .	81.841	-0.499	12.317	1.00 49.38
ATOM	3815	CG	LEU	500	80.901	-0.024	11.212	1.00 47.62
MOTA	3816	CD1	LEU	500	79.483	-0.454	11.543	1.00 47.25
ATOM	3817	CD2	LEU	500	80.992	1.486	11.081	1.00 47.38
ATOM	3818	C	LEU	500	84.060	-0.573	13.433	1.00 51.09
MOTA	3819	0	LEU	500	84.396	-1.734	13.670	1.00 53.76
MOTA	3820	N	PRO	505	87.588	-5.968	10.545	1.00 81.81
ATOM	3821	CD	PRO	505	88.588	-6.677	11.357	1.00.81.96
ATOM	3822	CA	PRO	505	88.105	-4.664	10.109	1.00 80.56
ATOM	3823	CB	PRO	505	89.501	-4.622	10.735	1.00 80.75
ATOM	3824	CG	PRO	505	89.868	-6.070	10.860	1.00 82.32
MOTA	3825	C	PRO	505	88.139	-4.477	8.588	1.00 78.53
ATOM	3826	0	PRO	505	88.462	-3.400	8.085	1.00 77.85
MOTA	3827	N	ASN	506	87.792	-5.532	7.865	1.00 77.09
ATOM	3829	CA	ASN	506	87.747	-5.484	6.411	1.00 75.57
MOTA	3830	CB	ASN	506	88.799	-6.415	5.806	1.00 75.80
MOTA	3831	C	ASN	506	86.347	-5.929	6.008	1.00 74.33
MOTA	3832	0	ASN	506	86.044	-6.117	4.826	1.00 73.76
MOTA	3833	N	ARG	507	85.496	-6.092	7.018	1.00 71.72
ATOM	3835	CA	ARG	507	84.120	-6.509	6.820	1.00 69.28
MOTA	3836	CB	ARG	507	83.619	-7.257	8.054	1.00 70.64
MOTA	3837	C	ARG	507	83.258	-5.284	6.605	1.00 65.87
ATOM	3838	0	ARG	507	83.445	-4.262	7.274	1.00 65.40
ATOM	3839	N	VAL	508	82.363	-5.358	5.628	1.00 62.01
MOTA	3841	CA	VAL	508	81.464	-4.248	5.381	1.00 58.41
MOTA	3842	CB	VAL	508	81.043	-4.136	3.915	1.00 57.18
MOTA	3843	CG1	VAL	508	82.251	-3.893	3.046	1.00 61.04

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2								
ATO			CG2 VA	L 508	80.3	10 -5.38	3 3.46	E 1 00 50
ATO			C VA	L 508	80.2			
ATO			AV C	L 508	79.9			· ·
ATO		47 I	HT V	R 509	79.5			
ATO		49 (CA TH	R 509	78.39			
ATO		50 C	CB TH	R 509	78.70			10 10 20
ATO		51 C	G1 TH	R 509	79.93			
OTA	M 385	33 C	G2 THE		77.60			
ATON		54 C	THE	₹ 509	77.38			,
ATON	1 385	55 0	THE		77.67			
ATOM	1 385	6 N			76.23			
ATOM	1 385	8 C	A LYS		75.20			
ATOM	1 385	9 C	B LYS		74.06			
ATOM	386	0 C						
ATOM	386	1 C			73.22			
ATOM	386	2 C:		•	73.82			
ATOM	386	3 N:			73.11			
ATOM	386	7 C	LYS		73.31			1.00 56.09
ATOM	386		LYS		74.73			1.00 40.83
ATOM			VAL		74.480		8.162	1.00 38.59
ATOM	387	L CZ		511	74.679	_	6.891	1.00 36.28
ATOM	3872			511	74.269		7.957	1.00 31.41
ATOM	3873		1 VAL	511	75.480		8.690	1.00 32.80
ATOM	3874		2 VAL	511	76.315		9.420	1.00 29.97
ATOM	3875		VAL	511	76.353		7.706	1.00 30.20
ATOM	3876	_	VAL	511	73.408		7.360	1.00 28.40
ATOM	3877	_	ALA	512	73.305		6.147	1.00 27 45
ATOM	3879				72.756		8.207	1.00 27.30
ATOM	3880			512 512	71.953		7.715	1.00 26.66
ATOM	3881		ALA		70.557		8.278	1.00 24.24
ATOM	3882		ALA	512	72.670	_	8.173	1.00 28.52
ATOM	3883	N	VAL	512	73.140		9.319	1.00 26.66
ATOM	3885	CA	VAL	513	72.768		7.275	1.00 29.18
ATOM	3886	CB	VAL	513 513	73.442	7.217	7.569	1.00 29.65
ATOM	3887		l VAL	513	74.631	7.482	6.601	1.00 28.93
ATOM	3888	CG2		513	75.384	8.722	7.015	1.00 25.51
ATOM	3889	C	VAL	513	75.570	6.292	6.550	1.00 29.45
ATOM	3890	0	VAL	513	72.509	8.407	7.476	1.00 30.45
ATOM	3891	N	LYS	513	71.900	8.646	6.431	1.00 30.15
ATOM	3893	CA	LYS	514	72.402	9.143	8.578	1.00 33.29
ATOM	3894	CB		514	71.575	10.357	8.654	1.00 33.28
ATOM	3895	CG	LYS	514	71.017	10.537	10.068	1.00 38.67
ATOM	3896	CD	LYS	514	70.074	9.456	10.531	1.00 45.73
ATOM	3897		LYS	514	69.462	9.860		1.00 53.93
ATOM	3898	CE NZ	LYS	514	68.450	8.840		1.00 63.59
ATOM	3902		LYS	514	67.206	8.823		1.00 71.90
ATOM	3902	C C	LYS	514	72.451	11.568		1.00 29.45
ATOM	3903	O N	LYS	514	73.584	11.673		1.00 25.64
MOTA		N	MET	515	71.918	12.495		1.00 29.42
ATOM	3906	CA	MET	515	72.668	13.690		1.00 30.46
ATOM	3907	CB	MET	515	73.464	13.391		1.00 29.63
ATOM	3908	CG	MET	515	72.557	13.070		1.00 32.48
ALOM	3909	SD	MET	515	73.391	12.475		1.00 33.06

MOTA	3910	CE	MET	515	73.734	10.809	3.715	1.00	30.26
MOTA	3911	С	MET	515	71.700	14.839	6.848	1.00	30.75
MOTA	3912	0	MET	515	70.478	14.654	6.867	1.00	33.07
ATOM	3913	N	LEU	516	72.238	16.027	6.608	1.00	30.32
MOTA	3915	CA	LEU	516	71.414	17.194	6.304	1.00	30.21
MOTA	3916	CB	LEU	516	72.112	18.487	6.748	1.00	26.54
MOTA	3917	CG	LEU	516	72.452	18.668	8.227	1.00	23.97
ATOM	3918	CD1	LEU	516	73.345	19.858	8.412	1.00	24.27
ATOM	3919	CD2	LEU	516	71.198	18.850	9.023	1.00	21.46
ATOM	3920	С	LEU	516	71.197	17.265	4.800	1.00	33.44
MOTA	3921	0	LEU	516	72.016	16.784	4.015	1.00	34.50
MOTA	3922	N	LYS	517	70.082	17.863	4.400	1.00	36.36
ATOM	3924	CA	LYS	517	69.783	18.048	2.993	1.00	34.58
ATOM	3925	CB	LYS	517	68.281	18.255	2.784	1.00	38.96
ATOM	3926	CG	LYS	517	67.409	17.155	3.380	1.00	44.34
ATOM	3927	CD	LYS	517	66.128	16.920	2.572	1.00	52.11
MOTA	3928	CE ·	LYS	517 .	65.138	18.083	2.637	1.00	58.29
ATOM	3929	NZ	LYS	517	63.915	17.833	1.786	1.00	60.90
MOTA	3933	C	LYS	517	70.567	19.304	2.597	1.00	33.51
ATOM	3934	0	LYS	517	71.024	20.064	3.460	1.00	30.34
ATOM	.3935	N	SER	518	70.701	19.539	1.296	1.00	34.39
MOTA	3937	CA	SER	518	71.444	20.693	0.788	1.00	35.84
ATOM	3938	CB	SER	518	71.537	20.618	-0.731	1.00	33.66
MOTA	3939	OG	SER	518	70.282	20.258	-1.266	1.00	38.73
ATOM	3941	C	SER	518	70.879	22.045	1.198	1.00	36.91
MOTA	3942	O	SER	518	71.591	23.050	1.205	1.00	37.32
MOTA	3943	N	ASP	519	69.598	22.069	1.538	1.00	37.88
ATOM	3945	CA	ASP	519	68.945	23.313	1.936	1.00	38.63
MOTA	3946	CB	ASP	519	67.517	23.364	1.375	1.00	42.23
ATOM	3947	CG	ASP	519	66.669	22.151	1.775	1.00	48.87
MOTA	3948	OD1		519	67.070	21.380	2.681	1.00	49.21
ATOM	3949	OD2		519	65.582	21.972	1.181	1.00	54.93
MOTA	3950	C	ASP	519	68.916	23.537	3.443	1.00	38.06
MOTA	3951	0	ASP	519	68.246	24.451	3.916	1.00	39.38
MOTA	3952	N	ALA	520	69.622	22.692	4.191	1.00	36.24
MOTA	3954	CA	ALA	520	69.631	22.795	5.648	1.00	34.69
MOTA	3955	CB	ALA	520	70.359	21.613	6.259	1.00	35.68
ATOM	3956	С	ALA	520	70.213	24.087	6.173		33.54
ATOM.	3957	0	ALA	520	71.039	24.718	5.522		34.83
MOTA	.3958	N	THR	521	69.815	24.452	7.384		34.45
ATOM	3960	CA	THR	521	70.315	25.668	8.001		36.51
ATOM	3961	CB	THR	521	69.148	26.592	8.493	1.00	39.14
MOTA	3962	OG1	THR	521	68.529	26.031	9.659	1.00	41.61
MOTA	3964	CG2	THR	521	68.081	26.750	7.409	1.00	40.14
MOTA	3965	С	THR	521	71.228	25.303	9.170	1.00	36.35
ATOM	3966	0	THR	521	71.376	24.125	9.510	1.00	32.23
MOTA	3967	N	GLU	522	71.868	26.310	9.756		39.33
MOTA	3969	CA	GLU	522	72.747	26.092	10.890	1.00	44.59
MOTA	3970	CB	GLU	522	73.364	27.424	11.335	1.00	51.80
ATOM	3971	CG	GLU	522	74.463	27.311	12.418		64.10
MOTA	3972	CD	GLU	522	75.811	26.815	11.886	1.00	69.12
MOTA	3973	OE1	GLU	522	76.784	27.605	11.869	1.00	69.26

ATO	M 39	74	OP2 at					
ATO			OE2 GL		75.90		29 11.5	02 1.00 73.62
ATO			C GL		71.95	3 25.4		
ATO		_	O GL		72.48	2 24.6		
ATO			7 LYS		70.67	9 25.8		
			CA LYS		69.82			
ATON			CB LYS		68.51			
ATON			G LYS	523	67.58			
ATOM			D LYS	523	66.29			
ATOM			E LYS	523	65.40			- · · • • •
ATOM		34 N	Z LYS	523	64.30			
ATOM	1 398	8 C	LYS		69.56			
ATOM	398	9 0	LYS		69.58	_		
ATOM	399	0 N	ASP		69.33			
ATOM	399	2 C	A ASP		69.122			51.51
ATOM	399	3 C						
ATOM	399	4 C			68.876			
ATOM	399		D1 ASP	524	67.482			
ATOM			D2 ASP	524	66.552			4 1.00 41.59
ATOM	399		ASP		67.307			
MOTA	3998	_	ASP	524	70.383			
ATOM.	3999			524	70.301			9 1.00 37.40
ATOM	400		LEU	525	71.554		9 11.40	4 1.00 32.39
. ATOM	4002			525	72.799	21.186	5 11.729	9 1.00 31.50
ATOM	4002			525	74.018	21.998		
ATOM				525	75.363	21.379		
	4004		1 LEU	525	75.521	19.990		
ATOM	4005			525	76:519	32.283		
ATOM	4006		LEU	525	72.848	20.941		1.00 30.27
ATOM	4007		LEU	525	73.104	19.828		
ATOM	4008		SER	526	72.563	21.982		• • • •
ATOM	4010			526	72.544	21.914		
ATOM	4011		SER	526	72.046	23.251		
ATOM	4012	OG	SER	526	71.923	23.199		
ATOM	4014	C	SER	526	71.640	20.796		
ATOM	4015	0	SER	526	71.924	20.162		· · -
ATOM	4016	N	ASP	527	70.525	20.588	16.998	1.00 27.54
ATOM	4018	CA	ASP	527	69.581	19.556	15.291	1.00 28.97
ATOM	4019	CB	ASP	527	68.289		15.664	1.00 29.28
ATOM	4020	CG	ASP	527	67.497	19.710	14.855	1.00 29.08
ATOM	4021	ODI	ASP	527	67.750	20.977	15.225	1.00 30.05
ATOM	4022		ASP	527	66.591	21.597	16.292	1.00 24.32
ATOM	4023	С	ASP	527		21.335	14.436	1.00 34.69
ATOM	4024	0	ASP	527	70.175	18.164	15.436	1.00 30.65
ATOM	4025	N	LEU	528	70.115	17.297	16.312	1.00 30.12
MOTA	4027	CA	LEU		70.769	17.958	14.265	1.00 30.50
ATOM	4028	CB		528	71.358	16.669	13.946	1.00 29.54
ATOM	4029	CG	LEU	528	71.850	16.647	12.487	1.00 26.03
ATOM	4030		LEU	528	72.409	15.320	11.942	1.00 24.26
ATOM			LEU	528	71.466	14.142	12.259	1.00 21.51
ATOM	4031		LEU	528	72.644	15.437	10.450	1.00 15.05
	4032	C	LEU	528	72.494	16.342	14.933	1.00 30.51
ATOM	4033	0	LEU	528	72.641	15.192	15.354	1.00 30.51
ATOM	4034	N	ILE	529		17.351	15.305	
ATOM	4036	CA	ILE	529		17.138	16.253	1.00 30.86
								1.00 28.41



MOTA	4037	CB	ILE	529	75.266	18.349	16.406	1.00 24.75	
ATOM	4038	CG2	ILE	529	76.355	18.064	17.432	1.00 25.51	
MOTA	4039	CG1	ILE	529	75.901	18.710	15.084	1.00 17.82	
ATOM	4040	CD1	ILE	529	76.912	19.806	15.251	1.00 18.14	
ATOM	4041	C	ILE	529	73.821	16.813	17.641	1.00 30.17	
ATOM	4042	0	ILE	529	74.286	15.873	18.285	1.00 30.11	•
ATOM	4043	N	SER	530	72.836	17.574	18.101	1.00 30.29	
ATOM	4045	CA	SER	530	72.271	17.310	19.418	1.00 33.14	
ATOM	4.046	CB	SER	530	71.158	18.293	19.735	1.00 36.09	
ATOM	4047	OG	SER	530	70.224	18.323	18.670	1.00 49.01	
MOTA	4049	C	SER	530	71.740	15.881	19.479	1.00 33.80	
MOTA	4050	0	SER	530	71.896	15.190	20.492	1.00 37.06	
MOTA	4051	N	GLU	531	71.156	15.413	18.378	1.00 30.13	
MOTA	4053	CA	GLU	531	70.629	14.065	18.351	1.00 29.18	•
ATOM	4054	CB	GLU	531	69.822	13.801	17.087	1.00 32.42	
MOTA	4055	CG	GLU	531	69.253	12.394	17.058	1.00 33.35	
MOTA	4056	CD	GLU .	531	68:354	12.131	15.883	1.00 34.76	
ATOM	4057	OE1	GLU	531	67.481	11.249	16.002	1.00 40.42	
ATOM	4058	OE2	GLU	531	68.516	12:793	14.847	1.00 35.88	
ATOM	4059	C	GLU	531	71.734	13.025	18.488	1.00 28.27	
MOTA	4060	0	GLU	531	71.569	12.032	19.192	1.00 26.75	
ATOM	4061	N	MET	532	72.842	13.235	17.786	1.00 27.80	
ATOM	4063	CA	MET	532	73.976	12.320	17.835	1.00 27.82	
ATOM	4064	CB	MET	532	75.080	12.813	16.890	1.00 29.43	
ATOM	4065	C.G	MET	532 .	76.461	12.225	17.138	1.00 24.34	
ATOM	4066	SD	MET	532	77.641	12.702	15.840	1.00 27.83	
MOTA	4067	CE	MET	532	77.791.	14.462	16.193	1.00 21.90	
ATOM	4068	C	MET	532	74.499	12.272	19.260	1.00 29.53	
ATOM	4069	0	MET	532	74.742	11.197	19.809	1.00 30.14	
ATOM	4070	N	GLU	533	74.610	13.445	19.871	1.00 30.25	
ATOM	4072	CA	GLU	533	75.109	13.570	21.233	1.00 31.95	
ATOM	4073	CB	GLU	533	75.300	15.039	21.594	1.00 32.55	
ATOM	4074	CG	GLU	533	76.391	15.724	20.765	1.00 35.71	
ATOM	4075	CD	GLU	533	77.766	15.087	20.951	1.00 36.71	
ATOM	4076		GLU	533	78.297	15.136	22.084	1.00 40.19	
ATOM	4077	OE2	GLU	533	78.322	14.555	19.969	1.00 33.99	
MOTA	4078	C	GLU	533	74.185	12.886	22.225	1.00 33.06	
ATOM	4079	0	GLU	533	74.642	12.197	23.147	1.00 33.49	
ATOM	4080	N	MET	534	72.883	13.052	22.025	1.00 33.12	
ATOM	4082	CA	MET	534	71.913	12.432	22.900	1.00 32.48	
ATOM	4083	CB	MET	534	70.484	12.859	22.533	1.00 30.60	
ATOM	4084	CG	MET.	534	69.591	12.915		0.50 28.70	PRT1
ATOM	4085	SD	MET	534	67.787	12.849	23.608	0.50 27.55	PRT1
ATOM	4086	CE	MET	534	67.409	14.560	23.291	0.50 26.84	PRT1
ATOM	4087	C	MET	534	72.102	10.908	22.785	1.00 31.10	
ATOM	4088	0	MET	534	72.258	10.224	23.791	1.00 32.80	
ATOM	4089	N	MET	535	72.194	10.394	21.563	1.00 30.50	
ATOM	4091	CA	MET	535	72.399	8.961	21.368	1.00 29.25	
ATOM	4092	CB	MET	535	72.577	8.623	19.884	1.00 28.10	
ATOM	4093	CG	MET	535	71.337	8.876	19.042	1.00 27.48	
MOTA	4094	SD	MET	535	71.377	7.980	17.502	1.00 26.94	
MOTA	4095	CE	MET	535	71.346	9.275	16.310	1.00 33.72	



ATOM	4096	C	MET	535		73.621	8.514	22.155	1.00	29.29
MOTA	4097	0	MET	535		73.640	7.412	22.710	1.00	29.06
ATOM	4098	N	LYS	536		74.644	9.367	22.185	1.00	
MOTA	4100	CA	LYS	536		75.869	9.073	22.930	1.00	33.24
MOTA	4101	CB	LYS	536		76.950	10.108	22.628	1.00	31.29
MOTA	4102	CG	LYS	536		77.602	10.007	21.258	1.00	31.09
ATOM	4103	CD	LYS	536		78.570	11.154	21.103	1.00	28.76
ATOM	4104	CE	LYS	536		79.219	11.220	19.755		26.70
ATOM	4105	NZ	LYS	536		80.059	12.461	19.742	1.00	27.38
ATOM	4109	C	LYS	536		75.630	9.014	24.451		35.30
ATOM	4110	0	LYS	536		76.201	8.172	25.137	1.00	35.61
MOTA	4111	N	MET	537		74.788	9.902	24.972		35.67
MOTA	4113	CA	MET	537	•	74.517	9.908	26.408	1.00	38.27
MOTA	4114	CB	MET	537		73.858	11.221	26.844	1.00	43.86
ATOM	4115	CG	MET	537		74.801	12.420	26.884	1.00	55.46
ATOM	4116	SD	MET	537		76.189	12.272	28.062	1.00	63.44
MOTA	4117	CE	MET	537		75.383	12.822	29.591		62.14
ATOM	4118	C	MET	537		73.657	8.734	26.845	1.00	37.10
MOTA	4119	0	MET	537		73.855	8.188	27.920	1.00	
ATOM	4120	N	ILE	538		72 723	8.320	26.003	1.00	34.96
ATOM	4122	CA	ILE	538		71.819	7.219	26.320	1.00	32.78
MOTA	4123	CB	ILE	538		70.618	7.202	25.342	1.00	32.48
ATOM	4124	CG2	ILE	538		69.782	5.943	25.537	1.00	32.27
ATOM	4125	CG1	ILE	538		69.756	8.449	25.538	1,00	31.77
ATOM	4126	CD1	ILE	538		68.746	8.651	24.409	1.00	34.25
ATOM	4127	C	ILE	538	•	72.456	5.823	26.365	1.00	30.54
ATOM	4128	0	ILE	538		72.146	5039	27.250	1.00	33.37
MOTA	4129	N	GLY	539		73.293	5.481	25.399	1.00	27.09
ATOM	4131	CA	GLY	539		73.892	4.162	25.419	1.00	28.72
MOTA	4132	C	GLY	539		73.173	3.135	24.552	1.00	31.16
MOTA	4133	0	GLY	539		72.069	3.379	24.060	1.00	32.94
ATOM	4134	N	LYS	540		73.808	1.981	24.370	1.00	31.68
ATOM	4136	CA	LYS	540		73.264	0.912	23.537	1.00	34.64
ATOM	4137	CB	LYS	540		74.399	0.032	23.029	1.00	33.47
ATOM	4138	CG	LYS	540		75.331	0.730	22.095	1.00	39.67
ATOM	4139	CD	LYS	540		76.396	-0.209	21.573	1.00	41.48
ATOM	4140	CE	LYS	540		77.228	0.475	20.501	1.00	48.72
ATOM	4141	NZ	LYS	540		76.442	0.800	19.254	1.00	54.86
ATOM	4145	C	LYS	540		72.206	-0.010	24.143		36.68
ATOM	4146	0	LYS	540		72.276	-0.370	25.324		41.03
ATOM	4147	N	HIS	541		71.233	-0.396	23.319		35.61
ATOM	4149	CA	HIS	541		70.190	-1.335	23.711		34.24
ATOM	4150	CB	HIS	541		69.074	-0.702	24.526		33.44
ATOM	4151	CG	HIS	541		68.118	-1.711	25.083		34.60
ATOM	4152	CD2		541		68.059	-2.310	26.292		33.77
ATOM	4153	ND1		541		67.143	-2.316	24.309	1.00	34.19
ATOM	4155	CE1		541		66.539	-3.248	25.020		36.87
ATOM	4156	NE2		541		67.074	-3.272	26.228		34.05
ATOM	4158	C	HIS	541		69.624	-2.023	22.474		36.31
ATOM	4159	0	HIS	541		69.342	-1.378	21.457		38.40
ATOM	4160	N	LYS	542		69.407	-3.331	22.586		36.42
ATOM	4162	CA	LYS	542		68.923	-4.155	21.469	1.00	35.10

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MOTA	4163	CB	LYS	542	68.680	-5.602	21.915	1.00 34.24
MOTA	4164	C	LYS	542	67.674	-3.646	20.802	1.00 32.40
ATOM	4165	0	LYS	542	67.507	-3.822	19.612	1.00 32.37
MOTA	4166	N	ASN	543	66.785	-3.046	21.580	1.00 32.12
MOTA	4168	CA	ASN	543	65.541	-2.561	21.015	1.00 33.01
ATOM	4169	CB	ASN	543	64.361	-3.081	21.842	1.00 34.26
ATOM	4170	CG	ASN	543	64.365	-4.597	21.979	1.00 32.20
ATOM	4171	OD1	ASN	543	64.633	-5.128	23.050	1.00 32.23
MOTA	4172	ND2	ASN	543	64.077	-5.292	20.904	1.00 30.50
ATOM	4175	C.	ASN	543	65.424	-1.050	20.719	1.00 32.21
ATOM	4176	0	ASN	543	64.326	-0.481	20.765	1.00 31.13
ATOM	4177	N	ILE	544	66.556	-0.419	20.397	1.00 30.52
ATOM	4179	C.A	ILE	544	66.611	1.002	20.028	1.00 29.01
ATOM	4180	СВ	ILE	544	67.040	1.962	21.208	1.00 25.83
ATOM	4181	CG2	ILE	544	66.244	1.682	22.467	1.00 24.46
ATOM	4182	CG1	ILE	544	68.532	1.848	21.522	1.00 27.54
ATOM	4183	CD1	ILE	544	69.008	2.839	22.581	1.00 22.70
ATOM	4184	C	ILE	544	67.617	1.118	18.870	1.00 22.70
ATOM	4185	0	ILE	544	68.410	0.194	18.633	1.00 27.26
ATOM	4186	N	ILE	545	67.504	2.184	18.078	1.00 27.28
ATOM	4188	CA	ILE	545	68.453	2.396	16.992	1.00 28.74
ATOM	4189	CB	ILE	545	67.913	3.350	15.921	1.00 27.08
ATOM	4190	CG2	ILE	545 545	69.027	3.727	14.955	
ATOM	4191	CG1	ILE	545				1.00 23.96
		CD1	ILE		66.754	2.692	15.167	1.00 23.13
ATOM	4192	CDI	ILE	545 545	67.152	1.481	14.339	1.00 20.61
ATOM	4193	C C		545	69.720	2.968	17.633	1.00 26.93
ATOM ATOM	4194	N	ILE ASN	545	69.719	4.075	18.160	1.00 28.63
	4195		ASN	546	70.800	2.200	17.560	1.00 28.53
ATOM	4197	CA	ASN	546	72.075	2.567	18.161	1.00 29.39
ATOM	4198	CB CG	ASN	546	72.752	1.308	18.718	1.00 29.14
ATOM	4199		ASN	546	71.908	0.613	19.772	1.00 30.21
ATOM	4200			546	71.804	1.088	20.899	1.00 30.74
ATOM	4201	ND2	ASN	546	71.290	-0.505	19.406	1.00 30.79
ATOM	4204	C	ASN	546	73.034	3.303	17.238	1.00 30.78
ATOM	4205	0	ASN	546	73.011	3.126	16.015	1.00 33.04
ATOM	4206	N	LEU	547	73.866	4.151	17.837	1.00 31.07
ATOM	4208	CA	LEU	547	74.880	4.904	17.101	1.00 31.37
ATOM	4209	CB	LEU	547	75.284	6.165	17.875	1.00 27.32
ATOM	4210	CG	LEU	547	76.413	7.032	17.297	1.00 24.17
ATOM	4211		LEU	547	75.953	7.768	16.069	1.00 18.06
ATOM	4212		LEU	547	76.864	8.014	18.348	1.00 22.50
ATOM	4213	C	LEU	547	76.107	3.999	16.861	1.00 33.38
MOTA	4214	0	LEU	547	76.610	3.343	17.789	1.00 33.58
MOTA	4215	N	LEU	548	76.543	3.919	15.607	1.00 32.72
MOTA	4217	CA	LEU	548	77.694	3.104	15.259	1.00 31.50
MOTA	4218	CB	LEU	548	77.388	2.244	14.029	1.00 26.30
MOTA	4219	CG	LEU	548	76.148	1.341	14.158	1.00 25.93
MOTA	4220	CD1	LEU	548	76.034	0.513	12.906	1.00 28.37
MOTA	4221	CD2	LEU	548	76.196	0.436	15.394	1.00 15.84
MOTA	4222	С	LEU	548	78.941	3.965	15.030	1.00 33.69
MOTA	4223	0	LEU	548	80.063	3.488	15.167	1.00 37.41
MOTA	4224	N	GLY	549	78.746	5.229	14.675	1.00 34.10

ATC		226	CA	GLY	549	79.8	771				
ATO		27	C	GLY		79.4		6.11			0 31.50
ATO		28	0	GLY	549			7.42			0 31.11
ATO	M 42	29	N	ALA	550	78.2 80.3		7.68			0 30.15
ATO	M 42	31	CA	ALA	550			8.26			0 31.02
ATO		32	CB	ALA	550	80.0		9.54		50 1.0	0 29.00
ATO	M 42	33	С	ALA	550	79.5		10.52		99 1.0	0 27.87
ATO	M 42	34	0	ALA	550	81.2		10.14		02 1.0	27.66
ATO		35	N	CYS	551	82.4		9.942		74 1.00	25.24
ATON		37	CA	CYS	551	80.9		10.810		84 1.00	27.61
ATOM	423	38	CB	CYS	551	81.92		11.540		70 1.00	25.02
ATOM		39	SG	CYS	551	81.75		11.237		30 1.00	22.41
ATOM	1 424	O		CYS	551	82.15		9.553		37 1.00	27.24
ATOM		1 (CYS	551	81.58		13.009		7 1.00	24.31
ATOM	424	2]		THR	552	80.56		13.525		8 1.00	23.55
ATOM	424	4 (THR	552 552	82.36		13.657		3 1.00	23.22
ATOM	424			THR	552 552	82.11		15.046		4 1.00	25.73
ATOM	424	6 (THR	552 552	82.13		15.215	13.20	2 1.00	26.50
ATOM	424			THR	552 552	83.47		15.031	13.66	4 1.00	26.31
ATOM	424	9 (THR	552	81.25		14.171	13.88	6 1.0C	26.64
ATOM	425	0 C		HR	552	83.13		16.014	11.09		27.93
ATOM	425	1 N		LN	553	82.89		17216	11.00	5 1.00	28.35
ATOM	425	3 C		LN	553	84.264		15.473	10.66	3 1.00	30.26
MOTA.	4254	1 C		LN	553	85.359		16.288	10.15	3 1.00	29.27
ATOM	4255	5 C		LN	553	86.669		15.768	10.763	3 1.00	29.54
ATOM	4256	G C:		LN	553	86.653		15.655	12.288	1.00	28.00
ATOM	4257	7 O:	E1 G		553	86.534		17.007	12.981	1.00	26.86
ATOM	4258			LN	553	87.440		17.821	12.902	1.00	30.85
ATOM	4261	C		LN	553	85.421		L7.239	13.676	1.00	
ATOM	4262	0		LN	553	85.475		16.316	8.634	1.00	
ATOM	4263	N	AS	SP	554	85.221 85.860		5.313	7.967		31.00
ATOM	4265	CZ	A AS	SP	554	86.070		7.480	8.119		
ATOM	4266	CE			554	87.370		7.725	6.695	1.00	
ATOM	4267	CG	AS	SP	554	88.534		7.081	6.257	1.00	
ATOM	4268	OD	1 AS	P	554	89.038		7.564	7.060	1.00	37.63
ATOM	4269	OD			554	88.929		8.664	6.763	1.00 4	2.66
ATOM	4270	C	AS		554	84.976		6.843	8.000	1.00 3	5.80
ATOM	4271	0	AS		554	85.193		7.341	5.715	1.00 2	8.04
MOTA	4272	N	GL		555	83.824		6.518	4.826		1.06
ATOM	4274	CA	GL		555	82.720		7.981	5.842	1.00 2	8.26
ATOM	4275	C	GL.		555	81.438		7.694	4.949	1.00 2	5.89
ATOM	4276	0	GL:		555	81.423		7.567	5.734	1.00 2	3.07
ATOM	4277	N	PRO		556	80.338		7.795	6.941	1.00 2	0.20
ATOM	4278	CD	PRO		556	80.280		7.185	5.076	1.00 2	2.81
MOTA	4279	CA	PRO		556	79.039		750	3.679	1.00 2	2.33
ATOM	4280	CB	PRO		56	78.154		.032	5.733	1.00 2	
ATOM	4281	CG	PRO		56			.499	4.612	1.00 22	
ATOM	4282	С	PRO		56	79.144 79.080		.801	3.698	1.00 24	1.36
ATOM	4283	0	PRO		56			.066	6.911	1.00 26	5.98
ATOM	4284	N	LEU		57	79.854 78.237		.111	6.934	1.00 28	
ATOM	4286	CA	LEU		5 <i>7</i>			.325	7.896	1.00 29	.25
ATOM	4287	CB	LEU	_	5 <i>7</i>	78.168 77.550			9.070	1.00 30	. 83
						//.550	т6.	.225 1	0.251	1.00 33	.20



ATOM	4288	CG	LEU	557	77.109	15.416	11.475	1.00	30.01
MOTA	4289	CD1	LEU	557	78.304	14.793	12.174	1.00	29.05
MOTA	4290	CD2	LEU	557	76.365	16.341	12.407	1.00	29.20
ATOM	4291	С	LEU	557	77.324	14.238	8.780	1.00	30.33
MOTA	4292	0	LEU	557	76.175	14.343	8.330	1.00	27.66
MOTA	4293	N	TYR	558	77.913	13.071	9.002	1.00	30.68
MOTA	4295	CA	TYR	558	77.214	11.823	8.812	1.00	29.26
MOTA	4296	CB	TYR	558	77.978	10.933	7.840	1.00	30.99
MOTA	4297	CG	TYR	558	78.066	11.481	6.430	1.00	35.01
ATOM	4298	CD1	TYR	558	79.108	11.109	5.592	1.00	36.17
MOTA	4299	CE1	TYR	558	79.198	11.600	4.296	1.00	41.40
MOTA	4300	CD2	TYR	558	77.109	12.368	5.941	1.00	36.44
ATOM	4301	CE2	TYR	558 .	77.188	12.871	4.648	1.00	40.96
MOTA	4302	CZ	TYR	558	78.237	12.484	3.825	1.00	43.59
ATOM	4303	ОН	TYR	558	78.298	12.965	2.525	1.00	42.91
ATOM	4305	C	TYR	558	77.081	11.125	10.164	1.00	28.18
ATOM	4306	0	TYR	558	78.077	10.855	10.835	1.00	28.06
ATOM	4307	N	VAL	559	75.842	10.879	10.574	1.00	26.72
ATOM	4309	CA	VAL	559	75.548	10.175	11.821	1.00	26.72
MOTA	4310	CB	VAL	559	74.326	10.813	1.2.552	1.00	28.03
ATOM	4311	CG1	VAL	559	73.915	9.992	13.771	1.00	29.85
ATOM	4312	CG2	VAL	559	74.655	12.236	12.982	1.00	29.37
MOTA	4313	C	VAL	559	75.238	8.723	11.443	1.00	25.58
MOTA	4314	0	VAL	559	74.131	8.402	10.988	1.00	25.73
ATOM	4315	N	ILE	560	76.214	7.851	11.642	1.00	24.35
MOTA	4317	CA	ILE	560	76.061	6.448	11.281	1.00	26.64
ATOM	4318	CB	ILE	560	77.441	5.781	11.002	1.00	26.53
ATOM	4319	CG2	ILE	560	77.252	4.359	10.465	1.00	27.80
MOTA	4320	CG1	ILE	560 .	78.254	6.620	10.004	1.00	24.69
ATOM .	4321	CDI	ILE	560	79.671	6.112	9.763	1.00	17.05
ATOM	4322	C	ILE	560	75.312	5.633	12.339	1.00	27.95
ATOM	4323	0	ILE	560	75.777	5.493	13.479	1.00	25.16
MOTA	4324	N	VAL	561	74.163	5.084	11.951	1.00	27.43
MOTA	4326	CA	VAL	561	73.352	4.265	12.847	1.00	27.69
ATOM	4327	CB	VAL	561	72.048	5.000	13.251	1.00	25.08
ATOM	4328	CG1	VAL	561	72.367	6.302	13.936	1.00	19.97
ATOM	4329	CG2	VAL	561	71.186	5.250	12.033	1.00	25.55
MOTA	4330	С	VAL	561	73.031	2.896	12.202	1.00	30.21
MOTA	4331	0	VAL	561	73.404	2.623	11.045	1.00	32.04
MOTA	4332	N	GLU	562	72.306	2.062	12.944	1.00	28.88
MOTA	4334	CA	GLU	562	71.940	0.714	12.509	1.00	27.69
MOTA	4335	CB	GLU	562	71.448	-0.081	13.712	1.00	26.79
MOTA	4336	CG	GLU	562	72.387	0.001	14.873	1.00	28.13
MOTA	4337	CD	GLU	562	72.012	-0.916	16.003	1.00	31.86
MOTA	4338	OE1	GLU	562	72.772	-1.876	16.255	1.00	33.17
MOTA	4339	OE2	GLU	562	70.974	-0.654	16.639	1.00	35.50
MOTA	4340	C	GLU	562	70.898	0.636	11.405	1.00	27.34
ATOM	4341	0	GLU	562	69.990	1.453	11.358	1.00	29.72
ATOM	4342	N	TYR	563	71.002	-0.392	10.568	1.00	28.07
MOTA	4344	CA	TYR	563	70.080	-0.626	9.455	1.00	32.50
ATOM	4345	CB	TYR	563	70.848	-1.236	8.269	1.00	28.32
MOTA	4346	CG	TYR	563	70.042	-1.427	7.007	1.00	26.56

7.00					
ATO		347	CD1 7		69.338 -0.378 6.448 1 00 30 40
ATO		348	CE1 1	YR 563	69 630 0 === 0.440 1.00 30.49
ATO	_	349		YR 563	3.230 1.00 32.83
ATC		350		YR 563	69 300 0 000
ATC		351	CZ T	YR 563	69 605 1 555
ATC		352		YR 563	67 976 1 000
ATO		354	C T	YR 563	69 030 1
ATO		355	O I.	YR 563	69 151 2 5570 1.00 36.30
ATO		56		LA 564	67 777 1 000 36.17
ATO		58	CA A	LA 564	66 530 3 00-
ATO		59	CB AI		65 557 3 000
ATO			C AI		65 910 2 260
ATO			O AI		64 950 1 555 1.00 41.61
ATON			n se		66 455 3 305
ATON			CA SE	R 565	66 019 2 225
ATOM			CB SE	R 565	66 672
ATOM	_		G SE	R 565	66 646 6 676 1.00 40.15
ATOM			SE		64 530
ATOM) SE	R 565	64 007 2 000
ATOM			LY:	S 56.6	63: 743 4 700
АТОМ		_	A LY	S 566	62, 212 4 24
ATOM			B LY	5 566	61 807 5 5 5 1
ATOM		_	G LYS	5 566	62 460 T = 71705 II.00 38.35
ATOM		_	D LYS	566	52 161 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
ATOM			E LYS	566	62 734 0 5 5 5
ATOM	437		Z LYS	566	62: 692 30 400
ATOM	438	_	LYS	566	61 400 2 075
ATOM	438		LYS	566	50 365 3 757
ATOM	438		GLY	567	62 166 1 22 1.00 39.48
ATOM	438		GLY	567	61 407 0 71
ATOM	4386		GLY	567	60 910 0 175
ATOM	4387	-	GLY	567	61 251 1 252
ATOM	4388		ASN	568	59 722
ATOM	4390			56.8	59 999 9 7 7 7 1.00 29.92
ATOM	4391			568	50 414
ATOM	4392			568	57 201 0 31.23
ATOM	4393	OD	1 ASN	568	56 005 2 7 7 7 1.00 34.16
MOTA	4394		2 ASN	568	57 304 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
ATOM ATOM	4397	С	ASN	568	57 950 0 405 5
	4398	0	ASN	568	57 525 1.00 31.60
MOTA	4399	N	LEU	569	E7 E17 0 51.76
ATOM	4401	CA	LEU	569	==1150 1.00 34.63
ATOM	4402	CB	LEU	569	=======================================
ATOM	4403	CG	LEU	569	55 500 0 7-5
ATOM	4404		LEU	569	56 010 34.78
ATOM	4405		LEU	569	EE 425 1.00 35.01
ATOM	4406	C	LEU	569	EE 141
ATOM	4407	0	LEU	569	E4 E10 37.34
ATOM	4408	N	ARG	570	54 636 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
ATOM	4410	CA	ARG	570	53 300 37.19
ATOM	4411	CB	ARG	570	52 070 1 100 39.79
ATOM	4412	CG	ARG	570	51 550 2 551 1.00 39.48
					51.558 1.638 9.887 1.00 41.93

MOTA	4413	CD	ARG	570	51.459	2.966	9.182	1.00	49.89
MOTA	4414	NE	ARG	570	52.329	2.991	8.009	1.00	55.25
MOTA	4416	CZ	ARG	570	53.121	4.008	7.693	1.00	57.90
MOTA	4417	NH1	ARG	570	53.145	5.093	8.455	1.00	56.93
ATOM	4420	NH2	ARG	570	53.921	3.920	6.637	1.00	57.58
ATOM	4423	С	ARG	570	53.219	-0.835	9.278	1.00	39.84
ATOM	4424	0	ARG	570	52.309	-1.644	9.060	1.00	42.48
ATOM	4425	N	GLU	571	54.208	-0.597	8.425	1.00	38.22
ATOM	4427	CA	GLU	571	54.292	-1.251	7.135	1.00	38.84
MOTA	4428	СВ	GLU	571	55.284	-0.492	6.266		40.72
MOTA	4429	CG	GLU	571	54.818	0.941	5.999		49.17
MOTA	4430	CD	GLU	571	55.845	1.798	5 284		58.95
ATOM	4431	OE1	GLU	571	57.047	1.434	5.278		67.07
MOTA	4432	OE2	GLU	571	55.455	2.854	4.736		61.02
ATOM	4433	C	GLU	571	54.617	-2.744	7.240		37.79
ATOM	4434	0	GLU	571	54.075	-3.558	6.488		37.63
ATOM	4435	N	TYR	572	55.462	-3.104	8.204		36.89
ATOM	4437	CA	TYR	572	55.841	-4.498	8.437		36.81
ATOM	4438	СВ	TYR	572	56.822	-4.584	9.612		33.24
ATOM	4439	CG	TYR	572	57.191	-5.987	10.080	1.00	33.42
ATOM	4440	CD1	TYR	572	58.209	-6.714	9.450	1.00	
ATOM	4441	CE1	TYR	572	58.623	-7.960	9.936	1.00	30.14
ATOM	4442	CD2	TYR	572	56586	-6.552	11.208	1.00	34.42
ATOM	4443	CE2	TYR	572	56.991	-7.799	11.704		32.29
ATOM	4444	CZ	TYR	572	58.012	-8.495	11.065	1.00	32.52
ATOM	4445	OH	TYR	572	58.427	-9.717	11.571		31.70
ATOM	4447	C	TYR	572	54.588	-5.310	8.754		37.64
ATOM	4448	0	TYR	572	54.387	-6.410	8.226		35.70
ATOM	4449	N	LEU	573	53.742	-4.740	9.608	1.00	
ATOM	4451	CA	LEU	573	52.498	-5.376	10.011	1.00	
ATOM	4452	CB	LEU	573	51.802	-4.532	11.067	1.00	35.40
ATOM	4453	CG	LEU	573	52.494	-4.421	12.419		34.55
ATOM	4454	CD1	LEU	573	51.755	-3.402	13.258	1.00	32.02
ATOM	4455		LEU	573	52.537	-5.788	13.238		34.58
ATOM	4456	CDZ	LEU	573	51.570	-5.549	8.818	1.00	38.11
ATOM	4457	0	LEU	573	51.144	-6.656	8.507	1.00	
ATOM	4458	N.	GLN	574	51.286			1.00	37.68
ATOM	4460	CA	GLN	574	50.402	-4.448 -4.476	8.138 6.982	1.00	40.92
ATOM	4461	CB	GLN	574	50.213				45.16
				574		-3.071	6.447		44.16
ATOM	4462	CG	GLN			-2.239	7.369		45.26
ATOM	4463	CD	GLN	574	49.222	-0.849	6.863		47.09
ATOM	4464	OE1		574	49.789	-0.483	5.838		50.83
ATOM	4465	NE2		574	48.450	-0.051	7.573		48.95
ATOM	4468	C	GLN	574	50.807	-5.419	5.861		45.21
MOTA	4469	0	GLN	574	49.951	-6.031	5.215		49.63
MOTA	4470	N	ALA	575	52.105	-5.562	5.646		43.35
ATOM	4472	CA	ALA	575	52.579	-6.446	4.604		42.62
ATOM	4473	CB	ALA	575	54.023	-6.130	4.284	1.00	
MOTA	4474	C	ALA	575	52.439	-7.906	5.022		42.85
MOTA	4475	0	ALA	575	52.771	-8.804	4.254		44.43
MOTA	4476	N	ARG	576	51.937	-8.142	6.229		42.24
MOTA	4478	CA	ARG	576	51.787	-9.494	6.747	1.00	41.58



ATC	M 44	79	CB AR	a ===	
ATO				•	52.813 -9.725 7.849 1.00 40.10
ATO				•	54.225 -9.694 7.314 1.00 40.58
ATO			CD AR	•	55.280 -9.604 8.392 1.00 42 40
ATO	_		NE AR		56.632 -9.607 7.826 1.00 41.95
ATO			CZ AR		57.110 -8.684 6.992 1.00 38.22
	-		NH1 ARC		56.359 -7.658 6.612 1.00 38.61
ATO			VH2 ARC		58.347 -8.787 6.541 1.00 34.50
ATO	_			- , -	EO 300 0 715
ATO				•	50 107 10 10
ATON					49.418 -9.057 6.684 1.00 44.65
ATON			'A ARG		48.023 -9.222 7.077 1.00 46.69
ATON			B ARG		47 707
ATOM		_	G ARG		47 350 1.00 45.24
ATOM		-	D ARG	577	46 570
ATOM			-,		16 120 1.00 44.63
ATOM					45 750
ATOM			H1 ARG	577	45 140
ATOM			H2 ARG	577	45 643
ATOM		_	ARG	577	47 400 10 71
ATOM			ARG	577	47 200 17.12
ATOM			GľM	594	F3 246 40 40.37
MOTA	451			594	E2 0F4 12 12 12 12 12 12 12 12 12 12 12 12 12
ATOM	451			594	52.054 -13.835
ATOM ATOM	4514		GLN	594	52.447 -14.127 10.174 1.00 64.01
ATOM	4515		GLN	594	52.962 -15.201 10.507 1.00 64.42
	4516		LEU	595	52.189 -13.154 11.031 1.00 61.45
ATOM ATOM	4518			595	52.524 -13.245 12.437 1.00 59.21
ATOM	4519			595	52.669 -11.826 12.979 1.00 57.54
ATOM	4520 4521			595	53.648 -11.043 12.099 1.00 56 37
ATOM	4522		1 LEU	595	53.442 -9.551 12.202 1.00 57 06
ATOM	4523		2 LEU	595	55.064 -11.430 12.465 1.00 55 57
ATOM	4524		LEU	595	51.509 -14.046 13.257 1.00 58 34
ATOM	4525		LEU	595	50.316 -14.039 12.953 1.00 58 21
ATOM	4527		SER	596	52.007 -14.740 14.280 1.00 58 00
ATOM	4528	CA CB	SER	596	51.182 -15.543 15.180 1.00 56 04
ATOM	4529	OG	SER	596	51.960 -16.770 15.667 1.00 57 98
ATOM	4531	C	SER SER	596	52.987 -16.403 16.580 1.00 58 94
ATOM	4532	0	SER	596	50.854 -14.681 16.383 1.00 54 65
ATOM	4533	N		596	51.479 -13.645 16.584 1.00 52 05
ATOM	4535	CA	SER SER	597	49.914 -15.133 17.208 1.00 56 10
ATOM	4536	CB	SER	597	49.525 -14.389 18.398 1.00 57 51
ATOM	4537	OG	SER	597 507	48.530 -15.196 19.236 1.00 58 60
ATOM	4539	C	SER	597	47.620 -15.914 18.421 1.00 61 95
ATOM	4540	0		597	50.//8 -14.094 19.220 1.00 57 75
ATOM	4541	N	SER LYS	597 598	50.934 -12.998 19.755 1.00 57.86
ATOM	4543	CA	LYS	598	51.692 -15.062 19.271 1.00 57 00
ATOM	4544	CB	LYS	598	52.930 -14.905 20.026 1.00 57 51
ATOM	4545	CG	LYS	598 500	53.690 -16.231 20.124 1.00 57.72
ATOM	4546	CD	LYS	598 598	54.470 -16.395 21.432 1.00 60.14
ATOM	4547	CE	LYS		55.227 -17.724 21.479 1.00 62.23
ATOM	4548	NZ	LYS	598 598	55.894 -17.989 22.834 1.00 60.79
		-		390	54.921 -18.149 23.949 1.00 61.46

4552 С LYS 598 53.809 -13.829 19.389 1.00 55.94 MOTA 4553 LYS 598 54.322 -12.955 20.089 1.00 55.84 MOTA 0 ATOM 4554 ASP 599 53.935 -13.866 18.061 1.00 53.32 N 4556 CA ASP 599 54.737 -12.882 17.334 1.00 50.30 ATOM ASP ATOM 4557 CB 599 54.688 -13.119 15.823 1.00 49.72 ATOM 4558 CG ASP 599 55.426 -14.383 15.394 1.00 53.97 1.00 58.12 ATOM 4559 OD1 ASP 599 56.176 -14.948 16.214 MOTA 4560 OD2 ASP 599 55.261 -14.822 14.233 1.00 55.58 MOTA 4561 C ASP 599 54.247 -11.474 17.636 1.00 49.53 MOTA 4562 0 ASP 599 55.054 -- 10.589 17.911 1.00 51.16 4563 LEU ATOM N 600 52.930 -11.281 17.634 1.00 47.50 **ATOM** 4565 CA LEU 600 52.354 -9.972 17.909 1.00 45.41 4566 1.00 43.77 **ATOM** CB LEU 600 50.850 -9.948 17.627 ATOM 4567 CG LEU 600 50.429 -10.121 16.169 1.00 41.05 CD1 LEU ATOM 4568 600 48.941 -9.904 16.048 1.00 41.04 MOTA 4569 CD2 LEU 600 51.160 -9.140 15.294 1.00 39.59 ATOM 4570 LEU 52.638 -9.485 19.318 1.00 46.77 C 600 LEU 52.964 -8.308 19.497 ATOM 4571 600 1.00 48.74 0 ATOM 4572 N VAL 601 52.524 ~10.372 20 314 1.00 47.64 21.716 ATOM 4574 CA VAL 601 52.804 -10.002 1.00 47.38 VAL 22.756 **ATOM** 4575 CB 601 52.321 -11.070 1.00 46.58 CG1 VAL 52.081 -10.403 24.114 MOTA 4576 601 1.00 45.07 ATOM 4577 CG2 VAL 601 51.058 -11.759 22.306 1.00 48.86 ATOM 4578 C VAL 601 54.321 -9.811 21.890 1.00 46.04 54.793 -8.935 22.622 MOTA 4579 Ö VAL 601 1.00 46.13 MOTA 4580 N SER 602 55.090 -10.624 21.183 1.00 44.21 4582 CA 56.534 -10.546 21.233 MOTA SER 602 1.00 42.78 ATOM CB 20.297 4583 SER 602 57.119 -11.594 1.00 43.98 MOTA 4584 OG SER 602 58.523 -11.615 20.355 1.00 51.02 ATOM 4586 С SER 602 56.954 -9.135 20.813 1.00 41.74 MOTA 4587 0 SER 602 57.709 -8.467 21.524 1.00 44.09 -8.667 19.685 ATOM 4588 N CYS 603 56.425 1.00 39.57 MOTA 4590 CYS 603 56.699 -7.317 19.177 CA 1.00 36.11 ATOM 4591 CB CYS 603 55.852 -7.058 17.924 1.00 34.72 ATOM 4592 SG CYS 603 55.760 -5.364 17.323 0.50 29.10 PRT1 MOTA 4593 C CYS 20.252 1.00 34.50 603 56.378 -6.272 MOTA 4594 0 CYS 603 57.174 -5.371 20.506 1.00 33.61 20.913 MOTA 4595 N ALA 604 55.236 -6.429 1.00 34.64 21.964 1.00 37.18 MOTA 4597 CA ALA 604 54.811 -5.506 4598 CB 53.386 -5.850 22.414 MOTA ALA604 1.00 38.20 **ATOM** 4599 С 55.786 -5.516 23.160 ALA 604 1.00 38.91 -4.481 ATOM 4600 56.026 23.790 0 ALA 604 1.00 38.29 4601 56.323 -6.693 23.477 MOTA N TYR 605 1.00 39.54 MOTA 4603 TYR 605 57.283 -6.854 24.565 1.00 39.29 CA MOTA 4604 TYR 57.573 -8.340 24.791 1.00 40.07 CB 605 ATOM 4605 CG TYR 605 58.663 -8.622 25.807 1.00 39.09 MOTA 4606 CD1 TYR 605 58.525 -8.236 27.137 1.00 38.50 ATOM 4607 CE1 TYR 605 59.526 -8.505 28.074 1.00 40.76 MOTA 4608 CD2 TYR 605 59.831 -9.283 25.435 1.00 39.73 MOTA 4609 CE2 TYR 605 60.834 -9.553 26.361 1.00 37.45 MOTA 4610 CZTYR 605 60.678 -9.166 27.677 1.00 40.34 MOTA TYR 605 61.666 -9.466 28.601 1.00 43.16 4611 OH

ATON	4 463							
ATOM					58.58	2 -6.11	3 24.22	1.00 39.45
					59.06	7 -5.29	1 25.022	
ATOM					59.12	9 -6.41		•
ATOM			'A GLN		60.36	1 ~5.78		
ATOM			B GLN		60.69	-6.303		
ATOM			G GLN	606	61.286			
ATOM			D GLN		61.502			
ATOM		1 0	E1 GLN	606	62.495			
ATOM		2 N	E2 GLN	606	60.568			
ATOM	462	5 C	GLN	606	60.286			
MOTA	462	6 O	GLN	606	61.209			
ATOM	462	7 N	VAL	607	59.188			
ATOM	4629	9 C	A VAL	607	58.979			
ATOM	4630	O CE	3 VAL	607	57.651			
ATOM	4633	L CC	31 VAL	607		_		
ATOM	4632		32 VAL	607	57.260			1.00 26.68
ATOM	4633		VAL	607	57.790			1.00 24.66
ATOM	4634		VAL	607	58.965		23.339	1.00 31.35
ATOM	4635		ALA	608	59.557		23.579	1.00 33.86
ATOM	4637				58.317	-2.402	24.270	1.00 30.17
MOTA	4638			608	58.235	-1.971	25.667	1.00 28.98
ATOM	4639	_	ALA	608	57.255	-2.836	26.440	1.00 28.30
ATOM	4640			608	59.598	-1.979	26.352	1.00 28.94
ATOM	4641		ALA	608	59.889	-1.091	27.155	1.00 27.83
ATOM	4643		ARG	609	60.436	-2.959	26.032	1.00 28.79
ATOM	4644			609	51.765	-3.023	26.628	1.00 30.90
ATOM	4645			609	62.499	-4.291	26.206	1.00 35.84
ATOM				609	61.787	-5.571	26.527	1.00 41.94
ATOM	4646	CD		609	62.782	-6.707	26.575	1.00 44.70
	4647	NE	ARG	609	63.392	-6.821	27.900	1.00 47.13
ATOM	4649	CZ	ARG	609	64.444	7.589	28.183	1.00 48.71
ATOM	4650		l ARG	609	65.025	-3.314	27.233	1.00 48.33
ATOM	4653		2 ARG	609	64.897	-7.655	29.428	1.00 49.11
MOTA	4656	C	ARG	609	62.602	-1.815	26.207	1.00 32.38
ATOM	4657	0	ARG	609	63.215	-1.148	27.058	1.00 32.63
ATOM	4658	N	GLY	610	62.636	-1.554	24.894	1.00 29.98
ATOM	4660	CA	GLY	610	63.384	-0.430	24.358	1.00 25.65
ATOM	4661	C	\mathtt{GLY}	610	62.969	0.837	25.061	1.00 25.44
ATOM	4662	0	GLY	610	63.791	1.640	25.463	1.00 23.44
ATOM	4663	N	MET	611	61.672	1.009	25.242	1.00 27.09
ATOM	4665	CA	MET	611	61.167	2.176	25.943	
ATOM	4666	CB	MET	611	59.653	2.233	25.832	1.00 31.34
ATOM	4667	CG	MET	611	59.195	2.595	24.449	1.00 28.39
ATOM	4668	SD	MET	611	59.904	4.182		1.00 25.17
ATOM	4669	CE	MET	611	59.458	5.158	24.005	1.00 26.65
ATOM	4670	C	MET	611	61.600		25.453	1.00 19.78
ATOM	4671	0	MET	611	62.008	2.176	27.412	1.00 34.05
ATOM	4672	N	GLU	612	61.500	3.211		1.00 33.79
ATOM	4674	CA	GLU	612		1.026		1.00 37.16
ATOM	4675	CB	GLU	612	61.893			1.00 38.85
ATOM	4676	CG	GLU	612	61.732			1.00 38.96
ATOM	4677	CD	GLU	612				1.00 35.19
ATOM	4678	OE1						1.00 35.26
		~~. <u>~</u>	320	612	62.605	-3.123	30.912	1.00 29.29

ATOM	4679	OE2	GLU	612	62.102	-2.588	32.982	1.00 37.85
ATOM	4680	C	GLU	612	63.353	1.364	29.628	1.00 40.01
ATOM	4681	0	GLU	612	63.720	2.060	30.584	1.00 38.27
MOTA	4682	N	TYR	613	64.176	0.972	28.662	1.00 40.33
ATOM	4684	CA	TYR	613	65.575	1.362	28.664	1.00 39.71
MOTA	4685	CB	TYR	613	66.333	0.722	27.494	1.00 39.03
ATOM	4686	CG	TYR	613	67.800	1.100	27.467	1.00 41.41
ATOM	4687	CD1	TYR	613	68.702	0.527	28.364	1.00 42.79
ATOM	4688	CE1	TYR	613	70.048	0.905	28.386	1.00 40.21
ATOM	4689	CD2	TYR	613	68.283	2.068	26.581	1.00 39.75
ATOM	4690	CE2	TYR	613	69.621	2.454	26.596	1.00 39.01
ATOM.	4691	CZ	TYR	613	70.499	1.868	27.503	1.00 39.56
ATOM	4692	OH	TYR	613	71.823	2.249	27.538	1.00 35.63
ATOM	4694	C	TYR	613	65.642	2.881	28.562	1.00 38.71
ATOM	4695	0	TYR	613	66.106	3.541	29.486	1.00 38.52
ATOM	4696	N	LEU	614	65.126	3.423	27.460	1.00 37.22
ATOM	4698	CA	LEU	614	65.128	4.864	27.212	1.00 35.66
ATOM	4699	СВ	LEU	614	64.223	5.202	26.025	1.00 35.27
ATOM	4700	CG	LEU	614	64.687	4.699	24.659	1.00 33.09
ATOM	4701	CD1	LEU	614	63.718	5188	23.612	1.00 33.31
ATOM	4702	CD2	LEU	614	66.099	5.184	24.363	1.00 31.20
ATOM	4703	С	LEU	614	64.672	5.653	28.430	1.00 35.64
ATOM	4704	0	LEU	614	65.298	6.639	28.816	1.00 34.54
ATOM	4705	N	ALA	615.	63.577	5.203	29.032	1.00 36.61
ATOM	4707	CA	ALA	615	63.028	5.835	30.222	1.00 37.74
ATOM	4708	СВ	ALA	615	61.682	5.187	30.608	1.00 37.74
ATOM	4709	C	ALA	615	64.021	5.776	31.389	1.00 37.30
ATOM	4710	0	ALA	615	64.111	6.731	32.175	1.00 37.29
ATOM	4711	N	SER	616	64.752	4.665	31.511	1.00 37.18
ATOM	4713	CA	SER	616	65.741	4.534	32.577	1.00 36.92
MOTA	4714	CB	SER	616	66.274	3.091	32.702	1.00 34.82
ATOM	4715	OG	SER	616	67.106	2.680	31.628	1.00 28.79
MOTA	4717	С	SER	616	66.870	5.516	32.287	1.00 38.57
MOTA	4718	0	SER	616	67.633	5.902	33.179	1.00 38.30
ATOM	4719	N	LYS	617	66.958	5.925	31.024	1.00 37.62
ATOM	4721	CA	LYS	617	67.965	6.876	30.606	1.00 36.13
MOTA	4722	CB	LYS	617	68.511	6.494	29.238	1.00 35.90
ATOM	4723	CG	LYS	617	69.274	5.206	29.236	1.00 34.58
MOTA	4724	CD	LYS	617	70.502	5.348	30.077	1.00 35.44
ATOM	4725	CE	LYS	617	71.201	4.022	30.232	1.00 38.54
ATOM	4726	NZ	LYS	617	72.566	4.211	30.790	1.00 41.54
ATOM	4730	С	LYS	617	67.378	8.275	30.564	1.00 36.55
ATOM	4731	0	LYS	617	67.943	9.155	29.934	1.00 40.26
MOTA	4732	N	LYS	618	66.221	8.468	31.187	1.00 36.42
ATOM	4734	CA	LYS	618	65.570	9.779	31.231	1.00 36.06
ATOM	4735	CB	LYS	618	66.543	10.833	31.746	1.00 42.22
ATOM	4736	CG	LYS	618	67.234	10.499	33.062	1.00 52.36
ATOM	4737	CD	LYS	618	66.301	10.668	34.236	1.00 61.51
ATOM	4738	CE	LYS	618	66.933	10.121	35.495	1.00 67.28
ATOM	4739	NZ	LYS	618	65.965	10.161	36.618	1.00 73.99
ATOM	4743	C	LYS	618	65.026	10.261	29.887	1.00 34.94
ATOM	4744	o	LYS	618	64.562	11.393	29.781	1.00 34.69

ATO		745	N	CYS	619	65.0	51	9.40	7 20 6				
ATO		147	CA	CYS	619	64.5		9.79				34.46	
ATO		48	CB	CYS	619	65.3		8.96				33.12	
ATO		49	SG (CYS	619	64.9		9.39				34.33	
ATO		50	C (CYS	619	63.0						35.64	
ATON		51	0 (CYS	619	62.4		9.69				32.13	
ATOM			N]	LE	620	62.4		8.64				30.72	
ATOM			CA]	LE	620	61.04		10.81				32.70	
ATOM	1 47	55	CB]	LE	620	60.44		10.90				32.75	
ATOM	1 47	56 (CG2 I	LE	620	59.00		12.12				33.55	
ATOM	47	57 (CG1 I	LE	620	60.48		12.33				38.39	
ATOM		58 (CD1 I	LE	620	59.99		11.91				30.71	
ATOM	475	59 (LE	620			13.084				30.11	
ATOM	476	50 C		LE	620	60.96		11.086			00	33.31	
ATOM	476	51 N	_	IS	621	61.51		12.040		4 1.0	0 3	33.40	
ATOM	476	3 (IS	621	60.35		10.114		3 1.0		33.56	
ATOM	476			IS	621	60.23		10.092				32.30	
ATOM	476			ſS	621	59.86		8.668		2 1.0		9.55	
ATOM	476		D2 H			60.04		8.402	,			7.32	
ATOM	476		D1 H		621	60.69		7.404	20.53			4.26	
ATOM	476		E1 H)		621 621	59.46		9.173	20.18	7 1.0	0 2	5.20	
ATOM	477		E2 H]			59.734		8.652	19.00	1.0	0 2	5.81	
ATOM	477		ні		621	60.48		7.579	19.18	1.0	0 2	6.65	
ATOM	477	_	HI		621	59.246		11.103	22.499			5.40	
ATOM	477	_	AR		621	59.459		11.574	21.388			9.18	
ATOM	4776				622	58.128		11.363	23.178			6.39	
ATOM	477	-			622	57.117		12.323	22.686			5.40	
ATOM	4778				622	57.694		13.732	22.617				
.ATOM	4779				622	58.171		14.253	23.937				
ATOM	4780				622	58.837		15.591	23.759	0.5.0			
ATOM	4782				622	59.315		16.101	25.032	0.50			
ATOM	4783		1 AR		622	60.487		L5.786	25.575	0.50			
ATOM	4786				622	61.326		14.965	24.952	0.50			
ATOM	4789		ARC		622	60.803	1	.6.268	26.769	0.50			
ATOM	4790	_	ARG		622	56.405	1	2.008	21.355	1.00	36	. 23	
ATOM	4791	N	ASI		622	55.527	1	2.763	20.936	1.00			
ATOM	4793	CA			623	56.806	1	0.938	20.668	1.00			
ATOM	4794	CB	ASP ASP		623	56.128	1	0.538	19.436	1.00			
ATOM	4795	CG	ASP		623	56.574	1	1.352	18.221		38		
ATOM	4796	OD			623	55.736	1	1.036	16.974	1.00			
ATOM	4797		ASP		523	56.277	1	1.082	15.851	1.00			
ATOM	4798	C			523	54.535	1	0.715	17.119	1.00			
ATOM	4799	0	ASP		523	56.271		9.052	19.162	1.00			
ATOM	4800		ASP		523	56.664	8	3.645	18.073	1.00			
ATOM	4802	N	LEU		24	56.015	8	3.244	20.179	1.00			
ATOM	4803	CA	LEU		24	56.099	6		20.029	1.00	31	71	
ATOM	4804	CB	LEU		24	56.070	6		21.407	1.00	22.	10	
ATOM		CG	LEU		24	56.049			21.514	1.00	20.	**0	
ATOM	4805		LEU		24	57.225			20.799	1.00	20. 27	T 2	
ATOM	4806 4807		LEU		24	56.072			22.987	1.00	4/.	10	
		C	LEU		24	54.917			19.185	1.00	27.	. T	
	4808	0	LEU		24	53.763			19.508	1.00			
	4809	N	ALA	6:	25	55.214			18.081	1.00		/4 00	
								•		±.00 2	: J . i	52	

ATOM	4811	CA	ALA	625	54.194	5.106	17.181	1.00	28.29
ATOM	4812	CB	ALA	625	53.682	6.182	16.245	1.00	26.72
ATOM	4813	C	ALA	625	54.895	4.031	16.395	1.00	28.40
MOTA	4814	0	ALA	625	56.118	4.028	16.343	1.00	32.12
MOTA	4815	N	ALA	626	54.131	3.135	15.770	1.00	28.55
MOTA	4817	CA	ALA	626	54.687	2.028	14.979	1.00	26.25
MOTA	4818	CB	ALA	626	53.577	1.169	14.365	1.00	23.54
ATOM	4819	С	ALA	626	55.569	2.573	13.892	1.00	23.68
ATOM	4820	0	ALA	626	56.544	1.944	13.519	1.00	26.07
ATOM	4821	N	ARG	627	55.208	3.744	13.378	1.00	23.80
MOTA	4823	CA	ARG	627	55.980	4.413	12.338	1.00	26.57
ATOM	4824	CB	ARG	627	55.289	5.728	11.914	1.00	25.91
MOTA	4825	CG	ARG	627	54.991	6.692	13.055	1.00	27.60
ATOM	4826	CD	ARG	627	54.711	8.130	12.584	1.00	33.01
ATOM	4827	NE	ARG	627	54.260	8.978	13.691	1.00	34.18
ATOM	4829	CZ	ARG	627	52.997	9.067	14.091	1.00	35.88
ATOM	4830	NH1	ARG	627	52.056	8.380	13.460	1.00	38.89
MOTA	4833	NH2	ARG	627	52.689	9.748	15.183	1.00	36.43
ATOM	4836	С	ARG	627	57.439	4.686	12.785	1.00	29.03
ATOM	4837	0	ARG	627	58.362	4.606	11.972	1.00	29.24
ATOM	4838	N	ASN	628	57.634	4.938	14.087	1.00	29.51
MOTA	4840	CA	ASN	628	58.954	5.234.	14.645	1.00	26.41
ATOM	4841	CB	ASN	628	58.864	6.359	15.676	1.00	25.32
ATOM	4842	CG	ASN	628	58.539	7.687	15.035	1.00	28.11
ATOM	4843	ODI	ASN	628	59.079	8.028	13.999	1.00	32.09
ATOM	4844	ND2	ASN	628	57.639	8.426	15.628	1.00	27.88
MOTA	4847	C	ASN	628	59.684	4.039	15.225	1.00	25.77
ATOM	4848	0	ASN	628	60.641	4.188	16.001	1.00	24.77
ATOM	4849	N	VAL	629	5.9.209	2.853	14.874	1.00	26.63
MOTA	4851	CA '	VAL	629	59.828	1.610	15.315	1.00	25.34
MOTA	4852	CB	VAL	629	58.812	0.693	16.007	1.00	21.26
ATOM	4853	CG1	VAL	629	59.492	-0.604	16.412	1.00	22.96
MOTA	4854	CG2	VAL	629	58.205	1.398	17.207	1.00	16.65
ATOM	4855	C	VAL	629	60.266	0.962	14.007	1.00	26.79
ATOM	4856	0	VAL	629	59.454	0.839	13.087	1.00	28.60
MOTA	4857	N	LEU	630	61.542	0.603	13.904	1.00	25.91
MOTA	4859	CA	LEU	630	62.062	-0.021	12.685	1.00	26.95
MOTA	4860	CB	LEU	630	63.297	0.733	12.210	1.00	22.79
MOTA	4861	CG	LEU	630	63.044	2.242	12.111	1.00	20.04
ATOM	4862	CD1	LEU	630	64.345	2.944	11.972	1.00	11.86
ATOM	4863	CD2	LEU	630	62.111	2.603	10.965	1.00	19.22
MOTA	4864	C	LEU	630	62.367	-1.492	12.961	1.00	28.01
MOTA	4865	0	LEU	630	62.629	-1.852	14.101	1.00	28.26
MOTA	4866	N	VAL	631	62.246	-2.346	11.946	1.00	30.82
MOTA	4868	CA	VAL	631	62.468	-3.790	12.098	1.00	31.75
ATOM	4869	CB	VAL	631	61.194	-4.607	11.659		30.04
MOTA	4870	CG1	VAL	631	61.346	-6.085	12.026	1.00	29.25
ATOM	4871	CG2	VAL	631	59.937	-4.030	12.290		24.59
MOTA	4872	С	VAL	631	63.697	-4.286	11.305	1.00	35.24
ATOM	4873	0	VAL	631	63.849	-3.999	10.097	1.00	34.02
MOTA	4874	N	THR	632	64.551	-5.052	11.979	1.00	36.24
MOTA	4876	CA	THR	632	65.770	-5.574	11.365	1.00	38.23

ATOM	4877	7 CB	THR	632	66.843	-5.836	5 12.416	5 1.00 38.21
ATOM	4878	og	1 THR	632	66.423			
ATOM	4880	CG	2 THR	632	67.069			
ATOM	4881	. C	THR	632	65.526			
ATOM	4882	0	THR	632	64.471			
ATOM	4883	N	GLU	633	66.496			···
ATOM	4885	CA	GLU	633	66.397			
ATOM	4886	CB	GLU	633	67.677			
MOTA	4887	CG	GLU	633	67.610	-9.884		
ATOM	4888	CD	GLU	633	66.825	-9.594		
ATOM	4889	OE:	L GLU	633	66.390	-8.444		
ATOM	4890	OE2	GLU	633		-10.536		
ATOM	4891	C	GLU	633	66.097	-9.722		
ATOM.	4892	0	GLÜ	633		-10.704		
MOTA	4893	N	ASP	634	66.415	-9.665	11.082	
ATOM	4895	CA	ASP	634		-10.784		
ATOM	4896	CB	ASP	634		-11.007	12.914	1.00 44.01
MOTA	4897	CG	ASP	634		-11.396	12.166	1.00 49.37
ATOM	4898	OD1	ASP	634		-12.515	11.595	1.00 54.70
ATOM	4899	OD2	ASP	634		-10.596	12.167	1.00 55.43
ATOM	4900	C	ASP	634		-10.507	12.801	1.00 56.17
ATOM	4901	0	ASP	634		-11.085	13.864	1.00 43.95
. ATOM	4902	N	ASN	635	64.075	-9.604	12.316	1.00 45.92
ATOM	4904	CA	ASN	635	62.822	-9.220	12.980	1.00 44.71 1.00 43.07
ATOM	4905	CB	ASN	635		-10.404	13.018	
ATOM	4906	CG	ASN	635		-10.994	11.653	1.00 45.50
ATOM	4907	OD1	ASN	635		-10.369	10.788	1.00 45.43 1.00 49.56
ATOM	4908	ND2	ASN	635		-12.190	11.435	1.00 48.18
ATOM	4911	C	ASN	635	62.927	-8.609	14.380	1.00 41.64
ATOM	4912	0	ASN	635 ⁻	62:050	-8.814	15.221	1.00 41.64
ATOM	4913	N	VAL	636	63.984	-7.843	14.627	1.00 41.89
ATOM	4915	C'A	VAL	636	64.177	-7.178	15.922	1.00 39.01
ATOM	4916	СВ	VAL	636	65.692	-7.002	16.259	1.00 40.66
ATOM	4917	CG1	VAL	636	65.882	-6.209	17.560	1.00 35.04
ATOM	4918	CG2	VAL	636	66.355	-8.360	16.367	1.00 41.69
ATOM	4919	C	VAL	636	63.544	5.789	15.925	1.00 36.77
ATOM	4920	0	VAL	636°	63.817	-4.989	15.045	1.00 38.35
ATOM	4921	N	MET	637	62.696	~5.518	16.908	1.00 35.71
ATOM	4923	CA	MET	637	62.049	-4.216	17.031	1.00 33.65
ATOM	4924	CB	MET	637	60.783	-4.319	17.884	1.00 38.24
ATOM	4925	CG	MET	637	59.737	-5.314	17.371	1.00 41.34
ATOM	4926		MET	637	59.128	-4.993	15.695	1.00 42.24
ATOM	4927		MET	637	59.249	-6.621	14.976	1.00 39.27
ATOM	4928		MET.	637	63.001	-3.209	17.668	1.00 32.62
ATOM	4929		MET	637	63.524	-3.436	18.765	1.00 30.56
ATOM	4930	N	LYS	638	63.173	-2.070	17.008	1.00 32.03
ATOM	4932		LYS	638	64.073	-1.027	17.492	1.00 28.77
ATOM	4933		LYS	638	65.351	-1.022	16.654	1.00 27.71
ATOM	4934		LYS	638	66.245	-2.211	16.896	1.00 25.04
ATOM	4935		LYS	638	67.429	-2.170	15.976	1.00 24.50
ATOM			LYS	638		-3.187	16.390	1.00 22.85
MOTA	4937	NZ :	LYS	638		-2.803	17.651	1.00 24.79
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ATOM	4941	С	LYS	638	63.443	0.364	17.446	1.00	28.00
ATOM	4942	0	LYS	638	62.977	0.799	16.391	1.00	25.60
MOTA	4943	N	ILE	639	63.410	1.032	18.601	1.00	25.32
ATOM	4945	CA	ILE	639	62.857	2.379	18.721	1.00	25.91
ATOM	4946	CB	ILE	639	62.800	2.875	20.201	1.00	25.56
ATOM	4947	CG2	ILE	639	62.074	4.208	20.279	1.00	22.82
ATOM	4948	CG1	ILE	639	62.142	1.835	21.118	1.00	28.00
ATOM	4949	CD1	ILE	639	60.634	1.748	21.003	1.00	33.25
ATOM	4950	C	ILE	639	63.739	3.363	17.955	1.00	26.87
ATOM	4951	0	ILE	639	64.968	3.381	18.125	1.00	24.13
ATOM	4952	N	ALA	640	63.108	4.170	17.108	1.00	26.74
MOTA	4954	CA	ALA	640	63.825	5.176	16.339	1.00	30.62
MOTA	4955	CB	ALA	640	63.624	4.939	14.851	1.00	30.31
MOTA	4956	C	ALA	640	63.338	6.572	16.739	1.00	32.53
ATOM	4957	0	ALA	640	62.289	6.706	17.371	1.00	33.83
ATOM	4958	N	ASP	641	64.082	7.605	16.351	1.00	33.05
MOTA	4960	CA	ASP	641	63.749	9.010	16.656	1.00	37.66
MOTA	4961	CB	ASP	641	62.539	9.489	15.840	1.00	42.62
ATOM	4962	CG	ASP	641	62.928	10.026	14.471	1.00	50.92
MOTA	4963	OD1	ASP	641	64.092	9.833	14.021	1.00	59.21
MOTA	4964	OD2	ASP	641	62.063	10.652	13.823	1.00	54.05
MOTA	4965	С	ASP	641	63.545	9.367	18.125	1.00	37.85
MOTA	4966	0	ASP	641	62.805	10.294	18.448	1.00	39.10
MOTA	4967	N	PHE	642	64.204	8.635	19.016	1.00	37.47
MOTA	4969	CA	PHE	642	64.099	8.874	20.456	1.00	36.47
MOTA	4970	CB	PHE	642.	64.403	7.581	21.226	1.00	32.22
ATOM	4971	CG	PHE	642	65.786	7.013	20.964	1.00	30.65
ATOM	4972	CD1	PHE	642	66.906	7.537	21.607	1.00	32.45
MOTA	4973	CD2	PHE	642	65.969	5.981	20.054	1.00	28.53
ATOM	4974	CE1	PHE	642	68.180	7.050	21.342	1.00	30.88
ATOM	4975	CE2	PHE	642	67.234	5.494	19.789	1.00	27.74
ATOM	4976	CZ	PHE	642	68.344	6.027	20.431	1.00	29.64
ATOM	4977	C	PHE	642	65.050	10.001	20.907	1.00	39.69
ATOM	4978	0	PHE	642	64.967	10.469	22.047	1.00	38.22
ATOM	4979	N	GLY	643	65.966	10.400	20.015	1.00	41.08
MOTA	4981	CA	GLY	643	66.925	11.447	20.324	1.00	40.65
ATOM	4982	C	GLY	643	66.694	12.747	19.571	1.00	43.53
ATOM	4983	0	GLY	643	67.500	13.666	19.688	1.00	41.10
MOTA	4984	N	LEU	644	65.617	12.825	18.786		48.35
MOTA	4986	CA	LEU	644	65.306	14.034	18.019	1.00	51.11
ATOM	4987	CB	LEU	644	63.962	13.907	17.314	1.00	50.28
ATOM	4988	CG	LEU	644	63.900	13.059	16.057	1.00	54.03
MOTA	4989	CD1	LEU	644	62.541	13.278	15.413	1.00	57.34
MOTA	4990	CD2	LEU	644	65.006	13.467	15.105	1.00	56.95
MOTA	4991	С	LEU	644	65.248	15.257	18.894	1.00	52.68
MOTA	4992	0	LEU	644	64.850	15.175	20.053	1.00	54.95
MOTA	4993	N	ALA	645	65629	16.399	18.332	1.00	54.61
MOTA	4995	CA	ALA	645	65.610	17.656	19.073	1.00	54.60
MOTA	4996	CB	ALA	645	66.495	18.684	18.382	1.00	53.32
MOTA	4997	C	ALA	645	64.178	18.185	19.215	1.00	54.09
MOTA	4998	0	ALA	645	63.716	18.488	20.322	1.00	53.14
MOTA	4999	N	ASP	652	52.340	21.795	14.895	1.00	91.33

ATOM	5001	CA	ASP	652	51.194	21.914	14.004	1.00 90.97
MOTA	5002	CB	ASP	652	51.650		12.555	
ATOM	5003			652	50.488		11.606	=
ATOM	5004		1 ASP	652	49.479	23.032	12.042	
ATOM	5005	OD:	2 ASP	652	50.586	22.075	10.414	1.00 94.81
ATOM	5006	C	ASP	652	50.352	20.652	14.103	1.00 90.61
ATOM	5007	0	ASP	652	50.645	19.641	13.463	1.00 91.26
ATOM	5008	N	TYR	653	49.289	20.737	14.895	1.00 89.65
MOTA	5010	CA	TYR	653	48.381	19.619	15.110	1.00 88.25
ATOM	5011	CB	TYR	653	47.306	20.003	16.133	1.00 88.16
ATOM	5012	CG	TYR	653	47.800	20.140	17.559	1.00 88.74
ATOM	5013	CD1	LTYR	653	47.047	20.818	18.513	1.00 90.00
ATOM	5014	CE	LTYR	653	47.477	20.915	19.839	1.00 90.70
ATOM	5015	CD2	YYR	653	49.006	19.559	17.964	1.00 89.14
ATOM	5016	CE2	TYR	653	49.443	19.649	19.280	1.00 89.49
ATOM	5017	CZ	TYR	653	48.675	20.325	20.214	1.00 89.80
ATOM	5018	OH	TYR	653	49.109	20.394	21.518	1.00 89.81
ATOM	5020	С	TYR	653	47.701	19.165	13.830	1.00 87.32
MOTA	5021	0	TYR	653	47.180	18.057	13.759	1 00 87.70
ATOM	5022	N	TYR	654	47.734	20.013	12.814	1.00 86.51
ATOM	5024	C'A	TYR	654	47.087	19.707	11.553	1.00 87.08
MOTA	5025	CB	TYR	654	46.387	20.959	11.028	1 00 88.45
MOTA	5026	CG	TYR	654	45.375	21.497	12.014	1.00 90.25
ATOM	5027	CD1		654	45.781	22.017	13.246	1.00 90.15
ATOM	5028	CE1	TYR	654	44.857	22.431	14.197	1.00 90.94
ATOM	5029	CD2	TYR	654	44.012	21.419	11.753	1.00 91.22
ATOM	5030	CE2	TYR	654	43.078	21.833	12.698	1.00 93.22
ATOM	5031	CZ	TYR	654	43.506	22.335	13.918	1.00 92.39
ATOM	5032	OH	TYR	654	42.588	22.717	14.872	1.00 94.38
ATOM	5034	C	TYR	654	48.C12	19.115	10.503	1.00 87.34
ATOM	5035	0	TYR	654	47.567	18.767	9.410	1.00 88.29
ATOM	5036	N	LYS	655	49.290	18.971	10.836	1.00 86.67
ATOM	5038	CA	LYS	655	50.233	18.406	9.887	1.00 87.62
ATOM	5039	CB	LYS	655	51.666	18.814	10.229	1.00 90.01
ATOM	5040	CG	LYS	655	52.688	18.252	9.251	1.00 95.23
ATOM	5041	CD	LYS	655	54.106	18.646	9.607	1.00 99.04
ATOM	5042	CE	LYS	655	55.108	17.832	8.789	1.00102.26
ATOM	5043	NZ	LYS	655	56.528	18.184	9.099	1.00104.44
ATOM	5047	C	LYS	655	50.102	16.890	9.896	1.00 87.61
ATOM	5048	0	LYS	655	50.233	16.259	10.945	1.00 87.58
ATOM	5049	N	LYS	656	49.787	16.319	8.737	1.00 87.88
ATOM	5051	CA	LYS	656	49.639	14.875	8.603	1.00 89.03
ATOM	5052	.CB	LYS	656	48.795	14.537	7.376	1.00 90.44
ATOM	5053	CG .	LYS	656	47.313	14.802	7.535	1.00 93.30
ATOM	5054	CD	LYS	656	46.590	14.599	6.213	1.00 96.87
MOTA	5055	CE	LYS	656	45.089	14.555	6.406	1.00 99.35
ATOM	5056	NZ	LYS	656	44.362	14.518	5.106	1.00102.42
ATOM	5060	С	LYS	656	51.004	14.206	8.487	1.00 88.57
ATOM	5061	0	LYS	656	51.915	14.749	7.855	1.00 88.38
ATOM	5062		GLY	660	49.270	10.021	5.735	1.00 61.58
ATOM	5064	CA	GLY	660	48.416	11.168	6.005	1.00 58.75
ATOM	5065	C	GLY	660	47.664	11.092	7.324	1.00 57.22

ATOM	5066	0	GLY	660	46.555	11.624	7.437	1.00	58.01
ATOM	5067	N	ARG	661	48.231	10.374	8.293	1.00	55.37
ATOM	5069	CA	ARG	661	47.631	10.247	9.622	1.00	51.19
MOTA	5070	CB	ARG	661	48.095	8.965	10.337	1.00	51.89
ATOM	5071	CG	ARG	661	47.756	7.663	9.612	1.00	51.56
MOTA	5072	CD	ARG	661	48.057	6.443	10.484	1.00	50.77
ATOM	5073	NE	ARG	661	47.834	5.181	9.772	1.00	50.04
ATOM	5075	CZ	ARG	661	48.015	3.974	10.307	1.00	48.12
ATOM	5076	NH1	ARG	661	48.421	3.855	11.569	1.00	43.28
MOTA	5079	NH2	ARG	661	47.788	2.882	9.578	1.00	43.69
ATOM	5082	C	ARG	661	48.041	11.463	10.446	1.00	46.22
ATOM	5083	0	ARG	661	48.998	12.162	10.097	1.00	44.78
MOTA	5084	N	LEU	662	47.328	11.703	11.542	1.00	41.80
ATOM	5086	CA	LEU	662	47.621	12.837	12.419	1.00	36.78
MOTA	5087	CB	LEU	662	46.342	13.596	12.758	1.00	33.05
ATOM	5088	CG	LEU	662	45.642	14.279	11.585	1.00	28.24
MOTA	5089	CD1	LEU	662	44.198	147.611	11.935	1.00	24.66
MOTA	5090	CD2	LEU	662	46.429	15.511	11.217	1.00	28.35
MOTA	5091	C	LEU	662	48.278	12.328	13.695	1.00	36.10
MOTA	5092	0	LEU	662	47.695	11.521	14.431	1.00	34.46
MOTA	5093	N	PRO	663	49.526	12.751	13.945	1.00	35.83
MOTA	5094	CD	PRO	663	50.360	13.537	13.022	1.00	37.72
MOTA	5095	CA	PRO	663	50.310	12.365	15.119	1.00	35.68
MOTA	5096	CB	PRO	663	51.611	13.130	14.914	1.00	35.23
MOTA	5097.	CG	PRO	663	51.756	13.134	13.437	1.00	36.10
MOTA	5098	C	PRO	663	49.660 .	12.703	16.453	1.00	35.87
ATOM	5099	0	PRO	663	49.958	12.069	17.469	1.00	39.86
MOTA	5100	N	VAL	664	48.787	13°. 705	16.466	1.00	33.54
MOTA	5102	CA	VAL	664	48.109	14.076	17.699	1.00	31.24
ATOM	5103	CB	VAL	664 ·	47.196	15.321	17.520	1.00	30.45
ATOM	5104		VAL	664	48.025	16.480	17.051	1.00	32.54
ATOM	5105	CG2	VAL	664	46.093	15.062	16.523	1.00	34.77
ATOM	5106	C		664	47.301	12.895	18.233	1.00	31.33
MOTA	5107	0	VAL	664	47.095	12.782	19.438	1.00	32.66
ATOM	5108	N	LYS	665	46.940	11.968	17.345	1.00	30.44
ATOM	5110	CA	LYS	665	46.153	10.795	17.719	1.00	28.43
MOTA	5111	CB	LYS	665	45.596	10.133	16.466	1.00	24.82
MOTA	5112	CG	LYS	665	44.700	11.080	15.687	1.00	27.50
MOTA	5113	CD	LYS	665	44.096	10.466	14.442	1.00	26.62
ATOM	5114	CE	LYS	665	42.967	11.326	13.909		21.64
ATOM	5115	NZ	LYS	665	42.479	10.850	12.584		25.29
ATOM	5119	C	LYS	665	46.889	9.794	18.615		29.56
MOTA	5120	0	LYS	665	46.295	8.836	19.095		29.57
MOTA	5121	N	TRP	666	48.183	10.020	18.826	1.00	30.12
MOTA	5123	CA	TRP	666	48.987	9.174	19.704		31.39
ATOM	5124	CB	TRP	666	50.329	8.845	19.059	1.00	30.40
MOTA	5125	CG	TRP	666	50.263	7.700	18.106		30.79
MOTA	5126	CD2	TRP	666	49.701	7.719	16.785		30.22
ATOM	5127	CE2	TRP	666	49.891	6.430	16.245		28.24
ATOM	5128		TRP	666	49.067	8.702	16.012		30.60
ATOM	5129		TRP	666	50.743	6.435	18.307		28.07
ATOM	5130	NE1	TRP	666	50.522	5.670	17.187	1.00	29.15

ATOM	5132		_	666	49.462	2 6.10°	7 14.954	1.00 29.38
ATOM	5133			666	48.640	8.374		
ATOM	5134		I2 TRP	666	48.845			
ATOM	5135		TRP	666	49.242			
ATOM	5136		TRP	666	49.591			
ATOM	5137		MET	667	49.028	3 11.214		
ATOM	5139		MET	667	49.260		_	
ATOM	5140	CB	MET	667	49.163			
ATOM	5141			667	50.510			
ATOM	5142		MET	667	50.358	15.906		
ATOM	5143		MET	667	50.914	15.810		
ATOM	5144	C	MET	667	48.389	11.839		
ATOM	5145	0	MET	667	47.186	11.646		
ATOM	5146	N	ALA	668	49.027		24.542	
ATOM	5148	CA	ALA	668	48.345	11.733	25.815	1.00 38.48
ATOM	5149	CB	ALA	668	49.351	11.537	26.929	1.00 37.61
ATOM	5150	C	ALA	668	47.603	13.038	26.014	1.00 37.61
ATOM	5151	О	ALA	668	48.059	14.090	25.566	1.00 39.40
ATOM	5152	N	PRO	669	46.474	13.001	26.731	1.00 42.22
ATOM	5153	CD	PRO	669	45.842	11.827	27.355	1.00 42.22
MOTA	5154	CA	PRO	669	45.677	14.204	26.980	1.00 43.91
ATOM	5155	CB	PRO	669	44.609	13.698	27.948	1.00 44.49
ATOM	5156	CG	PRO	669	44.421	12.279	27.499	1.00 43.59
ATOM	5157	С	PRO	669	46.476	15.372	27.570	1.00 44.89
ATOM	5158	Ö	PRO	669	.46.394	16.497	27.075	1.00 45.48
ATOM	5159	N	GLU	670	47.266	15.105	28.607	1.00 43.39
ATOM	5161	CA	GLU	670	48.050	16.158	29.244	1.00 42.97
ATOM	5162	CB	GLU	670	48.739	15.645	30.504	1.00 43.31
ATOM	5163	CG	GLU	670	49.864	14.646	30.252	1.00 44.78
ATOM	5164	CD	GLU	670	49.408	13.204	30.290	1.00 43.48
MOTA	5165	OE1	GLU	670	50.225	12.331	30.639	1.00 41.85
ATOM	5166	OE2	GLU	670	48.235	12.931	29.986	1.00 47.18
ATOM	5167	С	GLU	670	49.090	16.798	28.333	1.00 43.18
ATOM	5168	0	GLU	670	49.362	17.983	28.444	1.00 41.68
ATOM	5169	Ŋ	ALA	671	49.677	16.008	27.440	1.00 44.65
ATOM	5171	CA	ALA	671	50.686	16.512	26.513	1.00 44.44
ATOM	5172	CB	ALA	671	51.412	15.347	25.841	1.00 40.17
ATOM	5173	C	ALA	671	50.046	17.410	25.465	1.00 46.49
ATOM	5174	0	ALA	671	50.558	18.484	25.148	1.00 45.70
ATOM	5175	N	LEU	672	48.903	16.970	24.952	1.00 50.30
ATOM	5177	CA	LEU	672	48.163	17.702	23.925	1.00 52.07
MOTA	5178	CB	LEU	672	47.080	16.782	23.335	1.00 54.41
ATOM	5179	CG	LEU	672	46.388	17.103	22.005	1.00 57.12
ATOM	5180		LEU	672	47.404	17.316	20.912	1.00 57.65
ATOM	5181	CD2	LEU	672	45.459	15.951	21.640	1.00 56.14
ATOM	5182	C	LEU	672	47.535	18.964	24.512	1.00 52.42
ATOM	5183	0	LEU	672	47.683	20.058	23.969	1.00 52.42
ATOM	5184	N	PHE	673	46.863	18.803	25.645	1.00 52.71
ATOM	5186	CA	PHE	673	46.203	19.911	26.314	1.00 52.74
MOTA	5187	CB	PHE	673	44.995	19.394	27.104	1.00 54.32
MOTA	5188	CG	PHE	673	43.987	18.646	26.259	1.00 52.92
MOTA	5189	CD1	PHE	673	43.399	17.477	26.728	1.00 52.38
					_		720	2.00 33.49



ATOM	5190	CD2	PHE	673	43.624	19.109	24.999	1.00 5	1.61
MOTA	5191	CE1	PHE	673	42.468	16.779	25.957	1.00 50	0.49
MOTA	5192	CE2	PHE	673	42.698	18.420	24.229		0.91
MOTA	5193	CZ	PHE	673	42.118	17.250	24.710	1.00 50	0.09
ATOM	5194	C	PHE	673	47.138	20.732	27.220	1.00 56	5.29
ATOM	5195	0	PHE	673	47.289	21.938	27.026	1.00 58	3.05
MOTA	5196	N	ASP	674	47.808	20.076	28.165	1.00 56	5.38
ATOM	5198	CA	ASP	674	48.703	20.772	29.104	1.00 56	5.12
MOTA	5199	CB	ASP	674	48.644	20.101	30.485	1.00 5	3.81
ATOM	5200	CG	ASP	674	47.299	20.234	31.152	1.00 52	2.48
MOTA	5201	OD1	ASP	674	46.715	19.188	31.504	1.00 50	0.25
MOTA	5202	OD2	ASP	674	46.844	21.384	31.337	1.00 5	1.16
MOTA	5203	C	ASP	674	50.182	20.886	28.706	1.00 5	7.07
MOTA	5204	0	ASP	674	51.010	21.273	29.541	1.00 56	5.00
MOTA	5205	N	ARG	6 7 5	50.525	20.526	27.468	1.00 5	7.28
ATOM	5207	CA	ARG	675	51.915	20.576	26.995	1.00 59	5.64
MOTA	5208	CB	ARG	675	52341	22.020	26.692	1.00 58	3.95
MOTA	5209	CG	ARG	675	51.542	22.678	25.569	1.00 66	5.91
MOTA	5210	CD	ARG	675	52.082	24.066	25.202	1.00 72	2.90
MOTA	5211	NE	ARG	675	53.360	24.019	24.482	1.00 75	5.10
ATOM	5213	CZ	ARG	675	54.096	25.089	24.181	1.00 7	3.61
ATOM	5214	NH1	ARG	675	53.687	26.301	24.536	1.00 7	1.27
ATOM	5217	NH2	ARG	675	55.250	24.943	23.540	1.00 72	2.12
ATOM	5220	С	ARG	675	52.853	19.932	28,017	1.00 5	3.25
A'TOM	5221	O	ARG	675	53.988	20.366	28.211	1.00 52	2.13
MOTA	5222	N	ILE	676 .	52.359	18.883	28.664	1.00 53	1.44
MOTA	5224	CA	ILE	676	53.108	18.153	29.683	1.00 49	9.81
MOTA	5225	СВ	ILE	676	52.241	17.944	30.958	1.00 46	5.07
MOTA	5226	CG2	ILE	676	52.804	16.844	31.856	1.00 40	0.98
MOTA	5227	CG1	ILE	676	52.129	19.257	31.721	1.00 43	3.31
ATOM	5228	CD1	ILE	676 .	51.324	19.147	32.963	1.00 45	5.02.
MOTA	5229	C	ILE	676	53.572	16.800	29.144	1.00 5	1.20
MOTA	5230	0	ILE	676	52.770	15.892	28.951	1.00 52	2.37
MOTA	5231	N	TYR	677	54.865	16.675	28.890	1.00 52	2.81
ATOM	5233	CA	TYR	677	55.412	15.429	28.383	1.00 53	3.96
NTOM	5234	CB	TYR	677	56.296	15.700	27.167	1.00 5	7.26
MOTA	5235	CG	TYR	677	55.524	16.175	25.951	1.00 64	1.10
ATOM	5236	CD1	TYR	677	55.229	17.532	25.762	1.00 69	5.60
MOTA	5237	CE1	TYR	677	54.514	17.965	24.634	1.00 6	7.15
MOTA	5238	CD2	TYR	677	55.085	15.263	24.985	1.00 6	5.29
MOTA	5239	CE2	TYR	677	54.376	15.680	23.862	1.00 6	7.34
MOTA	5240	CZ	TYR	677	54.095	17.028	23.692	1.00 69	9.24
MOTA	5241	OH	TYR	677	53.399	17.414	22.573	1.00 73	3.55
MOTA	5243	С	TYR	677	56.192	14.713	29.482	1.00 52	2.30
MOTA	5244	0	TYR	677	57.053	15.309	30.124	1.00 5	3.73
ATOM	5245	N	THR	678	55.830	13.461	29.748	1.00 48	3.95
ATOM	5247	CA	THR	678	56.505	12.659	30.760	1.00 4	5.99
ATOM	5248	CB	THR	678	55.729	12.634	32.107	1.00 46	5.04
ATOM	5249	OG1	THR	678	54.663	11.676	32.046	1.00 49	9.79
ATOM	5251	CG2	THR	678	55.160	14.010	32.429	1.00 49	5.58
MOTA	5252	C	THR	678	56.656	11.221	30.261	1.00 43	3.81
MOTA	5253	0	THR	678	56.231	10.888	29.158	1.00 4	5.12

7.00								
ATOM				_	57.250	10.35	9 31.076	5 1.00 41.50
ATOM			A HIS		57.414	8.97		
ATOM			_		58.390	8.253		
ATOM	_				59.798	8.770		
ATOM			D2 HIS		60.456	9.690		
ATOM			D1 HIS		60.715	8.296		· · · —
ATOM			E1 HIS	679	61.880	8.892		
ATOM		3 N1	E2 HIS	679	61.747	9.742		
MOTA		5 C	HIS	679	56.068	8.279		
ATOM	5266	5 0	HIS	679	55.909	7.215		
MOTA	5267	7 N	GLN	680	55.108	8.863		
ATOM	5269	C C	GLN	680	53.773	8.290		
ATOM	5270) CE	GLN	680	53.021	8.705		
MOTA	5271	. CG	GLN	680	53.518	8.005		
ATOM	5272	CI	GLN	680	53.651	6.477		1.00 42.17
ATOM	5273	OE	1 GLN	680	52.686	5.737		1.00 43.35
MOTA	5274	NE	2 GLN	680	54.860	6.010	33.564	1.00 44.05
MOTA	5277	C	GLN	680	53.012	8.674	30.221	1.00 37.17 1.00 39.33
ATOM	5278		GLN	680	52.220	7.883	29.709	1.00 39.33
ATOM	5279		SER	681	53.299	9.854	29.673	1.00 38.00
ATOM	5281	CA	SER	681	52.636	10.251	28.441	1.00 37.44
MOTA	5282	CB	SER	681	52.963	11.698	28.078	1.00 37.44
MOTA	5283	OG	SER	681	54.349	11.937	28.102	1.00 37.67
MOTA.	5285	C	SER	681	53.095	9.278	27.356	1.00 38.03
ATOM	5286	0	SER	681	52.302	8.866	26.510	1.00 38.28
AT'OM	5287	N	ASP	682	54.362	8.866	27.431	1.00 36.81
ATOM	5289	CA	ASP	682	54.920	7.888	26.495	1.00 36.81
MOTA	5290	CB	ASP	682	56.404	7.655	26.765	1.00 37.18
ATOM	5291	CG	ASP	682	57.309	8.584	25.968	1.00 40.08
ATOM	5292		L ASP	682	58.528	8.317	25.959	1.00 41.94
. ATOM	5293		2 ASP	682	56.824	9.565	25.352	1.00 39.55
. ATOM	5294	C	ASP	682.	54.180	6.561	26.645	1.00 36.93
ATOM	5295	0	ASP	682	54.005	5.818	25.675	1.00 38.23
ATOM	5296	N	VAL	683	53.742	6.268	27.866	1.00 36.33
ATOM	5298	CA	VAL	683	53.000	5.040	28.143	1.00 36.29
MOTA	5299	CB	VAL	683	52.834	4.820	29.683	1.00 35.29
MOTA	5300		VAL	683	51.900	3.653	29.989	1.00 34.98
MOTA	5301		VAL	683	54.198	4.546	30.312	1.00 30.55
MOTA MOTA	5302	C	VAL	683	51.648	5.067	27.392	1.00 35.21
	5303	0	VAL	683	51.223	4.050	26.845	1.00 32.81
ATOM	5304	N	TRP	684	51.027	6.245	27.309	1.00 34.49
ATOM	5306	CA	TRP	684	49.759	6.412	26.602	1.00 36.39
MOTA	5307	CB	TRP	684	49.200	7.825	26.811	1.00 39.30
ATOM	5308	CG	TRP	684	48.006	8.174	25.947	1.00 41.47
ATOM ATOM	5309		TRP	684	46.651	8.381	26.384	1.00 42.41
	5310		TRP	684	45.896	8.744		1.00 41.76
ATOM	5311		TRP	684	46.004	8.298		1.00 42.06
ATOM	5312		TRP	684	48.010	8.410		1.00 40.55
ATOM	5313		TRP	684	46.749	8.756		1.00 42.32
ATOM	5315		TRP	684	44.522			1.00 41.35
ATOM	5316		TRP	684	44.638			1.00 41.99
ATOM	5317	CH2	TKP	684	43.917	8.933		1.00 41.07



MOTA	5318	С	TRP	684	49.964	6.125	25.115		36.12
MOTA	5319	0	TRP	684	49.152	5.410	24.511	1.00	38.69
ATOM	5320	N	SER	685	51.029	6.690	24.534	1.00	33.48
MOTA	5322	CA	SER	685	51.395	6.491	23.130	1.00	26.49
MOTA	5323	CB	SER	685	52.636	7.300	22.802	1.00	
MOTA	5324	OG	SER	685	52.403	8.688	22.992		30.31
MOTA	5326	С	SER	685	51.665	5.015	22.859	1.00	26.25
MOTA	5327	0	SER	685	51.377	4.510	21.782	1.00	28.78
ATOM	5328	N	PHE	686	52.214	4.319	23.846		28.14
MOTA	5330	CA	PHE	686	52.470	2.884	23.727		28.53
MOTA	5331	CB	PHE	686	53.245	2.399	24.947		27.34
ATOM	5332	CG	PHE	686	53.567	0.937	24.917		29.91
MOTA	5333	CD1	PHE	686	54.424	0.419	23.942	1.00	29.23
MOTA	5334	CD2	PHE	686	53.016	0.075	25.861	1.00	28.28
MOTA	5335	CE1	PHE	686	54.725	-0.936	23.908	1.00	
MOTA	5336	CE2	PHE	686	53.307	-1.274	25.840		27.18
MOTA	5337	CZ	PHE	686	54.166	-1.787	24.861		30.06
MOTA	5338	C	PHE	686	51.129	2.117	23.618	1.00	31.42
MOTA	5339	0	PHE	686	51.041	1.096	22.930	1.00	29.05
MOTA	5340	И	GLY	687	50.093	2.623	24.298		31.18
MOTA	5342	CA	GLY	687	48.783	2.000	24258		32.16
ATOM	5343 ⁻	C	GLY	687	48.276	2.026	22.825		35.0 <i>9</i>
MOTA	5344	0	GLY	687	47.805	1.011	22.289	1.00	36.38
MOTA	5345	7.i	VAL	688	48.378	3.188	22.186	1.00	33.72
MOTA	5347	CA	VAL	688	47.949	3.307	20.808	1.00	30.28
MOTA	5348	CB	VAL	688	47.996	4.761	20.322	1.00	28.62
MOTA.	5349	CG1	VAL	688	47.433	4.862	18.905	1.00	26.79
MOTA	5350	CG2	VAL	688	47.202	5.645	21.275		26.40
MOTA	5351	C	VAL	588	48.823	2.406	19.930		30.01
MOTA	5352	0	VAL	688	48.324	1.782	18.989		30.37
MOTA	5353	N	LEU	689	50.108	2.282	20.273		29.76
MOTA	5355	CA	LEU	689	51.022	1.418	19.510		29.37
MOTA	5356	CB	LEU	689	52.476	1.577	19.982		25.78
MOTA	5357	CG	LEU	689	53.564	0.944	19.097		23.00
MOTA	5358	CD1		689	54.855	1.741	19.153		24.44
MOTA	5359		LEU	689	53.823	-0.471	19.479		21.63
MOTA	5360	С	LEU	689	50.583	-0.043	19.634		29.98
MOTA	5361	0	LEU	689	50.708	-0.806	18.678	1.00	28.75
ATOM	5362	N	LEU	690	50.048	-0.409	20.803	1.00	32.38
ATOM	5364	CA	LEU	690	49.562	-1.764	21.060		32.66
ATOM	5365	CB	LEU	690	49.114	-1.929	22.517		32.33
ATOM	5366	CG	LEU	690	50.107	-2.192	23.658		32.00
ATOM	5367		LEU	690	49.330	-2.201	24.962		35.74
ATOM	5368		LEU	690	50.834	-3.513	23.475		30.76
ATOM	5369	C	LEU	690	48.369	-2.018	20.156		33.29
ATOM	5370	0	LEU	690	48.248	-3.079	19.550		35.08
MOTA	5371	N	TRP	691	47.490	-1.026	20.065		34.28
MOTA	5373	CA	TRP	691	46.304	-1.114	19.221		33.79
MOTA	5374	CB	TRP	691	45.483	0.172	19.364		32.68
MOTA	5375	CG	TRP	691	44.147	0.144	18.669		31.23
MOTA	5376	CD2		691	43.888	0.490	17.312		28.11
MOTA	5377	CE2	TRP	691	42.506	0.310	17.089	1.00	29.96





ATO		78	CE3 TR	P 691	44.68	6 0.94	9 16 25	
ATO			CD1 TR	P 691	42.93			
ATO			NE1 TR	P 691	41.95			
ATO			CZ2 TR		41.90			50.05
ATO		83 (CZ3 TR	P 691	44.09			
ATO	_	84 (CH2 TR	P 691	42.71			
OTA	- ·-	85 (TR		46.74			
ATO		B6 (TR	P 691	46.13			
ATO			J GL	J 692	47.81			
ATON			A GLU	J 692	48.35			
ATOM			B GLU	J 692	49.532			1.00 35.35
ATOM		91 C	G GLU	J 692	49.138			1.00 31.75
ATOM		-	D GLU		50.318			1.00 32.63
ATOM			E1 GLU		51.150			1.00 35.28
ATOM		4 0	E2 GLU	692	50.430		16.301	1.00 37.81
ATOM		5 C	GLU	692	48.810		14.237	1.00 34.85
ATOM		6 0	GLU		48.589		15.658	1.00 35.71
ATOM		7 N	ILE	693	49.439		14.544	1.00 37.26
MOTA			A ILE		49.944		16.610	1.00 35.05
MOTA			B ILE		50.843		16.396	1.00 35.00
ATOM	540	1 C	32 ILE	693	51.275	-6.064	17.575	1.00 35.88
ATOM	540		31 ILE	693	52.081	-3.711	17.400	1.00 36.03
ATOM	540	3 CI	ol ILE	693	52.814	-3.874	17.669	1.00 34.66
ATOM	5404	4 C	ILE	693	48.810	-5.153	18.943	1.00 35.52
ATOM	540		ILE	693	48.790	-5.943	16.232	1.00 34.29
ATOM	5406	2 N	PHE	694	47.837	-5.079	15.281	1.00 33.66
ATOM	5408			694	46.722	-5.999	17.127 17.082	1.00 34.44
ATOM	5409			694	46.156	-6.167	18.490	1.00 35.63
ATOM	5410			694 .	47.158	-6.787	19.428	1.00 35.26
ATOM	5411	_	1 PHE	694	47.796	-6.017	20.389	1.00 35.26
ATOM	5412		2 PHE	694	47.574	-8.111	19.237	1.00 33.07
ATOM	5413		1 PHE	694	48.837	-6.539	21.137	1.00 31.74
ATOM	5414			694	48.614	-8.643	19.982	1.00 31.01
ATOM	5415		PHE	694	49.254	-7.855	20.934	1.00 31.64
ATOM	5416		PHE	694	45.688	-5.771		1.00 31.84
ATOM	5417		PHE	694	44.844	-6.632		1.00 36.62
ATOM	5418	N	THR	695		-4.626		1.00 38.73
ATOM	5420	CA	THR	695	44.898	-4.331		1.00 35.76
MOTA	5421	CB	THR	695	44.245	-2.929		1.00 34.86 1.00 32.81
ATOM	5422		THR	695	45.246	_		1.00 32.81
ATOM	5424	CG2		695	43.497			1.00 31.61
ATOM	5425	С	THR	695	45.766			
ATOM	5426	0	THR	695	45.333			1.00 35.95
ATOM	5427	N	LEU	696	46.993			1.00 38.88
ATOM	5429	CA	LEU	696	47.979			.00 34.68
ATOM	5430	CB	LEU	696	47.622			.00 32.84
ATOM	5431	CG	LEU	696				00 32.65
ATOM	5432		LEU	696		_	L0.785 1	00 30.89
ATOM	5433		LEU	696				.00 31.30
ATOM	5434	C	LEU	696				.00 30.76
ATOM	5435	0	LEU	696		-3.931		.00 32.43
ATOM	5436	N	\mathtt{GLY}	697				.00 31.48
						, - 4		.00 33.65

MOTA	5438	CA	GLY	697	48.940	-1.529	11.188	1.00	32.78
MOTA	5439	C	GLY	697	47.742	-0.641	10.960	1.00	33.06
MOTA	5440	0	GLY	697	47.728	0.172	10.048	1.00	34.74
MOTA	5441	N	GLY	698	46.719	-0.798	11.782	1.00	35.53
MOTA	5443	CA	GLY	698	45.531	0.009	11.612	1.00	36.87
ATOM	5444	С	GLY	698	45.771	1.496	11.753	1.00	34.92
MOTA	5445	0	GLY	698	46.779	1.926	12.299	1.00	34.08
MOTA	5446	N	SER	699	44.814	2.271	11.265	1.00	36.45
MOTA	5448	CA	SER	699	44.858	3.725	11.318	1.00	35.36
ATOM	5449	CB	SER	699	44.363	4.290	9.995	1.00	34.58
MOTA	5450	OG	SER	699	44.126	5.684	10.087	1.00	41.43
MOTA	5452	C	SER	699	43.927	4.146	12.451	1.00	36.53
ATOM	5453	0	SER	699	42.734	3.812	12.438	1.00	37.58
MOTA	5454	И	PRO	700	44.471	4.799	13.491	1.00	36.03
MOTA	5455	CD	PRO	700	45.896	5.028	13.776	1.00	34.58
MOTA	5456	CA	PRO	700	43.630	5.228	14.611	1.00	35.47
ATOM	5457	CB	PRO	700	44.655	5.573	15.694	1.00	34.59
MOTA	5458	CG	PRO	700	45.840	5.990	14.919	1.00	34.18
MOTA	5459	C	PRO	700	42.742	6.411	14.247	1.00	34.66
ATOM	5460	0	PRO	700	43.194	7.363	13.616	1.00	34.39
MOTA	5461	N	TYR	701	41.462	6 293	.14.588	1.00	34.11
ATOM	5463	CA	TYR	701	40.459	7.324	14.338		33.11
ATOM	5464	CB	TYR .	701	40.713	8 548	15.225	1.00	38.13
MOTA	5465	CG	TYR	701	40.552	8.272	16.706	1.00	43.52
MOTA	5466	CD1	TYR	701	41.538	8.637	17.616	1.00	14.79
ATOM	546?	CE1	TYR	701	41.387	8.391	18.978	1.00	49.99
MOTA	5468	CD2	TYR	701 .	39.405	7.647	17.197	1.00	47.59
MOTA	5469	CE2	TYR	701	39.245	7.395	18.552		49.15
MOTA	5470	CZ	TYR	701	40.237	7.770	19.444	1.00	5C.84
ATOM	5471	OH	TYR	701	40.091	7.539	20.804	1.00	54.00
MOTA	5473	C	TYR	701	40.389	7.736	12.877	1.00	30.95
MOTA	5474	0	TYR	701	40.597	8.900	12.534	1.00	30.64
ATOM	5475	N	PRO	702	40.096	6.773	11.985	1.00	30.06
MOTA	5476	CD	PRO	702	39.887	5.336	12.192	1.00	25.47
ATOM	5477	CA	PRO	702	40.014	7.112	10.561	1.00	29.36
MOTA	5478	CB	PRO	702	39.836	5.744	9.899	1.00	25.86
MOTA	5479	CG	PRO	702	39.185	4.946	10.929		24.42
ATOM	5480	C	PRO	702	38.859	8.045	10.256		31.49
MOTA	5481	0	PRO	702	37.716	7.794	10.654	1.00	33.50
MOTA	5482	N	GLY	703	39.194	9.151	9.592		30.85
MOTA	5484	CA	GLY	703	38.210	10.149	9.212		27.67
MOTA	5485	С	GLY	703	37.985	11.230	10.250		27.39
MOTA	5486	0	GLY	703	37.270	12.194	9.981		26.56
ATOM	5487	N	VAL	704	38.627	11.100	11.412		27.05
ATOM	5489	CA	VAL	704	38.466	12.053	12.505		28.50
ATOM	5490	CB	VAL	704	38.576	11.364	13.876		28.95
ATOM	5491		VAL	704	38.509	12.397	14.990		29.36
ATOM	5492		VAL	704	37.475	10.338	14.045		29.64
MOTA	5493	С	VAL	704	39.473	13.194	12.493		30.95
MOTA	5494	0	VAL	704	40.669	12.977	12.661		32.90
MOTA	5495	N	PRO	705	39.001	14.428	12.269		31.09
MOTA	5496	CD	PRO	705	37.682	14.795	11.728	1.00	31.49

N COC								
ATC	_	197		RO 705	39.9	26 15.5	61 12.25	5 1 00 00 44
ATC		198		RO 705	39.1			
ATC		199		RO 705	37.7			30.10
ATO		00		RO 705	40.3			0.70
ATO		01		RO 705	39.6			
ATO	_	02		AL 706	41.3			,
ATO			CA V	AL 706	41.9			0
ATO				AL 706	43.02			
ATO			CG1 V	AL 706	43.68			
ATO			CG2 V	L 706	44.05		_ =	
ATO			C VA	L 706	40.97		· -	1.00 37.26
ATO	_		AV C	L 706	41.05		· · · ·	1.00 38.21
ATON		10 1	V GL	·Ū 707	40.06		_	1.00 37.65
MOTA			CA GL	U 707	39.04			1.00 40.27
ATOM			CB GL	U 707	38.18			1.00 40.57
ATOM		.4 (C GL	Ծ 707	38.16			1.00 40.56
ATOM		.5 () GL	U 707	37.87			1.00 41.60
ATOM		6 N	I GL	U 708	37.78			1.00 41.79
ATOM.		.8 C	A GL		36.94			1.00 42.54
MOTA		9 C	B GL		36509			1.00 44.09
ATOM		0 C	G GL		35.68			1.00 47.61
ATOM		1 C	D GL		34.511			1.00 50.42
ATOM			El GLU	J 708	33.856			1.00 55.51
ATOM	552.	3 0	E2 GLU		34.244			1.00 58.91
ATOM	552	4 C	GLU		37.661		_	1.00 60.06
ATOM	552	5 0	GLU		37.051			1.00 44.63
ATOM	5526		LEU		38.960			1.00 45.12
ATOM	5528		A LEU		39.768			1.00 43.72
ATOM	5529	C.E	3 LEU		41.212			1.00 39,85
MOTA	5530) C(LEU	709	42.037	14.243		1.00 34.99
ATOM	5531	. CI	1 LEU	709	41.619	13.359		1.00 31.80
ATOM	5532	CI	2 LEU	709	43.495	11.918 13.533	_	1.00 29.20
ATOM	5533	C	LEU	709	39.751		18.454	1.00 31.19
ATOM	5534	0	LEU	709	39.646	15.001	19.683	1.00 39.26
MOTA	5535	N	PHE	710	39.872	14.317	20.714	1.00 37.71
ATOM	5537	CA	PHE	710	39.862	16.327	19.691	1.00 38.62
MOTA	5538	CB	PHE	710	40.016	17.068	20.942	1.00 41.82
ATOM	5539	CG	PHE	710	41.383	18.567		1.00 42.02
ATOM	5540	CD:	l PHE	710	42.441	18.958		1.00 43.81
ATOM	5541	CD:	2 PHE	710	41.621	18.043		1.90 47.07
ATOM	5542		L PHE	710	43.716	20.234		1.00 42.91
ATOM	5543	CE	PHE	710	42.890	18.401		1.00 49.22
ATOM	5544	CZ	PHE	710	43.942	20.602		L.00 46.73
ATOM	5545	C	PHE	710	38.568	19.681		1.00 48.40
ATOM	5546	0	PHE	710	38.593	16.787		00 43.80
ATOM	5547	N	LYS	711		16.502	22.904 1	00 44.54
ATOM	5549	CA	LYS	711	37.452 36.148	16.790	20.968 1	.00 44.15
ATOM	5550	CB	LYS	711		16.539	21.569 1	.00 42.60
ATOM	5551	CG	LYS	711	35.029	16.855	20.577 1	.00 44.35
ATOM	5552	CD	LYS	711	33.661	16.781	21.200 1	.00 48.05
ATOM	5553	CE	LYS	711	32.560	17.205	20.263 1	.00 49.23
ATOM	5554	NZ	LYS	711	31.212	16.804	20.855 1	.00 50.61
			-		30.078	17.204	19.987 1	.00 56.56



MOTA	5558	C	LYS	711	36.045	15.105	22.084	1.00	41.50
ATOM	5559	0	LYS	711	35.589	14.875	23.202	1.00	41.06
ATOM	5560	N	LEU	712 .	36.489	14.144	21.282	1.00	41.61
MOTA	5562	CA	LEU	712	36.463	12.737	21.687	1.00	43.22
ATOM	5563	CB	LEU	712	37.070	11.841	20.600	1.00	41.69
ATOM	5564	CG	LEU	712	36.246	11.404	19.397	1.00	38.07
ATOM	5565	CD1	LEU	712	37.071	10°.460	18.527	1.00	34.55
ATOM	5566	CD2	LEU	712	34.990	10.714	19.891	1.00	37.28
ATOM	5567	С	LEU	712	37.253	12.536	22.982	1.00	43.94
ATOM	5568	0	LEU	712	36.804	11.832	23.900	1.00	41.71
ATOM	5569	N	LEU	713	38.444	13.129	23.029		45.26
ATOM	5571	CA	LEU	713	39.318	13.022	24.191	-	46.47
ATOM	5572	CB	LEU	713	40.647	13.728	23.925	1.00	46.32
ATOM	5573	CG	LEU	713	41.524	13.012	22.889	1.00	
ATOM	5574		LEU	713	42.853	13.737	22.734	1.00	39.96
ATOM	5575		LEU	713	41 758	11.571	23.328	1.00	
ATOM	5576	C ·	LEU	713	38.665	13.519	25.477		47.50
ATOM	5577	0	LEU	713	38.630	12.789	26.472	1.00	48.26
ATOM	5578	N	LYS	714	38.098	14.725	25.440	1.00	47.08
ATOM	5580	CA	LYS	714	37,41.9		26.600	1.00	45.59
ATOM	5581	CB	LYS	714	36.974	16.727.	26.293		47.53
ATOM	5582	CG	LYS	714		17.661	26.064		51.33
ATOM	5583	CD	LYS	714	37.647	19.044	25.689	1.00	59.12
ATOM	5584	CE	LYS	714	38.836	19.917	25.273	1.00	64.39
ATOM	5585	NZ	LYS	714	39.843	20.072	26.370	1.00	
ATOM	5589	C	LYS	714	36.217	14.476	27.056		44.19
ATOM	5590	Ō	LYS	714	35.895	14.447	28.244		43.04
ATOM	5591	N	GLU	715	35.565	13.805	26.112		43.89
ATOM	5593	CA	GLU	715	34.401	12.976	26.424		44.12
ATOM	5594	C.B	GLU	715	33.512	12.785	25.190		47.40
ATOM	5595	CG	GLU	715	32.860	14.053	24.623	1.00	52.31
ATOM	5596	CD	GLU	715	31.953	13.763	23.427	1.00	56.22
ATOM	5597	OE1		715	32.121	12.699	22.784	1.00	57.16
ATOM	5598	OE2	GLU	715	31.059	14.588	23.138		57.32
ATOM	5599	C	GLU	715	34.809	11.605	26.956		42.47
ATOM	5600	0	GLU	715	33.964	10.718	27.094		41.03
ATOM	5601	N	GLY	716	36.101	11.419	27.201	1.00	41.06
ATOM	5603	CA	GLY	716	36.593	10.150	27.718	1.00	41.58
ATOM	5604	C	GLY	716	36.548	8.985	26.739		41.60
ATOM	5605	o	GLY	716	36.640	7.816	27.141		38.34
ATOM	5606	N	HIS	717	36.469	9.303	25.450		42.80
ATOM	5608	CA	HIS	717	36.398	8.278	24.420		45.03
ATOM	5609	CB	HIS	717	36.082	8.894	23.052		46.28
ATOM	5610	CG	HIS	717	35.987	7.887	21.940		48.73
ATOM	5611		HIS	717	34.941	7.157	21.483		48.67
ATOM	5612		HIS	717	37.071	7.521	21.169		49.33
ATOM	5614		HIS	717	36.701	6.607	20.290		45.65
ATOM	5615		HIS	717	35.410	6.370	20.290		45.87
ATOM	5617	C	HIS	717	37.662	7.448	24.324		46.84
ATOM	5618	0	HIS	717	38.767		24.324		
			ARG			7.980			48.06
ATOM	5619	N CA		718	37.478	6.138	24.217		48.75
ATOM	5621	CA	ARG	718	38.573	5.181	24.091	1.00	49.16



ATC		522	CB A	RG 718	38.694 4.345 25.370 1.00 46 06
ATC		523	CG A	RG 718	39 000
ATO		524	CD A	RG 718	40 344 5 000
ATO		25	NE A	RG 718	40 724
ATO		27		RG 718	40 500 7 5-1
ATO		28	NH1 AF		40 004
ATO		31	NH2 AF	RG 718	41 025 2 555
ATO		34	C AR	RG 718	38 357 4 000
ATO		35	O AR		37 006 4 000
OTA	_	36	N ME		39 396 3 300
ATO		38	CA ME		39 006
ATON	M 56	39	CB ME		40 355 3 000
ATO		40	CG ME		40 740 4 200
ATOM	1 564	41 .	SD ME'		42 152
ATOM		12 (CE ME		42 48:
ATOM	1 564	13 (C ME		4.066 19.465 1.00 36.42
ATOM		4 () MET		38.649 1.671 21.312 1.00 51.07
ATOM		5 1			39.08/ 1.132 22.325 1.00 48.42
ATOM	564	7 (A ASE	. – •	37.797 1.096 20.462 1.00 53.92
. ATOM	564	8 0	B ASE		37.254 -0.253 20.648 1.00 55 90
ATOM	564	9 C	G ASF		30.221 -0.597 19.553 1.00 57.16
ATOM		0 0	D1 ASP		34.998 0.320 19.552 1.00 59.05
ATOM	565		D2 ASP		34.951 1.316 20.312 1.00 63.29
ATOM	565				34.0.74 0.042 18.758 1.00 54.85
ATOM	565	3 0			30.326 -1.343 20.638 1.00 55 89
ATOM	5654	4 N			39.397 -1.190 20.027 1.00 55.28
ATOM	5656	5 C		721	38.008 -2.450 21.304 1.00 56.09
ATOM	565	7 CI		721	38.892 -3.605 21.370 1.00 56.46
ATOM	5658	3 C		721	38.344 -4.606 22.378 1.00 58.16
MOTA	5659	CI		721	39.005 -5.977 22.316 1.00 62.49
ATOM	5660	CE		721	38.449 -6.873 23.401 1.00 66.40
ATOM	5661	N2		721	38.474 -8.329 22.995 1.00 68.27
MOTA	5665	C	LYS	721	38.107 -9.194 24.156 1.00 75.61
ATOM	5666	0	LYS	721	38.930 -4.241 19.985 1.00 56.00
ATOM	5667	N	PRO	722	37.884 -4.532 19.403 1.00 59.26
ATOM	5668	CD		722	40.133 -4.439 19.423 1.00 54.10
ATOM	5669	CA		722	11.461 -3.968 19.836 1.00 53.72
ATOM	5670	CB		722	40.208 -5.046 18.094 1.00 51.82
ATOM	5671	CG		722	41.702 -4.953 17.759 1.00 49.09
ATOM	5672	C	PRO	722	42.143 -3.768 18.501 1.00 49.06
ATOM	5673	0	PRO	722	39.765 -6.498 18.123 1.00 50.10
ATOM	5674	N	SER	723	39.678 -7.120 19.188 1.00 48.82
ATOM	5676	CA	SER	723	39.453 -7.020 16.945 1.00 49 87
ATOM	5677	CB	SER	723	39.079 -8.410 16.814 1.00 50.27
ATOM	5678	OG	SER	723	38.396 -8.643 15.473 1.00 48.56
ATOM	5680	C	SER	723	39.273 -8.323 14.404 1.00 48.93
ATOM	5681	Ō	SER	723	40.414 -9.144 16.872 1.00 51 33
ATOM	5682	N	ASN		12.400 -8.679 16.311 1.00 51.18
ATOM	5684	CA	ASN	724 724	40.445 ~10.284 17.551 1 00 54 65
ATOM	5685	CB	ASN	724	41.673 -11.062 17.706 1 00 56 76
ATOM	5686	CG	ASN	724	42.370 -11.286 16.359 1 00 59 06
ATOM	5687		ASN	724	41.698 -12.345 15.543 1 00 63 00
			WOIA.	724	41.645 -13.508 15.948 1.00 67.56

ATOM	5688	ND2	ASN	724	41.154	-11.960	14.403	1.00	60.12
ATOM	5691	С	ASN	724	42.622	-10.381	18.683	1.00	57.26
MOTA	5692	0	ASN	724	43.786	-10.131	18.383	1.00	58.40
ATOM	5693	N	CYS	725	42.089	-10.045	19.845	1.00	57.58
MOTA	5695	CA	CYS .	725	42.852	-9.418	20.908	1.00	57.02
MOTA	5696	CB	CYS	725	42.835	-7.885	20.803	1.00	55.65
ATOM	5697	SG	CYS	725	43.782	-7.034	22.119	1.00	52.17
ATOM	5698	С	CYS	725	42.158	-9.884	22.177	1.00	56.53
ATOM	5699	0	CYS	725	40.927	-9.954	22.240	.1.00	55.99
MOTA	5700	N	THR	726	42.957	-10.279	23.155	1.00	56.09
ATOM	5702	CA	THR	726	42.453	-10.773	24.423	1.00	57.09
ATOM	5703	CB	THR	726	43.551	-11.579	25.129	1.00	57.12
MOTA	5704	OG1	THR	726	44588	-10.696	25.562	1.00	59.14
ATOM	5706	CG2	THR	726	44.152	-12,587	24.154	1.00	55.09
ATOM	5707	C	THR	726	41.994	-9.608	25.288	1.00	57.58
ATOM	5708	0	THR	726	42.555	-8.518	25.195	1.00	58.49
ATOM	5709	N	ASN	727	40.979	-9.832	26.120	1.00	58.48
ATOM	5711	CA	ASN	727	40.482	-8.77.4	26.986	1.00	58.74
ATOM	5712	CB	ASN	727	39.331	-9.267	27.864	1.00	66.81
MOTA	5713	CG	ASN	727	39.674	-10.534	28.631	1.00	76.72
ATOM	5714	OD1	ASN	727	40.778	-10.689	29.161	1.00	80.48
MOTA	5715	ND2	ASN	727	38.716	-11.458	28.689	1.00	82.39
ATOM	5718	С	ASN	727 .	41.606	8.238	27.852	1.00	55.48
ATOM	5719	0	ASN	727	41.589	-7.080	28.255	1.00	51.24
MOTA	5720	N	GLU	728	42.589	-9.099	28.114	1.00	55.37
ATOM	5722	CA	GLU	728	43.757	-8.739	28.913	1.00	55.53
MOTA	5723	CB	GLU	728	44.611	-9.983	29.198	1.00	55.75
ATOM	5724	CG	GLU	728	45.881	-9.699	30.006	1.00	58.24
ATOM	5725	CD	GLU	728	46.606	-10.958	30.463	1.00	58.16
ATOM	5726	OE1	GLU	728	46.977	-11.796	29.611	1.00	56.39
ATOM	5727	OE2	GLU	728	46.816	-11.102	31.686	1.00	58.35
ATOM	5728	C	GLU	728	44.564	-7.685	28.153	1.00	54.11
ATOM	5729	O	GLU	728	44.790	-6.575	28.654	1.00	55.67
MOTA	5730	N	LEU	729	44.954	-8.020	26.926	1.00	49.65
MOTA	5732	CA	LEU	729	45.715	-7.106	26.086	1.00	46.10
ATOM	5733	CB	LEU	729	46.038	-7.766	24.742	1.00	39.77
MOTA	5734	CG	LEU	729	47.136	-8.836	24.848	1.00	36.12
ATOM	5735	CD1	LEU	729	47.118	-9.757	23.673	1.00	34.89
ATOM	5736	CD2	LEU	729	48.498	-8.193	24.987	1.00	33.47
MOTA	5737	С	LEU	729	44.950	-5.794	25.908	1.00	45.05
ATOM	5738	0	LEU	729	45.522	-4.713	26.019	1.00	45.58
ATOM	5739	N	TYR	730	43.640	-5.884	25.722	1.00	43.53
MOTA	5741	CA	TYR	730	42.831	-4.692	25.557	1.00	43.57
MOTA	5742	CB	TYR	730	41.414	-5.064	25.097	1.00	41.49
ATOM	5743	CG	TYR	730	40.492	-3.870	24.951	1.00	40.28
MOTA	5744	CD1	TYR	730	40.763	-2.865	24.013	1.00	36.86
ATOM	5745	CE1	TYR	730	39.937	-1.752	23.891	1.00	36.21
ATOM	5746	CD2	TYR	730	39.361	-3.730	25.768		39.44
ATOM	5747	CE2	TYR	730	38.522	-2.616	25.654	1.00	38.13
ATOM	5748	CZ	TYR	730	38.817	-1.632	24.712		38.79
ATOM	5749	ОН	TYR	730	37.974	-0.542	24.575		40.32
ATOM	5751	С	TYR	730	42.806	-3.866	26.856		44.45

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ATC	_	752	0	TYR	730	42.7	196 2				
ATO	_	753	N	MET	731	42.7				.00 43.	
AT(_	755	CA	MET	731	42.8			006 1	.00 46.	.44
ATO	_	756	CB	MET	731				279 1	.00 48.	
ATC)M 5	757	CG	MET	731	42.5		748 30.		.00 54.	
ATC	M 5	758	SD	MET	731	41.1		387 30.	398 1.	00 62.	
ATC		759	CE	MET	731	39.7		189 30.	392 1.	00 70.	49
ATO		760	C	MET	731	39.49			209 1.	00 72.	
ATO		61	0	MET	731	44.16				00 46.	
ATO		62	N	MET	732	44.28	-		86 1.	00 44.	
ATO	M 57	64	CA	MET	732	45.20			81 1.	00 43.8	
ATO		65	CB	MET	732	46.53			39 1.	00 43.0	
ATO	4 57	66	CG	MET	732	47.59			22 1.	00 39.4	44
ATON		67		MET	732	49.02			27 1.	00 36.0	02
ATON		68	_	MET	732	50.31			79 1.(
ATOM.		59		MET	732	50.54	_		30 1.(00 41.2	
ATOM		70	_	MET	732	46.47			98 1.0	00 42.0	9.
ATOM	577	71]	_	MET	733	46.99			59 1.0	0 42.1	.4
ATOM	577	73 (_	MET	733	45.77	_		54 1.0	0 43.1	4
ATOM	577	4 (/ET	733	45.608			57 1.0	0 42.2	4
MOTA	577	'5 (ÆT	733	44.852			17 1.0	0 41.4	
MOTA	577	6 5		ET	733	45.607		-	8 1.0	0 40.23	
ATOM	577	7 0		ET	733	44.669			9 1.0	0 38.02	
ATOM	577	8 C	M	ET	733	45.183	· -		2 1.0	0 28.12	
MOTA	577	9 0	M	EΤ	733	44.820			4 1.00	0 41.68	
MOTA	578	0 N		RG	734	45.215 43.713			6 2.00	0 43.78	
ATOM	5782	2 C.	A A	RG	734	42.893		_	5 1.00	42.59	
ATOM	5783	3 C:	B A	RG	734	41.642				42.92	<u>.</u>
ATOM	5784		G A	RG	734	40.753				42.35	
MOTA	5785) A	RG	734	40.360	-0.37			39.76	
ATOM	5786			RG	734	39.535	0.76 1.74			41.83	
ATOM	5788				734	38.207	1.69			45.36	
ATOM	5789		II AF		734	37.542	0.708			50.22	
MOTA	5792		12 AF	₹G	734	37.534	2.642	· - ·- ·		51.18	
ATOM	5795	_	AR	G '	734	43.719	1.385	-		53.24	
ATOM ATOM	5796		AR	.G '	734	43.610	2.571			42.42	
ATOM	5797		AS		735	44.591	0.544	-			
ATOM	5799	CA		-	735	45.464	0.959		_	41.40	
ATOM	5800	CB	AS		735	46.337	-0.194			43.33	
ATOM	5801	CG			35	45.556	-1.256		1.00	48.28	
ATOM	5802		l AS		35	45.903	-2.451		1.00	54.86	
ATOM	5803		2 AS		35	44.612	-0.900			53.49	
ATOM	5804	C	ASI		35	46.365	2.107	30.840	1.00	55.59	
ATOM	5805	0	ASI		35	46.484	3.124	31.543	1.00		
ATOM	5806	N	CYS		36	47.021	1.926	29.693	1.00	44.03	
ATOM	5808	CA	CYS		36	47.896	2.952	29.693	1.00		
ATOM	5809	CB	CYS		36	48.545	2.468	27.858	1.00	35.90	
ATOM	5810	SG	CYS		36	49.634	1.087	28.104	1.00	33.62	
ATOM ATOM	5811	C	CYS		36	47.100	4.208	28.104	1.00		
ATOM	5812	0	CYS		36	47.651	5.309	28.830	1.00 3		
ATOM	5813	N	TRP			45.793	4.039	28.668	1.00 3		
	5815	CA	TRP	73	7	44.906	5.156	28.372	1.00 3	8.02	
								-0.372	1.00 4	U.14	

ATOM	5816	CB	TRP	737	43.910	4.766	27.274	1.00 40.93
ATOM	5817	CG	TRP	737	44.563	4.379	25.977	1.00 42.36
MOTA	5818	CD2	TRP	737	44.018	3.518	24.969	1.00 43.84
MOTA	5819	CE2	TRP	737	44.972	3.437	23.929	1.00 46.42
MOTA	5820	CE3	TRP	737	42.817	2.806	24.845	1.00 42.43
MOTA	5821	CD1	TRP	737	45.793	4.775	25.519	1.00 42.57
ATOM	5822	NE1	TRP	737	46.043	4.214	24.292	1.00 44.22
MOTA	5824	CZ2	TRP	737	44.756	2.666	22.773	1.00 44.97
ATOM	5825	CZ3	TRP	737	42.606	2.042	23.699	1.00 40.74
ATOM	5826	CH2	TRP	737	43.571	1.978	22.682	1.00 40.75
MOTA	5827	C	TRP	737	44.157	5.706	29.584	1.00 40.62
ATOM	5828	0	TRP	737	43.085	6.285	29.437	1.00 41.37
ATOM	5829	N	HIS	738	44.706	5.533	30.783	1.00 42.09
ATOM	5831	C'A	HIS	738	44.044	6.059	31.966	1.00 43.78
ATOM	5832	CB	HIS	738	44.635	5.463	33.248	1.00 46.52
MOTA	5833	CG	HIS	738	43.878	5.844	34.486	1.00 52.24
ATOM	5834	C'D2	HIS	738	43.599	7.053	35.025	1.00 50.95
ATOM	5835	ND1	HIS	738	43.271	4 914	35.299	1.00 56.16
ATOM	5837	CEl	HIS	738	42.643	5.536	36.285	1.00 57.23
MOTA	5838	NE2	HIS	738	42.827	6.835	36.141	1.00 53.22
MOTA	5840	C.	HIS	738	44.183	7.57?	31.964	1.00 42.81
MOTA	5841	0	HIS	738	45.235	8.093	31.654	1.00 42.12
ATOM	5842	N	ALA	739 .	43.121	8.285	32.324	1.00 45.66
ATOM	5844	CA	ALA	739 .	43.130	9.750	32.350	1.00 49.42
MOTA	5845	CB	ALA	739	41.739	10.262	32.681	1.00 53.04
ATOM	5846	C	ALA	739	44.167	10.380	33.291	1.00 50.18
ATOM	5847	O	ALA	739 .	44.710	11.450	33.006	1.00 51.86
ATOM	5848	N	VAL	740	44.322	9.780	34.466	1.00 49.96
ATOM	5850	CA	VAL	740	45.299	10.219	35.467	1.00 50.17
ATOM	5851	CB	VAL	740	44.828	9.849	36.881	1.00 50.33
ATOM	5852	CG1	VAL	740	45.880	10.209	37.896	1.00 51.40
.ATOM	5853	CG2	VAL	740	43.534	10.559	37.193	1.00 50.86
ATOM	5854	C	VAL ·	740	46.626	9.497	35.196	1.00 49.81
ATOM	5855	0	VAL	740	46.749	8.295	35.472	1.00 49.85
ATOM	5856	N	PRO	741	47.646	10.230	34.713	1.00 47.92
ATOM	5857	CD	PRO	741	47.618	11.683	34.476	1.00 46.97
ATOM	5858	CA	PRO	741	48.968	9.686	34.393	1.00 46.47
ATOM	5859	CB	PRO	741	49.796	10.941	34.134	1.00 44.38
MOTA	5860	CG	PRO	741	48.800	11.877	33.561	1.00 44.86
ATOM	5861	C	PRO	741	49.593	8.815	35.480	1.00 47.21
ATOM	5862	0	PRO	741	50.243	7.816	35.176	1.00 46.77
MOTA	5863	N	SER	742	49.380	9.181	36.741	1.00 48.87
ATOM	5865	CA	SER	742	49.939	8.430	37.860	1.00 50.19
MOTA	5866	CB	SER	742	49.753	9.203	39.166	1.00 51.87
ATOM	5867	OG	SER	742	48.389	9.514	39.391	1.00 54.19
ATOM	5869	C	SER	742	49.331	7.040	38.010	1.00 51.30
MOTA	5870	0	SER	742	49.863	6.192	38.723	1.00 51.14
MOTA	5871	N	GLN	743	48.207	6.814	37.343	1.00 53.07
MOTA	5873	CA	GLN	743	47.531	5.531	37.414	1.00 53.50
ATOM	5874	CB	GLN	743	46.015	5.745	37.548	1.00 59.34
ATOM	5875	CG	GLN	743	45.412	5.307	38.898	1.00 66.19
MOTA	5876	CD	GLN	743	46.133	5.896	40.106	1.00 70.07



_											
		5877		GLN	743	46.	750				
		5878	NE2	~	743	46.	_	.170	40.885	1.00	73.86
		5881	C		743	46.0		.209	40.273	1.00	72.01
		5882	0		743	47.8		.613	36.236	1.00	51.14
		5883			744	47.5		.425	36.266	1.00	51.79
AI	OM 9	885			744	48.4		.153	35.196	1 00	48.31
ΤA	'OM g	8886				48.8		343	34.027	1 00	45.49
		887			744	49.3	26 5.	224	32.869	1.00	45.49
AT	OM 5	888		-	744	48.3		200	32.324	1 00	40.33
AT	OM 5	889			44	48.9	44 7.	100	31.262	1.00	36.32
AT		891		·-	44	48.0	50 8.	203	30.961	1.00	28.55
ATO		892	NH1 A	- ·	44	48.42		409	30.547	1.00	28.86
ATO		895	MILL W	-~	44	49.70		700	30.357	1.00	30.58
ATO		398	NH2 A		44	47.51	6 10.	354	30.386	1.00 2	26.02
ATC		399			44	50.01		154		1.00 3	0.62
ATC		900			14	50.79			34.452	1.00 4	7.35
ATO		901			15	50.13			35.334	1.00 5	2.01
ATO			CD PI		15	49.24			33.869	1.00 4	6.36
ATO		02	CA P		5	51.26	•		32.921	1.00 4	5.54
ATO		03	CB PF	20 74	5	50.97	_		34.271	1.00 4	3.41
ATO			CG PR	-	5	50.15			33.547	1.00 4	1.77
ATO			C PR		5	52.590			32.354	1.00 4:	2.26
			O PR	0 74	5	52.621			33.822	1.00 40	0.30
ATON			N TH	R 74	6	53.679			32.990 j	1.00 39	7.73
ATON			CA TH			54.997			4.433	1.00 39	.14
ATOM			CB TH	₹ 746		55.992			4.039 1	00 38	.35
ATOM			G1 TH	746		55.992	-		5.249 1	00 36	. 75
ATOM		.3 (G2 THE			56.202			5.769 <u>1</u>	.00 32	. 25
ATOM		.4 (THE			55.477			6.341 1	.00 30	31
ATOM			THE			55.568			2.987 1	.00 37	90
ATOM	591	6 N	PHE			55.185	-0.06		2.938 1	.00 37	90
ATOM	591	8 C	A PHE			56.490	1.58			.00 35	94
ATOM	591	9 C				57.106	0.71	6 31		.00 35.	00
ATOM	592	0 C		747		58.124	1.469	9 30		.00 30.	45
ATOM	592	L CI	D1 PHE	747		57.512	2.174	1 29		00 27.	40
ATOM	5922	CI	D2 PHE			56.950	1.450			00 27.	ρT
ATOM	5923		E1 PHE	747		57.468	3.558			00 23.	68
ATOM	5924	CF	2 PHE	747		56.352	2.088			00 27.	97
ATOM	5925			747		56.869	4.209			00 23.	56
ATOM	5926		PHE	747		56.312	3.470			00 26.	92
ATOM	5927		PHE	747		57.766	-0.477			00 26.2	21
ATOM	5928	N		747		57.920	-1.525			00 36.3	37
ATOM	5930	CA	LYS	748		58.177	-0.312			00 37.1	.1
ATOM	5931	CB		748		58.797	-1.411			00 39.6	8
ATOM	5932		LYS	748			-0.895			00 42.2	0
ATOM	5933	CG	LYS	748			-1.991		095 1.0	0 46.1	7
ATOM	5934	CD	LYS	748			-1.428		984 1.0	0 54.7	8
ATOM		CE	LYS	748		- -		37.		0 58.5	3
ATOM	5935	NZ	LYS	748			-2.537	38.		0 59.3	3
ATOM	5939	C	LYS	748		_	-2.025	39.	120 1.0	0 62.3	5
	5940	0	LYS	748			-2.463	34.	111 1.0	0 42.78	3
ATOM	5941	N	GLN	749			-3.664	34.0	075 1.0	0 37.97	7
ATOM	5943	CA	GLN	749			1.992	34.3	392 1.0	0 43.27	,
ATOM	5944	CB	GLN	749			2.866	34.6	71 1.00	43.39)
				•		~	2.056	35.1	46 1.00	47.37	
										,	

ATOM	5945	CG	GLN	749	54.236	-1.504	36.569	1.00 51.86
MOTA	5946	CD	GLN	749	53.036	-0.639	36.938	1.00 54.76
MOTA	5947	OE1	GLN	749	53.181	0.504	37.350	1.00 58.36
MOTA	5948	NE2	GLN	749	51.846	-1.179	36.769	1.00 59.25
MOTA	5951	C	GLN	749	55.006	-3.607	33.389	1.00 41.66
MOTA	5952	0	GLN	749	54.978	-4.841	33.355	1.00 40.25
MOTA	5953	N	LEU	750	54.759	-2.843	32.327	1.00 41.47
MOTA	5955	CA	LEU	750	54.398	-3.387	31.018	1.00 40.00
MOTA	5956	CB	LEU	750	54.366	-2.279	29.966	1.00 40.55
MOTA	5957	CG	LEU	750	53.316	-1.174	30.112	1.00 39.94
MOTA	5958	CD1	LEU	750	53.714	0.019	29.257	1.00 41.03
MOTA	5959	CD2	LEU	750	51.952	-1.696	29.722	1.00 37.80
MOTA	5960	С	LEU	750	55.383	-4.452	30.581	1.00 39.61
MOTA	5961	0	LEU	750	54.990	-5.470	30.027	1.00 42.08
MOTA	5962	N	VAL	751	56.670	-4.207	30.804	1.00 40.63
ATOM	5964	CA	VAL	751	57.691	-5.177	30.422	1.00 39.65
MOTA	5965	CB	VAL	751	59.115	-4.639	30.677	1.00 33.44
ATOM	5966	CG1	VAL	751	60.142	-5.694	30.351	1.00 31.57
ATOM	5967	CG2	VAL	751	59.372	-3.433	29.825	1.00 25.19
ATOM	5968	C	VAL	751	57.458	-6.468	31.204	1.00 43.58
MOTA	5969	0	VAL	751	57.530	-7.563	30.646	1.00 44.81
ATOM	5970	N	GLU	752	57.116	6.339	32.481	1.00 46.24
MOTA	5972	CA	GLU	752	56.869	-7.518	33.301	1.00 50.55
ATOM	5973	CB	GLU	752	56.781	-7.137	34.783	1.00 53.70
ATOM	5974	CG	GLU	752	58.090	-6.541	35.310	1.00 56.60
ATOM	5975	CD	GLU	752	58.079	-6.243	36.792	1.00 56.20
ATOM	5976	OE1	GLU	752	58.387	-5.092	37.178	1.00 53.45
ATOM	5977	OE2	GLU	752	57.789	-7.170	37.573	1.00 60.28
ATOM	5978	C	GLU	752	55.622	-8.275	32.837	1.00 50.90
ATOM	5979	0	GLU	752	55.689	-9.474	32.555	1.00 51.03
MOTA	5980	N	ASP	753	54.501	-7.570	32.708	1.00 51.12
ATOM	5982	CA	ASP	753	53.251	-8.184	32.265	1.00 48.76
ATOM	5983	CB	ASP	753	52.122	-7.160	32.249	1.00 51.11
ATOM	5984	CG	ASP	75.3	51.646	-6.805	33.636	1.00 54.97
ATOM	5985	OD1	ASP	753	51.592	·-7.715	34.495	1.00 58.37
ATOM	5986	OD2	ASP	753	51.319	-5.618	33.864	1.00 56.38
ATOM	5987	C	ASP	753	53.381	-8.790	30.881	1.00 48.02
ATOM	5988	0	ASP	753	52.991	-9.935	30.672	1.00 48.32
MOTA	,5989	N	LEU	754	53.925	-8.020	29.940	1.00 45.16
ATOM	5991	CA	LEU	754	54.111	-8.490	28.571	1.00 44.82
MOTA	5992	CB	LEU	754	54.696	-7.387	27.691	1.00 42.70
ATOM	5993	CG	LEU	754	53.736	-6.263	27.298	1.00 42.92
ATOM	5994	CD1	LEU-	754	54.500	-5.236	26.495	1.00 41.44
ATOM	5995	CD2	LEU	754	52.537	-6.822	26.502	1.00 42.86
ATOM	5996	С	LEU	754	55.001	-9.716	28.529	1.00 46.00
ATOM	5997	0	LEU	754	54.815	-10.606	27.708	1.00 45.88
ATOM	5998	N	ASP	755	55.975	-9.752	29.424	1.00 47.37
ATOM	6000	CA	ASP	755		-10.873	29.516	1.00 48.88
ATOM	6001	СВ	ASP	755		-10.584	30.628	1.00 49.89
MOTA	6002	CG	ASP	755	58.998	-11.616	30.717	1.00 51.73
ATOM	6003		ASP	755		-11.680	31.785	1.00 55.47
ATOM	6004		ASP	755		-12.354	29.738	1.00 50.98
		-		=				



7.00	0 14	_			
AT		005	C A	SP 755	56.024 -12.093 29.864 1 00 51 26
AT(O A	SP 755	56 021 12 100
ATO			N A	RG 756	55 227 71 81-
ATO	_		CA A	RG 756	54 333 10 11 11 11 11 11 11 11 11 11 11 11 11
ATO			CB AI	RG 756	53 556 13 504
ATC		11 (CG AI	RG 756	52 300 13 300
ATC		12 (CD AF	RG 756	52.389 -13.380 33.029 1.00 54.26
ATC		13 1	VE AF		51.672 -12.772 34.215 1.00 56.76
ATO		15 (ZZ AR		51.293 -11.382 33.969 1.00 61.39
ATO		16 N	JH1 AR	G 756	50.259 -11.002 33.221 1.00 62.60
ATO	M 60:		IH2 AR	_	10.007 -11.909 32.642 1.00 61.18
ATO	M 602	22 C	. AR		53.586 "9.711 33.064 1.00 63.72
ATO	M 602	23 C	AR		53.337 =13.420 30.297 1.00 53.03
ATO		24 N			53.243 -14.607 30.000 1.00 54.82
ATO	M 602	6 C	A IL		52.687 -12.452 29.680 1.00 51.18
MOTA	√I 602	7 C		. • ,	51.709 -12.732 28.630 1.00 48.68
ATON		8 C	G2 ILI		31.025 -11.435 28.120 1 00 47 00
ATOM	4 602	9 C	G1 ILE		30.112 -11.752 26.953 1 00 45 56
ATOM	1 603	0 CI	O1 ILE		30.247 -10.763 29.258 1.00 47 77
ATOM	1 603		ILE		9.414 28.914 1 00 46 00
ATOM	603	2 0	ILE	. • .	32.314 - 13.482 27.449 1 00.49 30
ATOM		3 N	VAL		31.834 ~14.409 26.937 1 00 45 61
ATOM	603	5 CA			33,523 -13.094 27.038 1 00 48 88
ATOM	6036				34.202 -1.3.734 25.912 1 00 40 00
ATOM	6037		1 VAL		33.602 -13 101 25.615 1 20 47 20
ATOM	6038		2 VAL	758	56.313 -13.864 24.502 1 00 44 77
MOTA	6039		VAL	758	33.461 -11.660 25.188 1 00 45 cc
ATOM	6040		VAL	758 758	34.378 -15.217 26.196 1 00 54 00
ATOM	6041		ÄLA	759	34.210 -16.050 25.306 7 20 52 52
ATOM	6043	CA	ALA	759 .	34.09/ -15.540 27.445 1 CO 57 CD
ATOM	6044	CB	ALA	759	34.038 -16.926 27.844 1 00 51 04
ATOM	6045	С	ALA	759	33.44/~16.987 29.257 7.00.62 30
ATOM	6046	0	ALA	759	33.392 -17.702 27.761 1 00 65 00
MOTA	6047	N	LEU	760	33.335 -18.823 27.254 1 00 66 30
MOTA	6049	CA	LEU	760	32.319 -17.090 28.248 1 00 66 00
ATOM	6050	СВ	LEU	760	31.209 .17.720 28.246 1 00 69 70
ATOM	6051	CG	LEU	760	30.314 -17.090 29.320 3 00 68 07
ATOM	6052		LEU	760	30.729 ~17.330 30.777 1.00 67.01
ATOM	6053		LEU	760	**************************************
ATOM	6054	C		760	30.701 -18.819 31.083 1 00 65 17
ATOM	6055	0	LEU	760	30.310 -1/.666 26.892 1 00 71 10
ATOM	6056	N	THR	761	49.342 -18.039 26.787 1 00 72 15
ATOM	6058	CA	THR		31.210 -17.201 25.860 1 00 73 70
ATOM	6059	СВ	THR	761 761	30.626 -17.113 24.518 1 00 73 00
ATOM	6060	OG1		761 761	30.963 -15.760 23.829 1 00 72 65
ATOM	6062	CG2		761 761	50.353 -14.690 24.555 1 00 74 44
ATOM	6063	C	THR	761	50.435 -15.731 22.420 1 00 70 32
ATOM	6064	0	THR	761 761	51.080 -18.276 23.636 1 00 74 66
ATOM	6065			761	52.276 -18.520 23.463 1.00 75.00
ATOM	6066		CYS MET	1603	19.100 -9.073 19.903 0 50 30 04 777
ATOM	6067	_		534	69.385 12.295 23.393 0.50 33.64 PRT2
ATOM	6068		MET MET	534	69.112 13.312 24.832 0.50 34.44 ppm
	200	. ند	MET	534	70.067 12.429 26.060 0.50 36.92 PRT2
					5.30 30.32 PRT2

ATOM	6069	SG CYS	603	56.370	-7.959	16.451	0.50	41.20	PRT2
MOTA	2716	OH2 TIP3	1	71.864	25.128	2.721		26.20	
ATOM	2719	OH2 TIP3	2	39.862	4.160	16.115	1.00	42.43	
ATOM	2722	OH2 TIP3	3	83.875	19.969	10.572		23.41	
MOTA	2725	OH2 TIP3	4	83.585	20.356	7.953	1.00	30.15	
MOTA	2728	OH2 TIP3	5	75.100	16.407	6.948	1.00	46.78	
MOTA	2731	OH2 TIP3	6	86.616	19.701	9.707	1.00	44.37	
MOTA	2734	OH2 TIP3	7	52.270	10.726	24.472	1.00	40.13	
MOTA	2737	OH2 TIP3	8	55.346	9.394	22.489	1.00	29.09	
MOTA	2740	OH2 TIP3	9	56.794	4.380	32.527	1.00	28.02	
MOTA	2743	OH2 TIP3	10	52.425	4.653	13.421	1.00	18.63	
MOTA	2746	OH2 TIP3	11	41.527	5.347	22.682	1.00	32.60	
MOTA	2749	OH2 TIP3	12	44.868	9.058	21.659	1.00	34.90	
ATOM	2752	OH2 TIP3	13	64.548	-2.881	29.048	1.00	32.56	
MOTA	2755	OH2 TIP3	14	. 77.179	13.205	23.892	1.00	30.36	
MOTA	2758	OH2 TIP3	1.5	79.309	16.826	18.132	1.00	55.69	
ATOM	2761	OH2 TĮP3	16	83.279	11.681	16.069	1.00	21.18	
MOTA	2764	OH2 TIP3	17	13.978	-9.614	0.374	1.00	23.81	
MOTA	2767	OH2 TIP3	18	38.294	0.616	5.237	1.00	48.89	
MOTA	2770	OH2 TIP3	19	27.114	6.248	5.051	1.00	19.82	
MOTA	2773	OH2 TIP3	20	34.369	-1.759	16.798	1.00	43.83	
MOTA	2776	OH2 TIP3	21	20.500	2.296	28.237	1.00	53.46	
MOTA	2779	OH2 TIP3	22	50.938	-11.733	38.257	1.00	51.73	
ATOM	2782	OH2 TIP3	23	17.066	-5.917	-2.027	1.00	29.88	
MOTA	2785	OH2 TIP3	24	27.873	8.078	15.136	1.00	46.40	
ATOM	2788	OH2 TIP3	25	31.459	0.037	6.873	1.00	33.38	
ATOM	2791	OH2 TIP3	26	27.088	-12.845	27.724	1.00	37.01	
MOTA	2794	OH2 TIP3	27	28.577	-17.329	12.884	1.00	37.31	
MOTA	2797	OH2 TIP3	28	88.863	14.111	8.054	1.00	41.25	
MOTA	2800	OH2 TIP3	29	2.311	-3.712	11.489		30.72	
MOTA	2803	OH2 TIP3	30	34.895	.4.269	18.658		28.99	
MOTA	2806	OH2 TIP3	31	80.531	18.007	9.739		23.83	
MOTA	2809	OH2 TIP3	32		3.787	10.628		20.39	
ATOM	2812	OH2 TIP3	33	-10.523	5.304	11.469		20.31	
ATOM	2815	OH2 TIP3	34	29.538	-8.848	20.187		43.26	
MOTA	2818	OH2 TIP3	35	5.866	3.469	13.367		21.16	
MOTA	2821	OH2 TIP3	36	31.810	3.038	0.203		65.03	
MOTA	2824	OH2 TIP3	37	19.879	2.087	-3.828		34.62	
MOTA	2827	OH2 TIP3	38	61.882	2.577	32.790		43.01	
ATOM	2830	OH2 TIP3	39	21.062	-6.897	-4.255		26.18	
ATOM	2833	OH2 TIP3	40	-15.562	8.847	22.744		40.33	
ATOM	2836	OH2 TIP3	41	40.043	2.380	8.610		65.14	
ATOM	2839	OH2 TIP3	42	19.176	11.322	0.332		33.04	
MOTA	2842	OH2 TIP3	43	67.221	8.965	17.535		14.78	
MOTA	2845	OH2 TIP3	44	87.877	18.828	18.789		50.00	
ATOM	2848	OH2 TIP3	45	74.676	17.083	4.253		43.45	
MOTA	2851	OH2 TIP3	46	29.458	16.709	10.527		37.44	
ATOM	2854	OH2 TIP3	47	66.590	7.242	15.359		27.63	
MOTA	2857	OH2 TIP3	48	85.038	21.651	5.881		27.12	
MOTA	2860	OH2 TIP3	49	-4.762	3.091	3.313		13.83	
ATOM	2863	OH2 TIP3	50	19.509	4.951	5.063		33.74	
ATOM	2866	OH2 TIP3	51	34.833	5.465	24.635	1.00	32.77	



AT		69	OH2 T		34.907 -17.187 13.739 1 00 30 47
ATO			OH2 T		60 000 7 550
ATO			OH2 T	IP3 54	7.368 27.982 1.00 31.38
ATO		78	OH2 T	IP3 55	55 219 12 165
ATO			OH2 T	IP3 56	68 507 6 25.430 1.00 40.99
ATC		84	ОН2 Т	IP3 57	73 496 22 25 1.00 45.39
ATC			ОН2 Т		73.400 20.957 19.260 1.00 49 23
ATO				P3 59	30.070 -8.367 -8.166 1.00 20.02
ATO		3		P3 60	38.079 10.933 5.669 1.00 27.07
ATO		6	ОН2 ТІ	P3 61	10.617 -9.690 -1.649 1.00 44.28
ATO	M 289		OH2 TI	_	1.501 12.262 1.00 42.78
ATO		2 (OH2 TI		3.969 28.834 1 00 37 60
IOTA	M 290		OH2 TI		10.52.3 -13.468 0.864 1.00 45 10
OTA	M 290		DH2 TI		1.001 -4.658 21.574 1.00 35 50
ATON	M 291		H2 TI		30.278 16.435 13.217 1.00 48 75
ATOM	1 291		H2 TI		3.317 1.00 16 04
ATOM.	1 291		H2 TI		73.400 18.707 22.744 1.00 34 79
ATOM	í 2920		H2 TI		3.041 -3.332 24.939 1.00 44 96
ATOM	1 2923	3 0	H2 TI	23 70	28.739 1 00 52 20
ATOM	2926		H2 TIP		21.770 "20.943 4.990 1.00 32 ag
ATOM	2929		H2 TIF	_	55.567 -6.482 5.018 1 00 37 70
ATOM			H2 TIP		16.676 13.158 -3.023 1.00 42 74
ATOM	2935		H2 TIP	_	-15.177 7.529 4.524 1 00 10 20
ATOM			H2 TIP	_	33.105 2.738 13.267 1.00 40 43
ATOM			12 TIP	_	0.334 -2.795 10 999 1 00 22 22
ATOM			E2 TIP	_	17.489 2.568 5.445 1.00 16.30
ATOM	2947		2 TIP		27.373 3.870 6.168 1.00 30 50
ATOM	2950	ОН		_	-8.546 6.378 9.673 1.00 17.89
ATOM	2953	ОН			1.508 -1.891 8.809 1.00 33 71
ATOM	2956	ОН			4·305 -3.024 6.965 1.00 30 cm
ATOM	2959	ОН	-		17.673 3.029 1.736 1.00 22 72
ATOM	2962		2 TIP3		20.319 3.536 2.883 1.00 20 20
ATOM	2965		2 TIP3		0.366 -2.419 22 243 1 00 22 15
ATOM	2968	OH			19.688 -6.134 -1.678 1 00 13 33
ATOM	2971		2 TIP3		10.581 -15.481 6.681 1 00 42 14
ATOM	2974		TIP3		4.476 -12.368 11.861 1 00 30 30
ATOM	2977		TIP3		6.421 1.053 -3.368 1.00 21.50
ATOM	2980		TIP3	88	-13.766 1.683 5.565 1.00 30 45
ATOM	2983		TIP3	89	13.089 -7.291 -0.140 1 00 30 37
ATOM	2986		TIP3	90	-1.762 -5.389 3 937 1 00 25
ATOM	2989		TIP3	91	12.642 5.184 -4.424 1 00 37 04
ATOM	2992		TIP3	92	69.601 27.513 2.309 1.00 44.55
ATOM	2995		TIP3	93	24.342 -13.465 -0.010 1.00 50.74
ATOM	2998			94	60.354 -4.675 33.978 1.00 30.74
ATOM	3001		TIP3	95	10.408 5.632 3.428 1.00 51.37
ATOM		OHZ	TIP3	96	-9.676 -3.916 4.621 1.00 34.12
ATOM			TIP3	97	73 207 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
ATOM			TIP3	98	-3 043 5 13-
ATOM	3010	OH2	TIP3	99	36 627 0 200
ATOM			TIP3	100	21 605 6 5 1.00 41.40
ATOM			TIP3	101	31 434 0 20.93
ATOM			TIP3	102	5 703
-11011	3022	UH2	TIP3	103	-13 037 0 1-1
					13.037 8.412 17.695 1.00 25.61

ATOM	3025	OH2 TIP3	104	26.597	-10.647	-1.184	1.00	25.85
MOTA	3028	OH2 TIP3	105	24.406	1.951	18.037	1.00	30.72
ATOM	3031	OH2 TIP3	106	-1.809	12.914	3.754	1.00	43.57
MOTA	3034	OH2 TIP3	107	59.590	13.738	33.131	1.00	26.96
MOTA	3037	OH2 TIP3	108	4.442	-11.011	1.724	1.00	46.96
MOTA	3040	OH2 TIP3	109	8.101	2.869	0.801	1.00	37.28
MOTA	3043	OH2 TIP3	110	76.065	1.631	26.158	1.00	46.49
ATOM	3046	OH2 TIP3	111	48.821	15.839	14.239	1.00	34.18
ATOM	3049	OH2 TIP3	112	2.703	-11.324	8.959	1.00	39.16
ATOM	3052	OH2 TIP3	113	82.922	26.478	12.953	1.00	43.77
ATOM	3055	OH2 TIP3	114	8.998	-6.359	-3.309	1.00	39.51
ATOM	3058	OH2 TIP3	115	-8.590	4.563	4.397	1.00	32.53
ATOM	3061	OH2 TIP3	116	8.115	-1.3.800	8.351	1.00	41.64
ATOM	3064	OH2 TIP3	117	51.643	6.187	10.821	1.00	31.70
MOTA	3067	OH2 TIP3	118	20.737	3.915	15.522	1.00	17.40
ATOM	3070	OH2 TIP3	119	73.254	3.698	20.947	1.00	27.49
ATOM	3073	OH2 TIP3	120	5.343	-11.780	22.588	1.00	36.63
ATOM	3076	OH2 TIP3	121	34.390	2.307	16.660	1.00	64.04
ATOM	3079	OH2 TIP3	122	9.552	-11.846	6.934	1.00	28.23
ATOM	3082	OH2 TIP3	123	8.463	4.098	-1.454	1.00	30.21
ATOM	3085	OH2 TIP3	124	7.397	6.952	2.826	1.00	33.87
ATOM	3088	OH2 TIP3	125	35.796	-1.428	0.072	1.00	30.27
ATOM	3091	OH2 TIP3	126	. 45.044	10.052	11.102	1.00	28.75
ATOM	3094	OH2 TIP3	127	45.209	11.756	21.279	1.00	31.80
ATOM	3097	OH2 TIP3	128	-2.800	15.170	16.902	1.00	32.72
ATOM	3100	OH2 TIP3	1.29	85.885	11.248	9.428	1.00	25.28
ATOM	3103	OH2 TIP3	130	13.136	-2.420	1.867	1.00	20.56
ATOM	3106	OH2 TIP3	131	75.900	3.542	20.641	1.00	39.79
ATOM	3109	OH2 TIP3	132	13.075	7.580	-2.817	1.00	34.49
ATOM	3112	OH2 TIP3	133	11.166	-10.189	0.573	1.00	36.71
ATOM	3115	OH2 TIP3	134	13.814	-16.459	3.327	1.00	21.18
ATOM	3118	OH2 TIP3	135	-6.419	-3.460	16.599	1.00	32.62
MOTA	3121	OH2 TIP3	136	25.578	-12.834	3.624	1.00	43.32
MOTA	3124	OH2 TIP3	137	-16.472	. 11.136	6.388	1.00	64.77
MOTA	3127	OH2 TIP3	138	86.531	12.711	7.151	1.00	28.72
ATOM	3130	OH2 TIP3	139	32.292	-4.665	1.511	1.00	30.98
MOTA	3133	OH2 TIP3	140	45.116	7.369	11.774	1.00	30.59
MOTA	3136	OH2 TIP3	141	81.035	12.317	16.907	1.00	41.72
MOTA	3139	OH2 TIP3	142	2.905	-7.019	-2.101		26.20
MOTA	3142	OH2 TIP3	143	31.895	-6.253	20.885	1.00	36.12
MOTA	3145	OH2 TIP3	144	74.974	-2.640	12.464	1.00	58.90
MOTA	3148	OH2 TIP3	145	7.514	6.734	-1.116	1.00	37.81
MOTA	3151	OH2 TIP3	146	71.606	5.595	22.198	1.00	54.82
MOTA	3154	OH2 TIP3	147	68.337	-5.037	8.955	1.00	40.80
MOTA	3157	OH2 TIP3	148	0.191	-9.669	6.903	1.00	47.40
MOTA	3160	OH2 TIP3	149	68.043	18.153	10.710	1.00	36.67
MOTA	3163	OH2 TIP3	150	3.644	8.512	4.478	1.00	40.16
MOTA	3166	OH2 TIP3	151	52.117	11.302	18.644	1.00	40.22
ATOM	3169	OH2 TIP3	152	-10.220	6.750	4.981		25.00
MOTA	3172	OH2 TIP3	153	76.944	1.425	-0.793	1.00	46.95
MOTA	3175	OH2 TIP3	154	10.053	-11.958	17.014	1.00	38.99
MOTA	3178	OH2 TIP3	155	34.348	14.128	18.169	1.00	42.98



AT		181	OH2 T	IP3	156	2.472 -8.230 16.520 1 00 -
AT		.84		IP3	157	29 961 1 76.
ATO	_	.87	OH2 T	IP3	158	32 600 17 37
ATO		90	OH2 T	IP3	159	42 409 10 045
ATO		93		IP3	160	88 070 70 10 1.00 39.61
ATO		96	OH2 T	IP3	161	70 091 4 755
ATC			OH2 T	[P3	162	77 322 5 424
ATC			OH2 T		163	-0.743
ATO			OH2 TI		164	34 224 35 5.436 1.00 61.30
ATO			OH2 TI		165	79 610 7 500
ATO			OH2 TI		166	11 725 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
ATO			OH2 TI		167	-8 402 34 5-5
ATO			OH2 TI		168	32 002 3 37
ATO			OH2 TI		L69	19 471
ATO)H2 'TI	P3]	170	-1 100 6 21.233 1.00 41.24
ATOM			H2 TI		.71	80 411 0 500
ATON			H2 TI	P3 1	.72	67 266 22 262
ATOM			H2 TI		.73	-0.460 1.00 43.71
ATOM	_	_	H2 TI		74	-0.107 6.701
ATOM			H2 TI		75	-0.955
ATOM			H2 TIE		76	-5 369 0 000
ATOM			H2 TIP		77	-7 000 30 dos
ATOM			H2 TIP	3 1	78	2 219 7 225 1.00 55.41
ATOM			H2 TIP		79	5 370 10 015
ATOM			H2 TIP		30	63 920 12 700
ATOM			12 TIP	3 18	31	79 461 0 075
ATOM			12 TIP	3 18	32	59 121 11 00-
MOTA	3262			3 1.8	13	14 249 1 00-
MOTA	3265		2 TIP	3 I8	4	59 294 2 200
MOTA	3268			3 18	5	32 370 53 653
ATOM	3271	OH			6	72 000 16 732
ATOM	3274		2 TIP3		7	1 039 0 505
ATOM	3277		2 TIP3		8 .	-0.494 5.055
ATOM ATOM	3280	OH			9	81 532 15 000
ATOM	3283		2 TIP3		0	-17 539 3 073
ATOM	3286	OH:		19:	1	27 542 10 56.21
ATOM	3289	OH:	•	192	2	34 363 4 353 1.00 53.58
ATOM	3292	OH2		193	3	-3 244 2 242
ATOM	3295		TIP3	194		42 673 7 005
ATOM	3298		TIP3	195		52 965 10 07.44
ATOM	3301		TIP3	196		26 701 12 22 1.00 35.63
ATOM	3304		TIP3	197		7 504 0 1.00 76.14
ATOM	3310		TIP3	198		55 300 15 07-
ATOM	3313		TIP3	199		51 654 10 00.69
ATOM	3316 3319		TIP3	200		20 000 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
ATOM			TIP3	201		28 200 1 75
ATOM	3322		TIP3	202		26 350 2 7.13, 1.00 42.52
ATOM	3325 3328		TIP3	203		36 927 0 7-1
ATOM			TIP3	204		17 012 20 715
ATOM	3331		TIP3	205		27 990 14 995
ATOM			TIP3	206		31 306 1 50-
	3337	OH2	TIP3	207		10 244 16 05
						10.244 -16.264 15.463 1.00 43.25

ATOM	3340	OH2	TIP3	208	7.255	-11.909	5.440	1.00	45.52
MOTA	3343	OH2	TIP3	209	-12.421	14.520	11.103	1.00	56.32
ATOM	3346	OH2	TIP3	210	11.250	9.879	-1.498	1.00	28.34
ATOM	3349	OH2	TIP3	211	11.426	12.574	-1.341	1.00	37.79
MOTA	3352	OH2	TIP3	212	34.344	13.104	-1.291	1.00	51.83
MOTA	3355	OH2	TIP3	213	31.230	18.082	8.054	1.00	44.77
MOTA	3358	OH2	TIP3	214	37.062	12.036	-1.875	1.00	53.61
MOTA	3361	OH2	TIP3	215	. 35.231	3.150	10.692	1.00	60.59
MOTA	3364	OH2	TIP3	216	63.913	13:371	26.770	1.00	59.44
MOTA	3367	OH2	TIP3	217	36.511	6.165	15.409	1.00	70.98
MOTA	3370	OH2	TIP3	218	90.623	4.459	6.671	1.00	52.23
ATOM	3373	OH2	TIP3	219	49.822	-11.758	10.881	1.00	46.12
MOTA	3376	OH2	TIP3	220	60.367	-10.286	16.662	1.00	68.41
MOTA	3379	OH2	TIP3	221	17.954	-21.378	7.048	1.00	68.51
MOTA	3382	OH2	TIP3	222	66.176	-1.266	30.784	1.00	39.19
ATOM	3385	OH2	TIP3	223	75.201	19.402	20.800	1.00	43.98
MOTA	3388	OH2	TIP3	224	-2.895	10.302	3.534	1.00	44.97
MOTA	3391	OH2	TIP3	225	6.045	-4.015	25.279	1.00	63.74
ATOM	3394	OH2	TIP3	226	36.238	5.898	12.819	1.00	32.89
ATOM	3397	OH2	TIP3	227	-5.516	16.713	14.089	1.00	51.60
ATOM	3400	OH2	TIP3	228	46.577	-11.931	26.964	1.00	37.76
MOTA	3403	OH2	TIP3	229	6.496	6.048	13.722	1.00	27.51
MOTA	3406	OH2	TIP3	230	-3.691	-5.054	20.691	1.00	38.16
MOTA	3409	OH2	TIP3	231	1.811	-3.444	-0.149	1.00	54.03
ATOM	3412	OH2	TIP3	232	86.148	11.480	23.402	1.00	57.66
MOTA	3415	OH2	TIP3	233	10.549	7.581	5.716	1.00	48.49
MOTA	3421	OH2	TIP3	234	64.680	-8.130	20.697	1.00	69.67
MOTA	3424	OH2	TIP3	235	11.380	-17.736	13.500	1.00	54.61
MOTA	3427	OH2	TIP3	236	3.136	-4.782	21.980	1.00	57.12
ATOM	3430	OH2	TIP3	237	72.296	1.006	-1.987		41.40
MOTA	3433	OH2	TIP3	238	50.258	-3.179	32.723		74.99
MOTA	3436	OH2	TIP3	239	58.051	9.469	11.776		44.10
ATOM	3439	OH2	TIP3	240	43.530	20.498	30.344	1.00	43.69
MOTA	3442	OH2	TIP3	241	67.081	16.597	15.934		45.80
MOTA	3445	OH2	TIP3	242	87.660	21.694	5.373	1.00	
ATOM	3448	OH2	TIP3	243	71.779	28.586	7.932		61.12
MOTA	3451	OH2	TIP3	244	25.965	-8.124	27.084		42.13
ATOM	3454	OH2	TIP3	245	-18.336	10.487	12.859	1.00	73.36
MOTA	3457	OH2	TIP3	246	30.703	11.410	16.381	1.00	39.24
MOTA	3460	OH2	TIP3	247		-16.025	-2.906		63.22
MOTA	4620	C	SUG	1000	67.815	4.441	11.493		20.00
MOT'A	4621	C1	SUG	1000	67.387	3.706	10.364		20.00
MOTA	4622	N	SUG	1000	67.823	2.445	9.937		20.00
MOTA	4623	C2	SUG	1000	66.401	4.224	9.501		20.00
MOTA	4624	C3	SUG	1000	65.825	5.499	9.765		20.00
MOTA	4625	C4	SUG	1000	66.259	6.212	10.884		20.00
MOTA	4626	C5	SUG	1000	67.239	5.690	11.736		20.00
MOTA	4627	C6	SUG	1000	66.155	3.220	8.401		20.00
MOTA	4628	0	SUG	1000	67.372	1.047	8.275		20.00
ATOM	4629	C7	SUG	1000	67.155	2.121	8.828		20.00
MOTA	4630	C8	SUG	1000	63.369	2.460	5.852		20.00
MOTA	4631	C9	SUG	1000	65.284	3.356	7.382	1.00	20.00



I I I I I I I I I I I I I I I I I I I	ATOM ATOM ATOM ATOM ATOM ATOM ATOM ATOM	463 463 463 463 463 4641 4642 4643 4644 4645 4647 4648 4649 4651 4653 4655 4655 4655 4655 4655 4655 4659 4660	3 C C C C C C C C C C C C C C C C C C C	SUG	G 1000 G 1000 G 1000 G 1000 G 1000 G 1000 G 1000 G 1000 G 1000	64.603 64.167 63.106 65.103 61.898 62.476 61.259 60.814 60.520 59.496 5.413 5.891 5.553 6.828 7.304 6.822 5.890 7.145 6.101 6.237 9.967 7.997 8.753 9.331 10.320 8.354 11.547 10.759 11.987	0.393 1.251 1.023 0.897 3.715 3.598 5.963 4.912 4.795 2.967 2.927 2.021 3.875 4.884 4.909 3.964 3.576 1.678 2.343 4.392 4.264 3.835 2.736 3.689 2.808 3.900 5.550	2 5.48 5.206 6.293 4.346 5.826 6.771 6.429 6.988 7.873 18.087 19.417 20.431 19.872 18.988 17.678 17.233 21.318 22.552 21.530 23.809 22.102 23.357 25.189 24.962 24.203 25.843 23.175	1.00 20.00 1.00 20.00
P	MOTA						2.808	24.203	
A A A					1001		5.550 5.063 7.308 6.142	23.175 22.373 21.475 21.504	1.00 20.00



TABLE 4

Atom		tom	A.A		х	Y	z	occ	В	
No.		ype	Туре							
ATOM	1	N	GLU	1464	-13.576	17.066	8.598		57.39	
MOTA	2	CA	GLU	1464	-12.446	17.198	7.684		55.83	
MOTA	3	CB	GLU	1464	-11.381	18.127	8.275		56.73	
MOTA	4	C	GLU	1464	-11.845	15.833	7.341		55.07	
ATOM	5	0	GLU	1464	-11.722	15.504	6.165		59.74	
MOTA	6	N	LEU	1465	-11.518	15.023	8.347		50.12	
ATOM	7	CA	LEU	1465	-10.950	13.699	8.087		44.43	•
ATOM	8	CB	LEU	1465	-10.155	13.196	9.291		43.28	
ATOM	9	CG	LEU	1465	-8.630	13.316	9.227		43.70	
ATOM	10		LEU	1465	-8.222	14.754	9.013		47.59	
MOTA	11		LEU	1465	-8.017	12.803	10.506		42.63	
ATOM	12	Ċ	LEU	1465	-12.046	12.697	7.739	1.00	40.93	
ATOM	13	0	LEU	1465	-13.139	12.730	8.301	1.00	39.13	
MOTA	14	N	PRO	1466	-11.794	11.852	6.726	1.00	40.49	
MOTA	15	CD	PRO	1466	-10.612	11.884	5.844	1.00	39.07	
ATOM	16	CA	PRO	1466	-12.754	10.831	6.284	1.00	40.14	
MOTA	17	CB	PRO	1466	-12.152	10.331	4.981	1.00	40.90	
MOTA	18	CG	PRO	1466	-10.664	10.518	5.202	1.00	41.39	•
ATOM	19	С	PRO	1466	-12.862	9.701	7.305	1.00	40.06	
ATOM	20	0	PRO	1466	-11.857	9 290	7.883	1.00	40.71	•
ATOM	21	N	GLU	1467	-14.064	9.175	7.491	1.00	38.65	
ATOM	22	CA	GLU	1467	-14.255	8.126	8.467	1.00	39.24	
ATOM	23	CB	GLU	1467	-15.722	8.054	8.873	1.00	45.06	
ATOM	24	CG	GLU	1467	-16.314	9.365	9.353	1.00	50.91	
MOTA	25	CD	GLU	1467	-17.789	9.252	9.699	1.00	53.51	
MOTA	26	OE1	GLU	1467	-18.379	8.170	9.504	1.00	54.15	
ATOM	27		GLU	1467	-18.369	10.250	10.160	1.00	53.10	
MOTA	28	С	GLU	1467	-13.808	6.777	7.914	1.00	36.09	
ATOM	29	0	GLU	1467	-13.922	6.529	6.711	1.00	38.58	
MOTA	30	N	ASP	1468	-13.272	5.929	8.791	1.00	30.71	
ATOM	31	CA	ASP	1468	-12.839	4.592	8.407	1.00	28.23	
ATOM	32	CB	ASP	1468	-11.328	4.515	8.186		25.51	
ATOM	33	CG	ASP	1468	-10.885	3.207	7.529	1.00	27.68	
MOTA	34		ASP	1468	-11.623	2.199	7.572	1.00	26.01	
ATOM	35		ASP	1468	-9.777	3.187	6.962	1.00	28.87	
MOTA	36	С	ASP	1468	-13.274	3.627	9.493	1.00	27.74	
MOTA	37	0	ASP	1468	-12.570	3.405	10.493	1.00	25.83	
MOTA	38	N	PRO	1469	-14.450	3.019	9.305	1.00	25.88	
MOTA	39	CD	PRO	1469	-15.396	3.175	8.183	1.00	24.25	
MOTA	40	CA	PRO	1469	-14.963	2.079	10.294	1.00	26.69	
MOTA	41	CB	PRO	1469	-16.255	1.586	9.641	1.00	28.81	
MOTA	42	CG	PRO	1469	-16.702	2.776	8.816		24.20	
MOTA	43	С	PRO	1469	-14.012	0.925	10.625	1.00	27.51	
MOTA	44	0	PRO	1469	-14.172	0.285	11.657	1.00	27.60	
MOTA	45	N	ARG	1470	-13.075	0.642	9.720	1.00	26.49	
MOTA	46	CA	ARG	1470	-12.108	-0.435	9.935	1.00	27.60	



ATOM	1 47	CB	ARG 147	20 13 005
ATOM	1 48	CG	ARG 147	8.668 1.00 26 00
ATOM	1 49		ARG 147	7.439 1.00 30 77
ATOM			ARG 147	0 10.153 -1.257 6.213 1.00 31.66
ATOM			ARG 147	0.001 5.915 1.00 30.94
ATOM	52	NH1		0.167 4.941 1.00 33 30
ATOM	53	NH2		20.846 4.144 1.00 32 78
MOTA	54	_	ARG 1470	1.346 4.779 1.00 27 16
ATOM	55	_	ARG 1470	11.110 -0.163 11.069 1.00 28 73
ATOM	56	_	TRP 1471	10.300 -1.091 11.673 1 00 27 20
ATOM	57		RP 1471	10.071 11.363 1 00 27 00
MOTA	58	_	RP 1471	1.430 12.375 1.00 26 22
ATOM	59	_	RP 1471	-8.642 1.964 11.671 1.00 23 87
ATOM	60			-7.998 0.947 10.795 1.00 24 61
ATOM	61			-7.110 -0.104 11.205 1.00 23 32
ATOM	62	_		-6.732 -0.807 10.041 1 00 24 34
MOTA			,-	-6.589 -0.509 12.438 1.00 21 39
ATOM				-8.129 0.831 9.446 1.00 3F 0F
ATOM				-7.369 -0.220 8.980 1.00 26.82
ATOM		CZ3 TI		-5.860 -1.898 10.083 1 00 33 10
ATOM		CH2 TE		-5.722 -1.589 12.473 1.00 24 22
ATOM		C TF	· · -	-5.364 -2.265 11.306 1.00.01
A'TOM		o ir	· -	-10.292 2.384 13.478 1 00 36 03
AT'OM		V GL		-9.551 2.544 14.452 1.00.25 25
ATOM		CA GL		-11.464 2.975 13.364 1 00 36 40
ATOM	_	B GL		-11.909 3.959 14.341 1.00 27 -2
MOTA				-13.168 4.674 13.821 1.66 22 22
ATOM		D GL		-13.497 6.026 14.498 1.00 27.45
ATOM	_	E1 GL		-12.611 7.180 14.042 1 00 34 64
ATOM		E2 GL		-11.877 7.038 13.042 1.00 24.52
ATOM	77 C			-12.658 8.247 14.683 1 00 22 72
ATOM	78 0			-12.179 3.421 15.735 1.00 25.00
ATOM	79 N			-12.795 2.373 15.891 1 00 27 7
ATOM	80 C		•	-11.689 4.121 16.745 1 00 35 0-
ATOM	81 CI			-11.961 3.740 18.129 1.00 27.45
ATOM	82 CC			-10.707 3.311 18.890 1 00 24 00
ATOM		Ol LEU	•	-10.958 3.090 20.392 1.00 37.00
MOTA	84 CI		-	-11.551 1.696 20.627 1 00 20 62
ATOM	85 C	LEU		-9.646 3.199 21.157 1.00 22 a
ATOM	86 0	LEU		-12.478 5.008 18.752 1.00 29 33
ATOM	87 N	PRO		-12.007 6.101 18.405 1.00 27 56
ATOM	88 CD		1474	-13.529 4.896 19.585 1.00 30 07
ATOM	89 CA		1474	-14.380 3.704 19.737 1.00 20.10
ATOM	90 CB	PRO	1474	-14.124 6.051 20.267 1.00 20.02
ATOM	91 CG		1474	-15.266 5.406 21.062 1.00 25.05
ATOM	92 C	PRO	1474	-15.701 4.307 20 158 3 00 26 83
ATOM	93 0	PRO	1474	-13.099 6.715 21.178 1.00 21.05
ATOM	94 N	PRO	1474	-12.310 6.042 21.850 1.00 22 4
ATOM	95 CA	ARG	1475	-13.110 8.038 21 178 3 00 31
ATOM	96 CB	ARG	1475	-12.181 8.810 21.973 1.00 33.33
ATOM	97 CG	ARG	1475	-12.442 10.292 21.791 1.00 35.09
ATOM	98 CD	ARG	1475	-12.082 10.729 20.413 1 00 43 00
	-0 CD	ARG	1475	-11.984 12.228 20.247 1.00 44.84
				4.00 44.84

ATOM	99	NE	ARG	1475	-11.665	12.499	18.846	1.00	48.59
ATOM	100	CZ	ARG	1475	-10.435	12.663	18.374	1.00	46.00
ATOM	101	NH1	ARG	1475	-9.400	12.618	19.202	1.00	46.56
MOTA	102	NH2	ARG	1475	-10.241	12.746	17.065	1.00	44.18
MOT'A	103	С	ARG	1475	-12.175	8.456	23.442	1.00	35.47
MOTA	104	0	ARG	1475	-11.115	8.400	24.072	1.00	37.44
MOTA	105	N	ASP	1476	-13.347	8.134	23.974	1.00	35.04
ATOM	106	CA	ASP	1476	-13.468	7.800	25.380	1.00	34.30
ATOM	107	CB	ASP	1476	-14.940	7.853	25.797	1.00	36.89
ATOM	108	CG	ASP	1476	-15.796	6.818	25.089	1.00	38.67
ATOM	109	OD1	ASP	1476	-15.288	6.056	24.234	1.00	41.19
MOTA	110	OD2	ASP	1476	-16.995	6.758	25.406	1.00	48.08
MOTA	111	C	ASP	1476	-12.858	6.457	25.770	1.00	33.67
ATOM	112	O	ASP	1476	-12.830	6.109	26.949	1.00	36.57
MOTA	113	N	ARG	1477	-12.441	5.670	24.781	1.00	32.72
MOTA	114	CA	ARG	1477	-11.828	4.370	25.033	1.00	29.68
MOTA	115	CB	ARG	1477	-12.1.17	3.418	23.886	1.00	25.53
MOTA	116	CG	ARG	1477	-13.564	3.189	23.599	1.00	23.83
MOTA	11.7	CD	ARG	1477	-14.234	2.525	24.772	1.00	26.80
ATOM	118	NE	ARG	1477	-14.493	3.485	25.842	1.00	27.24
ATOM	119	CZ	ARG	1477	-14.818	3.145	27.085	1.00	27.41
MOTA	120	NH1	ARG	1477	-14.931	1.874	27.438	1.00	29.00
ATOM	121	NH2	ARG	1477	-15.005	4:095	27.985	1.00	25.85
ATOM	122	c ·	ARG	1477	-10.316	4.489	25.177	1.00	30.44
ATOM	123	0	ARG	1477	-9.616	3.515	25.461	1.00	32.78
ATOM	124	N	LEU	1478	-9.800	5.690	25.002	1.00	30.39
MOTA	125	CA	LEU	1478	-8.370	5.883	25.080	1.00	31.96
ATOM	126	СВ	LEU	1478	~7.886	6.508	23.771	1.00	30.43
ATOM	127	CG	LEU	1478	-6.400	6.424	23.431	1.00	31.90
ATOM	128	CD1	LEU	1478	-5.939	4.964	23.382	1.00	28.92
MOT'A	129	CD2	LEU	1478	-6.159	7.115	22.102	1.00	33.55
ATOM	130	С	LEU	1478	-7.974	6.757	26.265	1.00	33.60
ATOM	131	0	LEU	1478	-8.193	7.972	26.251	1.00	33.96
ATOM	132	N	VAL	1479	-7.416	6.140	27.305	1.00	33.54
ATOM	133	CA	VAL	1479	-6.974	6.902	28.468	1.00	32.52
ATOM	134	CB	VAL	1479	-7.085	6.089	29.757	1.00	32.76
MOTA	135	CG1	VAL	1479	-6.728	6.973	30.926	1.00	33.27
ATOM	136	CG2	VAL	1479	-8.493	5.537	29.913	1.00	30.15
MOTA	137	С	VAL	1479	-5.529	7.341	28.239	1.00	34.24
ATOM	138	0	VAL	1479	-4.581	6.546	28.350	1.00	32.24
ATOM	139	N	LEU	1480	-5.381	8.607	27.867		35.88
ATOM	140	CA	LEU	1480	-4.077	9.192	27.569	1.00	38.43
ATOM	141	CB	LEU	1480	-4.241	10.541	26.855		36.93
ATOM	142	CG	LEU	1480	-4.828	10.535	25.435		35.67
ATOM	143		LEU	1480	-4.762	11.952	24.907		32.47
ATOM	144		LEU	1480	-4.037	9.613	24.499		33.60
ATOM	145	C	LEU	1480	-3.144	9.324	28.768		39.70
ATOM	146	0	LEU	1480	-3.511	9.912	29.784		39.88
ATOM	147	N	GLY	1481	-1.912	8.842	28.610		39.70
ATOM	148	CA	GLY	1481	-0.960	8.896	29.700		41.31
ATOM	149	C	GLY	1481	0.349	9.633	29.474		44.39
ATOM	150	0	GLY	1481	0.429	10.626	28.744		45.69
		-					-		

ATOM	1 15	1 N	L	79 1400		
ATOM				-	1.389 9.122 30.1	
ATOM					2.728 9.700 30.0	069 1.00 46.91
ATOM					3.649 8.934 31.0	123 1.00 51.20
ATOM					5.135 9.056 30.7	
ATOM					5.878 7.826 31.2	48 1.00 60.81
ATOM	15				5.430 6.567 30.5	15 1.00 61.24
ATOM	158	-	LY	_	6.235 5.375 30.9	12 1.00 65.39
ATOM	159		LY		3.370 9.782 28.6	81 1.00 46.09
ATOM	160		PRO		3.440 8.782 27.9	44 1.00 42.98
ATOM	161				3.886 10.969 28.3	24 1.00 46.65
ATOM	162				3.910 12.184 29.1	52 1.00 46.11
ATOM	163				4.536 11.212 27.0	36 1.00 45.96
ATOM	164				5.015 12.660 27.1	72 1.00 43.59
ATOM	165		PRO		4.041 13.253 28.12	22 1.00 45.37
ATOM	166		PRO		5.739 10.279 26.91	2 1.00 46.43
ATOM	167		LEU		6.506 10.139 27.86	1.00 44.77
ATOM	168		LEU		5.844 9.579 25.78	6 1.00 48.21
ATOM	169		LEU		6.978 8.684 25.55	4 1.00 50.46
ATOM	170		LEU		6.543 7.426 24.81	1 1.00 49.38
ATOM	171		LEU		5.655 6.437 25.57	6 1.00 50.15
ATOM	172		LEU		5.067 5.422 24.61	
ATOM	173	C	LEU		6.446 5.750 26.66	9 1.00 44.60
ATOM	174	0	LEU		8.058 9.419 24.76	4 1.00 53.33
ATOM	175	N	GLY	1484 1485 .	9.241 9.115 24.89	6 1.00 51.94
ATOM	176	CA	GLY	1485	7.643 10.376 23.93	1 1.00 57.68
ATOM	177	C	GLY		8.603 11.140 23.149	3 1.00 60.27
ATOM	178	Ö	GLY	1485 1485	7.997 11.946 22.016	1.00 62.66
ATOM	179	N	GL _I N		6.774 12.090 21.924	1.00 64.91
ATOM	180	C'A	GLN	1491 1491 .	4.704 14.425 18.904	
ATOM	181	CB	GLN	1491	4.339 13.868 20.206	1.00 44.42
ATOM	182	C	GLN	1491	3.373 14.829 20.918	1.00 44.31
ATOM	183	Ō	GLN	1491	3.755 12.433 20.170	1.00 43.09
ATOM	184	N	VAL	1492	2.807 12.150 19.426	1.00 43.67
ATOM	185	CA	VAL	1492	4.338 11.542 20.974	1.00 40.40
ATOM	186	CB	VAL	1492	3.903 10.143 21.101	1.00 39.95
ATOM	187	CG1		1492	4.962 9.119 20.673	1.00 37.64
ATOM	188	CG2		1492	4.416 7.721 20.897	1.00 34.94
ATOM	189		VAL	1492	5.336 9.296 19.233	1.00 40.26
ATOM	190	0	VAL	1492	3.720 9.905 22.586	1.00 40.23
ATOM	191		VAL	1493	4.679 10.038 23.355	1.00 40.41
ATOM	192		VAL	1493	2.516 9.518 22.993	1.00 38.15
ATOM	193		VAL	1493	2.250 9.291 24.405	1.00 37.11
ATOM		CG1			1.131 10.245 24.924	1.00 37.83
ATOM		CG2		1493	1.386 11.656 24.422	1.00 36.45
ATOM			VAL	1493	-0.252 9.769 24.508	1.00 39.28
ATOM				1493	1.854 7.844 24.701	1.00 36.02
ATOM			_	1493	1.450 7.118 23.797	1.00 37.17
ATOM				1494	2.052 7.418 25.944	1.00 32.77
ATOM		_		1494	1.645 6.081 26.335	1.00 30.87
ATOM				1494	2.445 5.587 27.550	1.00 27.22
ATOM		CD1 I		1494	1.970 4.250 28.141	1.00 28.67
	\		J 1	1494	2.124 3.132 27.129	1.00 27.40

ATOM	203	CD2	LEU	1494	2.736	3.904	29.377	1.00 28.84
ATOM	204	C	LEU	1494	0.173	6.256	26.701	1.00 31.18
ATOM	205	0	LEU	1494	-0.249	7.344	27.119	1.00 30.88
MOTA	206	N	ALA	1495	-0.626	5.223	26.477	1.00 30.40
MOTA	207	CA	ALA	1495	-2.044	5.307	26.817	1.00 28.30
MOTA	208	CB	ALA	1495	-2.815	5.999	25.691	1.00 27.35
ATOM	209	С	ALA	1495	-2.608	3.919	27.057	1.00 26.32
MOTA	210	0	ALA	1495	-1.926	2.915	26.846	1.00 24.54
MOTA	211	N	GLU	1496	-3.836	3.867	27.552	1.00 28.11
MOTA	212	CA	GLU	1496	-4.514	2.603	27.793	1.00 29.22
ATOM	21.3	CB	GLU	1496	-4.841	2.441	29.272	1.00 31.77
ATOM	214	CG	GLU	1496	-3.627	2.233	30.140	1.00 37.26
ATOM	215	CD	GLU	1496	-3.950	2.405	31.613	1.00 39.77
ATOM	216	OE1	GLU	1496	-4.322	3.534	31.999	1.00 37.54
ATOM	217	OE2	GLU	1496	-3.835	1.417	32.378	1.00 41.52
ATOM	218	С	GLU	1496	-5.799	2.594	26.970	1.00 29.76
ATOM	219	0	GLU	1496	-6.593	3.543	27.020	1.00 31.39
ATOM	220	N	ALA	1497	-5.961	1.561	26.153	1.00 29.55
ATOM	221	CA	ALA	1497	-7.139	1.426	25.324	1.00 28.69
ATOM	222	CB	ALA	1497	-6.742	0.969	23.930	1.00 23.86
ATOM	223	C	ALA	1497	-8.068	0.418	25.965	1.00 29.51
ATOM	224	0	ALA	1497	-7.657	-0.702	26.278	1.00 30.40
ATOM	225	N	ILE	1498	-9.313	0.823	26.201	1.00 31.33
ATOM	226	CA	LLE	1498	-10.302	-0.064	26.811	1.00 32.30
ATOM	227	CB	ILE	1.498	-11.359	0.727	27.619	1.00 33.61
ATOM	228	CG2	ILE	1498	-12.233	-0.246	28.439	1.00 34.55
ATOM	229	CG1	ILE	1498	-10.690	1.745	28.545	1.00 31.99
ATOM	230	CD1	ILE	1498	-11.663	2.730	29.155	1.00 26.68
ATOM	231	C	ILE	1498	-11.023	-0.777	25.673	1.00 32.69
ATOM	232	0	ILE	1498	-11.644	-0.134	24.838	1.00 32.03
MOTA	233	N	GLY	1499	-10.917	-2.095	25.610	1.00 37.34
ATOM	234	CA	GLY	1499	-11.588	-2.822	24.554	1.00 44.45
MOTA	235	C	GLY	1499	-10.709	-3.193	23.372	1.00 50.75
MOTA	236	0	GLY	1499	-9.993	-4.205	23.438	1.00 53.68
ATOM	237	N	LEU	1500	-10.729	-2.370	22.321	1.00 51.14
ATOM	238	CA	LEU	1500	-9.963	-2.613	21.087	1.00 51.15
MOTA	239	CB	LEU	1500	-8.445	-2.677	21.345	1.00 50.85
ATOM	240	CG	LEU	1500	-7.516	-1.463	21.166	1.00 49.05
ATOM	241	CD1	LEU	1500	-6.082	-1.946	21.263	1.00 44.92
ATOM	242	CD2	LEU	1500	-7.703	-0.783	19.824	1.00 44.03
ATOM	243	C	LEU	1500	-10.420	-3.891	20.376	1.00 50.50
ATOM	244	0	LEU	1500	-10.544	-4.966	20.984	1.00 49.92
ATOM	245	N	PRO	1505	-13.321	-5.777	25.373	1.00 48.57
ATOM	246	CD	PRO	1505	-13.937	-7.111	25.286	1.00 50.09
ATOM	247	CA	PRO	1505	-14.289	-4.776	25.848	1.00 46.31
ATOM	248	CB	PRO	1505	-15.630	-5.503	25.710	1.00 45.25
MOTA	249	CG	PRO	1505	-15.271	6.918	26.025	1.00 48.85
ATOM	250	С	PRO	1505	-14.010	-4.321	27.294	1.00 43.31
ATOM	251	0	PRO	1505	-14.001	-3.122	27.571	1.00 42.84
ATOM	252	N	ASN	1506	-13.712	-5.272	28.178	1.00 40.46
ATOM	253	CA	ASN	1506	-13.430	-4.945	29.571	1.00 42.33
ATOM	254	СВ	ASN	1506	-14.302	-5.776	30.512	1.00 43.55

ATOM			SN 1506	-15.76	0 -5.43	<i>c</i>	
ATOM		OD1 A	SN 1506				
ATOM		ND2 A	SN 1506		_		
ATOM		C A	SN 1506	-11.96	-		
ATOM	259	O A	SN 1506	-11.61	_		
ATOM	260	N AI	RG 1507	-11.09		,	
ATOM	261	CA A		-9.66			1.00 42.72
ATOM	262	CB AF					1.00 42.24
ATOM	263	CG AR		-9.144	_		1.00 50.39
ATOM	264	CD AR		-9.407			1.00 60.88
ATOM	265	NE AR		-8.357			1.00 67.47
ATOM		CZ AR	•	-8.566		_	1.00 74.19
ATOM		NH1 AR		-8.012			1.00 79.97
ATOM		NH2 AR		-7.193		32.406	1.00 81.67
ATOM		C AR		-8.338	-11.068		1.00 82.38
ATOM		O AR	,	-8.982		28.611	1.00 38.15
ATOM		VAI		-9.458	-3.354	27.642	1.00 36.46
ATOM				.7.927	-3.491	29.279	1.00 35.19
ATOM				-7.190	-2.335	28.782	1.00 33.82
ATOM				-6.824	-1.296	29.883	1.00 30.19
ATOM		G1 VAI G2 VAI		-8.072	-0.723	30.498	1.00 34.68
ATOM	276 C		_	-5.948	-1.900	30.938	1.00 28.53
ATOM	277 O			-5.912	-2.869	28.155	1.00 33.91
ATOM				-5.392	-3.926	28.555	1.00 34.02
ATOM			_	-5.427	-2.152	27.154	1.00 31.32
ATOM				-4.206	-2.527	26.476	1.00 30.47
ATOM				-4.492	-3.015	25.031	1.00 30.88
ATOM		G1 THR	•	-5.522	-4.008	25.066	1.00 30.88
ATOM		G2 THR		~3.255	-3.648		1.00 24.49
ATOM	283 C	THR		-3.323	-1.300		1.00 24.49
ATOM	284 0	THR	1509	-3.774	-0.219		1.00 28.74
ATOM	285 N	LYS	1510	-2.092	-1.432		1.00 27.29
ATOM	286 CZ		1510	-1.162	-0.325		
ATOM	287 CE		1510	0.092	-0.595		1.00 30.55
ATOM	288 CG		1510	-0.117	-0.460	_	1.00 27.23
ATOM	289 CE		1510	1.191	-0.614		1.00 34.33
ATOM	290 CE		1510	1.065	-1.603		1.00 40.49
ATOM	291 NZ		1510	0.318	-1.067		1.00 48.28
	292 C	LYS	1510	-0.813			1.00 51.03
ATOM ATOM	293 0	LYS	1510	-0.521			.00 29.64
	294 N	VAL	1511	-0.904		_	00 28.00
ATOM	295 CA		1511	-0.625			.00 30.10
ATOM	296 CB		1511	-1.951			.00 30.13
ATOM		l VAL	1511	-2.719			.00 31.39
ATOM		2 VAL	1511	-2.829			.00 30.42
ATOM	299 C	VAL	1511	0.150			.00 28.08
ATOM	300 O	VAL	1511	0.274			.00 30.51
ATOM	301 N	ALA	1512	0.679		24.360 1	.00 31.09
ATOM	302 CA	ALA	1512	1.408		22.185 1	.00 28.30
ATOM	303 CB	ALA	1512	2.740		1.979 1	.00 25.23
ATOM	304 C	ALA	1512	0.535		1.331 1.	.00 23.82
ATOM	305 O	ALA	1512	0.033		1.057 1.	00 25.50
ATOM	306 N		1513	0.033		0.061 1.	00 27.06
			- 	0.331	6.281 2	1.404 1.	00 29.37

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MOTA	307	CA	VAL	1513	-0.477	7.199	20.625	1.00 31.53
MOTA	308	CB	VAL	1513	-1.588	7.843	21.504	1.00 32.26
MOTA	309	CG1	VAL	1513	-2.453	8.775	20.684	1.00 34.37
MOTA	310	CG2	VAL	1513	-2.452	6.776	22.152	1.00 33.42
MOTA	311	C	VAL	1513	0.347	8.328	20.006	1.00 33.34
ATOM	312	0	VAL	1513	1.030	9.064	20.719	1.00 32.35
MOTA	313	N	LYS	1514	0.321	8.423	18.680	1.00 36.65
ATOM	314	CA	LYS	1514	1.022	9.466	17.929	1.00 37.26
MOTA	315	CB	LYS	1514	1.541	8.917	16.606	1.00 36.21
MOTA	316	CG	LYS	1514	2.524	7.792	16.800	1.00 39.32
MOTA	317	CD	LYS	1514	2.725	6.998	15.535	1.00 42.59
MOTA	318	CE	LYS	1514	3.245	7.860	14.416	1.00 44.71
MOTA	319	NZ	LYS	1514	4.408	8.680	14.844	1.00 38.78
ATOM	320	C	LYS	1514	0.020	10.574	17.653	1.00 37.21
MOTA	321	0	LYS	1514	-1.095	10.305	17.192	1.00 37.39
ATOM	322	N	MET	1515	0.433	11.812	17.908	1.00 39.05
MOTA	323	CA	MET	1515	-0.419	12.981	17.713	1.00 41.68
ATOM	324	CB	MET	1515	-1.162	13.299	18.991	1.00 41.07
ATOM	325	CG	MET	1515	-0.251	13.641	20.139	1.00 40.69
MOTA	326	SD	MET	1515	-1.271	13.763	21.571	1.00 41.18
MOTA	327	CE	MET	1515	-1.523	12.018	21.959	1.00 40.98
MOTA	328	C	MET	1515	0.397	14.197	17.321	1.00 44.66
ATOM	329	0	MET	1515	1.606	14.255	17.550	1.00 43.83
ATOM	330	N	LEU	1516	-0.288	15.182	16.747	1.00 50.63
ATOM	331	CA	LEU	1516	0.349	16.423	16.312	1.00 52.21
ATOM	332	CB	LEU	1516	-0.513	17.129	15.255	1.00 50.18
ATOM	333	CG	LEU	1516	-0.757	16.463	13.904	1.00 50.25
MOTA	334	CD1	LEU	1516	-1.733	17.298	13.114	1.00 51.02
ATOM	335	CD2	LEU	1516	0.555	16.329	13.163	1.00 51.60
MOTA	336	С	LEU	1516	0.549	17.391	17.473	1.00 54.25
ATOM	337	0	LEU	1516	-0.143	17.326	18.488	1.00 52.52
ATOM	338	N	LYS	1517	1.500	18.299	17.302	1.00 59.09
MOTA	339	CA	LYS	1517	1.773	19.315	18.313	1.00 62.57
MOTA	340	CB	LYS	1517	3.220	19.813	18.222	1.00 66.29
MOTA	341	CG	LYS	1517	4.281	18.810	18.663	1.00 70.96
ATOM	342	CD	LYS	1517	5.666	19.197	18.130	1.00 74.61
ATOM	343	CE	LYS	1517	6.711	18.118	18.414	1.00 78.21
ATOM	344	NZ	LYS	1517	8.020	18.410	17.751	1.00 77.95
MOTA	345	C	LYS	1517	0.824	20.474	18.037	1.00 63.07
MOTA	346	0	LYS	1517	0.226	20.557	16.960	1.00 63.68
MOTA	347	N	SER	1518	0.720	21.391	18.987	1.00 64.54
ATOM	348	CA	SER	1518	-0.167	22.543	18.848	1.00 67.29
MOTA	349	CB	SER	1518	-0.085	23.439	20.090	1.00 65.14
ATOM	350	С	SER	1518	0.124	23.382	17.609	1.00 69.48
MOTA	351	0	SER	1518	-0.798	23.843	16.938	1.00 71.85
MOTA	352	N	ASP	1519	1.402	23.530	17.280	1.00 70.88
MOTA	353	CA	ASP	1519	1.802	24.326	16.127	1.00 72.00
MOTA	354	CB	ASP	1519	3.162	24.973	16.385	1.00 72.61
MOTA	355	C	ASP	1519	1.861	23.548	14.817	1.00 72.32
MOTA	356	0	ASP	1519	2.432	24.035	13.844	1.00 73.72
MOTA	357	N	ALA	1520	1.322	22.332	14.798	1.00 72.11
MOTA	358	CA	ALA	1520	1.344	21.508	13.595	1.00 71.13

ATOM	359		ALA	1520		0.65	59	20.17	3 13.85			
ATOM	360	C	ALA	1520		0.66		22.242				71.01
ATOM	361	0	ALA	1520		-0.31		22.962				69.96
ATOM	362	N	THR	1521		1.23						71.41
ATOM	363	CA	THR	1521		0.67		22.101				57.39
ATOM	364	CB	THR	1521		1.79		22.726				56.23
ATOM	365		THR	1521				23.167				6.40
ATOM	366		THR	1521		2.52		22.016			0 7	70.07
ATOM	367		THR	1521		2.74		24.070				6.67
ATOM	368		THR	1521		-0.15		21.665				5.62
ATOM	369		3LU	1522		-0.09		20.493			0 6	6.78
ATOM	370		3LU	1522		-0.89		22.057	8.33	0 1.0	0 6	3.60
ATOM	371		LU	1522		-1.698		21.095	7.584	4 1.00) 6	2.25
ATOM	372		LU	1522		-2.560		21.802	6.53		6 (4.02
ATOM	373	-	LU	1522		-0.768		20.051	6.942	2 1.00		0.41
ATOM	374	-	YS			-1.161		18.906	6.738	3 1.00		1.94
ATOM	375	_	YS	1523		0.475		20.441	6.662			6.47
ATOM	376			1523		1.449		19.529	6.080			
ATOM	377			1523		2.739		20.273	5.713	1.00		
ATOM	378			1523		3.897		19.381	5 219			
ATOM	379	_		1523		3.482	!	18.451	4.071			
ATOM	380			1523		4.681		17.723	3.469	1.00		
ATOM	381			1523		4.252		16.704	2:458	1.00		
ATOM	382			1523		1.728		18.474	7.135			
ATOM	383			1523		1.757		17.280	6.832			
ATOM				1524		1.899		18.921	8.376	1.00		
ATOM	384 385			1524		2.147		18.023	9.493	1.00		
ATOM	386			1524		2.380	:	18.815	10.783	1.00		
ATOM	387	CG AS		1524		3.744	•	19.511	10.817	1.00		
ATOM	388	OD1 AS		L524·		3.849	2	20.580	11.460	1.00		
ATOM	389	OD2 AS		.524		4.715	1	18.984.	10.230	1.00		
ATOM		C AS		.524		0.968	1	L7.054	9.661	1.00		
ATOM		O AS		.524	•	1.157	1	15.890	10.007	1.00		
ATOM		N LE		525		-0.240	1	7.541	9.391	1.00		
ATOM		CA LE		525		-1.438	1	6.713	9.483			.28
ATOM		CB LE		525 .		-2.701	1	7.592	9.411	1.00		
ATOM		CG LE		525		-4.100	1	6.957	9.403	1.00		
ATOM		CD1 LE		525		-4.289	1	5.933	10.514	1.00		
ATOM		CD2 LE		525		-5.120		8.044	9.524	1.00		
ATOM		C LE		525		-1.417		5.699	8.343	1.00		
ATOM		O LE		525		-1.682	1.	4.525	8.557	1.00		
ATOM		N SE		526		-1.064	1	6.158	7.147	1.00		
ATOM		CA SEI		526		-1.002		5.315	5.954	1.00		
		CB SEI		526		-0.582		6.136	4.723	1.00		
ATOM		OG SEI		526		-1.538		7.100	4.352	1.00		
ATOM		SEI	15	526		-0.007		4.193	6.144			
ATOM	404 () SEF	15	526		-0.297		3.047	5.840	1.00 4		
ATOM	405 N		15	27		1.167		1.527	6.655	1.00 4		
ATOM		A ASI	15	27		2.210		3.546		1.00 4		
ATOM		B ASP		27		3.497		2.235	6.867	1.00 4		
ATOM	408 C	G ASP		27		4.083		5.147	7.316	1.00 4		
ATOM	409 O	D1 ASP		27				5.041	6.235	1.00 4		
ATOM		D2 ASP						.966		1.00 4		
						/	+ 3	. 500	6.600	1.00 4	9.1	L1

MOTA	411	С	ASP	1527	1.782	12.485	7.858	1.00 39.01
MOTA	412	0	ASP	1527	2.021	11.298	7.651	1.00 40.04
MOTA	413	N	LEU	1528	1.094	12.917	8.909	1.00 35.93
MOTA	414	CA	LEU	1528	0.594	12.004	9.927	1.00 36.48
MOTA	415	CB	LEU	1528	-0.008	12.784	11.107	1.00 36.51
MOTA	416	CG	LEU	1528	-0.436	11.961	12.326	1.00 40.56
ATOM	417	CD1	LEU	1528	0.650	10.955	12.692	1.00 42.00
ATOM	418	CD2	LEU	1528	-0.770	12.877	13.499	1.00 38.25
MOTA	419	C	LEU	1528	-0.453	11.065	9.309	1.00 35.25
ATOM	420	0	LEU	1528 .	-0.442	9.855	9.566	1.00 36.37
ATOM	421	N	ILE	1529	-1.311	11.614	8.453	1.00 33.10
ATOM	422	CA	ILE	1529	-2.365	10.839	7.805	1.00 32.32
ATOM	423	CB	ILE	1529	-3.364	11.732	7.012	1.00 31.17
ATOM	424	CG2	ILE	1529	-4.311	10.861	6.1.87	1.00 32.01
MOTA	425	CG1	ILE	1529	-4.193	12.579	7.983	1.00 31.35
MOTA	426	CD1	ILE	1529	-5.024	13.662	7.335	1.00 32.59
ATOM	427	C	ILE	1529	-1.732	9.825	6.877	1.00 33.44
ATOM	428	0	ILE	1529	-2.148	8:667	6.860	1.00 35.41
ATOM	429	N	SER	1530	-0.733	10.269	6.108	1.00 33.40
ATOM	430	CA	SER	1530	0.007	9.414	5.171	1.00 34.34
ATOM	431	СВ	SER	1530	1.126	10.197	4.495	1.00 38.37
ATOM	432	OG	SER	1530	0.605	11.332	3.835	1.00 46.02
ATOM	433	С	SER	1530	0.614	8.208	5.868	1.00 30.41
ATOM	434	0	SER	1530	0.494	7.083	5.376	1.00 30.50
ATOM	435	N	GLU	1531	1.256	8.449	7.010	1.00 27.40
ATOM	436	CA	GLU	1531	1.865	7.369	7.766	1.00 28.90
ATOM	437	СВ	GLU	1531	2.629	7.907	8.973	1.00 28.45
ATOM	438	CG	GLU	1531	3.263	6.812	9.825	1.00 29.33
ATOM	439	CD	GLU.	1531	4.094	7.344	10.979	1.00 31.14
ATOM	440			1531	4.913	6.561	11.495	1.00 33.14
ATOM	441		GLU	1531	3.940	8.522	11.378	1.00 31.11
ATOM	442	С	GLU	1531	0.824	6.351	8.215	1.00 30.88
ATOM	443	0	GLU	1531	1.118	5.146	8.259	1.00 32.35
ATOM	444	N	MET	1532	-0.377	6.832	8.553	1.00 29.86
ATOM	445	CA	MET	1532	-1.476	5.966	8.996	1.00 30.01
ATOM	446	СВ	MET	1532	-2.608	6.800	9.596	1.00 29.58
ATOM	447	CG	MET	1532	-3.761	5.968	10.146	1.00 31.20
ATOM	448	SD	MET	1532	-5.095	6.973	10.779	1.00 29.37
MOTA	449	CE	MET	1532	-5.271	8.228	9.489	1.00 21.59
ATOM	450	C	MET	1532	-2.002	5.145	7.814	1.00 29.60
ATOM	451	0	MET	1532	-2.131	3.923	7.893	1.00 29.68
MOTA	452	N	GLU	1533	-2.257	5.824	6.702	1.00 30.38
ATOM	453	CA	GLU	1533	-2.755	5.176	5.495	1.00 30.38
ATOM	454	CB	GLU					
				1533	-2.987	6.221	4.423	1.00 25.79
ATOM	455	CG	GLU GLU	1533	-4.117	7.154	4.784	1.00 26.67
MOTA	456	CD		1533	-5.420	6.405	5.064	1.00 29.90
ATOM	457		GLU	1533	-5.923	5.696	4.166	1.00 29.93
ATOM	458		GLU	1533	-5.939	6.518	6.197	1.00 29.10
ATOM	459	C	GLU	1533	-1.787	4.120	5.003	1.00 30.32
ATOM	460	0	GLU	1533	-2.197	3.043	4.563	1.00 32.06
ATOM	461	N	MET	1534	-0.500	4.435	5.136	1.00 29.97
ATOM	462	CA	MET	1534	0.606	3.571	4.737	1.00 31.22

MOTA	463	CB	MET	1534		1.9	1 8	4 20	F 4 0	.	
ATOM	464	CG	MET	1534		3.13		4.30			
MOTA	465	SD	MET	1534		3.52		3.48	_		
ATOM	466	CE	MET	1534		5.21		3.62			
ATOM	467		MET	1534				4.25			
ATOM	468		MET	1534		0.56		2.30			
ATOM	469		MET	1535		0.59		1.19			
ATOM	47.0		MET	1535		0.49		2.48			57
ATOM	471	-	ÆT.	1535		0.41		1.354		.3 1.00 28.8	32
ATOM	472	_	ÆT	1535		0.32		1.829			
ATOM	473		ET.	1535		1.62		2.434		3 1.00 28.1	
ATOM	474		ET			1.67				5 1.00 30.9	
ATOM	475	-	ET	1535		1.39		4.335	11.72	9 1.00 27.6	
MOTA	476	-	ET	1535		-0.77		0.460		5 1.00 28.5	
ATOM	477	-	YS	1535		-0.68		-0.774			
ATOM	478			1536		-1.88		1.072	7.01		
ATOM	479		YS	1536		-3.078		0.315	6.60	8 1.00 27.6	
ATOM	480		YS	1536		-4.237		1.253	6.283	3 1.00 25.8	
ATOM	481	_	YS	1536		-4.807		1.947			
ATOM	482		YS	1536		-5.925	5	2.857			
ATOM	483			1536		6.402		3674	8.225	1.00 21.8	
ATOM				1536		-7.469	•	1.594	7.796		
ATOM		_		1536		-2.813	}	-0.573	5.397		
ATOM				1536		-3.150		-1.756	5 393		
ATOM				1537		-2.186		-0.014	4.372		
A TOM		CA MI		1537		-1.890		-0.783	3.172		
ATOM		CB ME		1537		-1.321		0.136	2.085		
ATOM		CG ME		1537		-2.282		1.208	1.566		
ATOM		SD ME		L53 _, 7		-3.740		0.505	0.744		
ATOM		CE ME		L537		-2.964		-0.152.	-0.698	1.00 43.04	
ATOM		C ME		1537		-0.903		-1.920	3.447		
ATOM) ME		.537		-1.102		-3.049	2.996	1.00 27.53	
ATOM		1 IL		.538		0.142		-1.626	4.223	1.00 28.64	
ATOM		CA IL		538		1.189		-2.609	4.533	1.00 26.88	
		B IL		538		2.381		1.948	5.280	1.00 25.23	
ATOM		G2 IL		538		3.380		2.989	5.745	1.00 25.23	
ATOM		G1 IL		538		3.097		0.968	4.345	1.00 27.31	
ATOM		D1 IL		538		4.445		0.465	4.874	1.00 22.70	
ATOM	500 C			538		0.756		3.911	5.224	1.00 23.44	
ATOM	501 0			538		1.274		4.980	4.909		
ATOM	502 N			539		-0.200			6.137	1.00 28.60	
ATOM	503 C	_		539		-0.625		5.069	6.812	1.00 27.19	
ATOM	504 C	GL	1.	539 .		0.207		5.369	8.039	1.00 26.88	
ATOM	505 0	GLY	1!	539	•	1.220		4.708	8.281	1.00 26.04	
ATOM	506 N	LYS	15	540		-0.195		6.396	8.788	1.00 27.96	
ATOM	507 C	A LYS	1.5	540 .		0.461				1.00 23.25	
ATOM	508 CI	B LYS	15	540		-0.573			10.052	1.00 21.53	
MOTA	509 CC	3 LYS	15	40		-1.530			11.028	1.00 20.48	
ATOM	510 CI	LYS		40		-2.542		_	11.563	1.00 28.42	
MOTA	511 CE	LYS	15	40		-3.568			12.502	1.00 36.24	
MOTA	512 NZ	LYS		40		-2.973			12.994	1.00 41.05	
ATOM	513 C	LYS		40		1.577			13.836	1.00 41.25	
ATOM	514 0	LYS	15			1.536		7.796 3.723	9.974	1.00 19.96	
						550	- 0	. 143	9.176	1.00 21.51	

ATOM	515	N	HIS	1541	2.514	-7.670	10.905	1.00 19.82
ATOM	516	CA	HIS	1541	3.622	-8.613	11.040	1.00 21.35
ATOM	517	CB	HIS	1541	4.704	-8.411	9.972	1.00 21.39
ATOM	518	CG	HIS	1541	5.747	-9.490	9.963	1.00 17.07
ATOM	519	CD2	HIS	1541	5.810	-10.667	9.292	1.00 18.04
ATOM	520	ND1	HIS	1541	6.891	-9.428	10.727	1.00 19.05
ATOM	521	CE1	HIS	1541	7.609	-10.522	10.535	1.00 19.63
ATOM	522	NE2		1541	6.975	-11.293	9.668	1.00 18.32
ATOM	523	С	HIS	1541	4.198	-8.456	12.449	1.00 23.61
ATOM	524	Q	HIS	1541	4.231	-7.352	13.002	1.00 25.66
ATOM	525	N	LYS	1542	4.587	-9.577	13.045	1.00 24.32
ATOM	526	CA	LYS	1542	5.141	-9.610	14.396	1.00 27.04
ATOM	527	CB	LYS	1542		-11.044	14.742	1.00 30.70
ATOM	528	CG	LYS	1542		-11.239	16.150	1.00 40.75
ATOM	529	CD	LYS	1542		-12.719	16.420	1.00 48.24
ATOM	530	CE	LYS	1542	6.995	-13.414	15.183	1.00 56.89
ATOM	531	NZ	LYS	1542	7.457	-14.831	15.421	1.00 60.99
ATOM	532	C	LYS	1542	6.318	-8.674	14.608	1.00 24.59
ATOM	533	0	LYS	1542	6.462	-8.067	15.676	1.00 23.35
ATOM	534	N	ASN	1543	7.147	-8.546	13.576	1.00 22.05
ATOM	535	CA	ASN	1543	8.333	-7.702	13.689	1.00 21.40
ATOM	536	CB	ASN	1543	9.558	-8.482	13.217	1.00 20.89
ATOM	537	CG	ASN	1543	9.721	-9.811	13.945	1.00 20.37
ATOM	538		ASN	1543	9.501	-1.0.883	13.372	1.00 24.97
ATOM	539		ASN	1.543	10.016	-9.741	15.230	1.00 21.56
ATOM	540	C	ASN	1543	8.312	-6.268	13.155	1.00 20.38
ATOM	541	0	ASN	1543	9.353	-5.733	12.776	1.00 20.03
ATOM	542	N	ILE	1544	7.153	-5.624	13.180	1.00 20.02
ATOM	543	CA	ILE	1544	7.037	-4.226	12.771	1.00 21.14
ATOM	544	CB	ILE	1544	6.545	-4.029	11.292	1.00 22.97
ATOM	545	CG2	ILE	1544	7.436	-4.810	10.334	1.00 23.27
MOTA	546	CG1	ILE	1544	5.082	-4.447	11.096	1.00 22.85
ATOM	547	CD1	ILE	1544	4.485	-3.974	9.760	1.00 18.94
MOTA	548	C	ILE	1544	6.044	-3.590	13.757	1.00 20.02
MOTA	549	o	ILE	1544	5.342	-4.309	14.466	1.00 21.00
ATOM	550	Ŋ	ILE	1545	6.103	-2.275	13.943	1.00 20.09
MOTA	551	CA	ILE	1545	5.140	-1.608	14.826	1.00 22.82
ATOM	552	CB	ILE	1545	5.586	-0.161	15.198	1.00 23.07
MOTA	553	CG2	ILE	1545	4.399	0.652	15.718	1.00 21.94
ATOM	554		ILE	1545	6.759	-0.178	16.193	1.00 20.49
ATOM	555	CD1	ILE	1545	6.450	-0.730	17.579	1.00 15.00
ATOM	556	C	ILE	1545	3.853	-1.555	14.010	1.00 24.18
ATOM	557	o	ILE	1545	3.809	-0.954	12.920	1.00 25.68
ATOM	558	N	ASN	1546	2.829	-2.236	14.514	1.00 25.69
ATOM	559	CA	ASN	1546	1.528	-2.311	13.853	1.00 24.23
ATOM	560	СВ	ASN	1546	0.866	-3.697	14.060	1.00 25.21
ATOM	561	CG	ASN	1546	1.690	-4.834	13.481	1.00 23.21
MOTA	562		ASN	1546	1.764	-4.997	12.274	1.00 21.10
ATOM	563		ASN	1546	2.324	-5.606	14.343	1.00 23.44
ATOM	564	C C	ASN	1546	0.567	-1.235	14.345	1.00 13.20
ATOM	565	0	ASN	1546	0.709	-0.682	15.426	1.00 23.12
	566	N	LEU	1547	~0.382	-0.882	13.426	1.00 24.14
MOTA	200	TA	UEU	704/	-0.362	-0.320	10.400	1.00 23.43

ATOM			EU 1547	-1.4	17 0.06	9 12 710	
ATOM		_	EU 1547	-1.9			
ATOM			EU 1547	-3.18			
ATOM		_		-2.83			,
ATOM		CD2 L	EU 1547	-3.71			00 21.70
ATOM		C L	EU 1547	-2.51			21.31
ATOM		O L	EU 1547	-2.84			
ATOM		N L	EU 1548	-3.01			- · · · · · · · · · · · · · · · · · · ·
ATOM	575	CA L	EU 1548	-4.04			1.00 25.96
ATOM	576	CB L	EU 1548	-3.68			1.00 22.37
ATOM	577		EU 1548	-2.34			1.00 17.76
ATOM	578	CD1 L		-2.15			1.00 17.12
MOTA	579	CD2 L	EU 1548	-2.26			1.00 18.81
ATOM	580	C LE	TU 1548	-5.39			1.00 16.20
ATOM	581	O LE	W 1548	-6.41			1.00 23.30
ATOM	582	N GI	Y 1549	-5.39	5 1.228	_	1.00 24.18
ATOM	583	CA GL	Y 1549	-6.636			1.00 21.53
ATOM	584	C GL	Y 1549	-6.392		15.485	1.00 22.47
ATOM	585	O GL	Y 1549	-5.245		15.340	1.00 24.62
ATOM	586	N AL	A 1550	-7.459		15.163	1.00 25.06
ATOM	587	CA AL	A 1550	- 7.362		15.409	1.00 24.15
ATOM	588	CB AL	A 1550	-7.063		15.313 13.890	1.00 22.20
ATOM	589	C AL	A 1550	-8.602			1.00 19.97
ATOM	590	O AL	A 1.550	-9.707		15.802	1.00 23.75
ATOM	591	N CY	5 1551	-8.383		15.804	1.00 26.43
ATOM	592	CA CYS	5 1551	-9.425		16.213	1.00 25.34
ATOM	593	CB CYS	3 1551	-9.160		16.678 18.127	1.00 27.17
ATOM		SG CYS	1551	-9.246	7.802	19.448	1.00 26.84
ATOM		C CYS	1551	-9.294	9.787	15.719	1.00 30.32
ATOM		O CYS		-8.364	10.575	15.827	1.00 28.42
ATOM		N THR		10.145	9.823	14.702	1.00 27.28
ATOM		CA THR	1552	-10.076	10.873		1.00 30.47
ATOM		CB THR		-10.061	10.219		1.00 30.58
ATOM		OG1 THR		-11.266	9.465		1.00 30.58
ATOM		CG2 THR		-8.895	9.255		1.00 31.11
ATOM		THR	1552	-11.241	11.847		1.00 27.59
ATOM ATOM) THR	1552	-11.192	12.911		1.00 32.24 1.00 28.56
ATOM		4 GLN	1553	-12.339	11.408		1.00 28.56
ATOM		CA GLN	1553	-13.529	12.233		
ATOM		B GLN	1553	-14.775	11.359		1.00 38.72 1.00 38.66
ATOM		G GLN	1553	-14.811			L.00 38.66 L.00 41.41
		D GLN	1553	-14.695			1.00 41.41
ATOM		E1 GLN	1553	-15.442			
ATOM		E2 GLN	1553	-13.746			.00 45.08
ATOM	611 C		1553	-13.658			00 43.32
ATOM	612 0		1553	-13.230			00 41.20
ATOM	613 N		1554	-14.225			.00 39.89
ATOM	614 C		1554	-14.474			.00 44.03
ATOM	615 C		1554	-15.778	`		.00 46.94
ATOM	616 C		1554	-17.007			.00 49.94
ATOM		O1 ASP	1554	-17.966			.00 56.68
ATOM	618 OI	D2 ASP	1554	-17.030			.00 64.76
						<u>-</u>	.00 60.79

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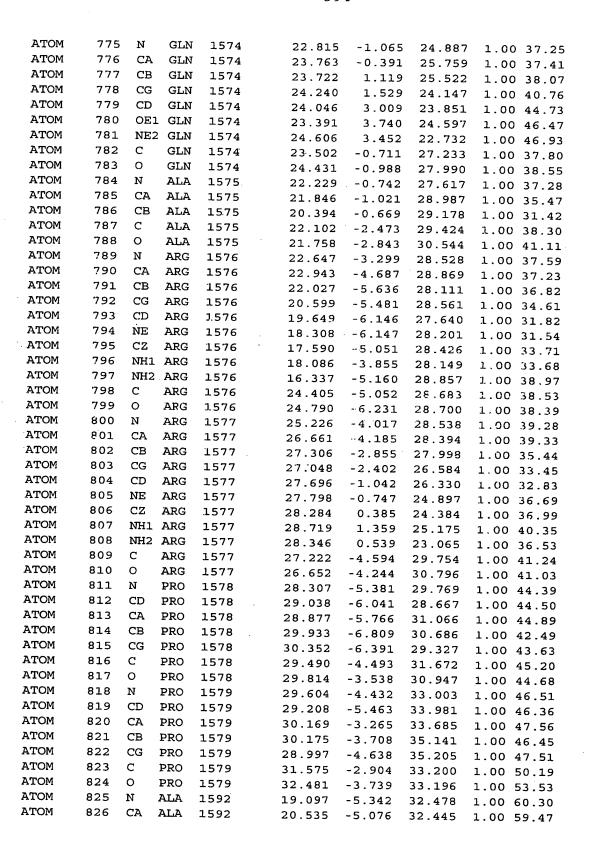
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ATOM	619	C	ASP	1554	-13.343	15.563	17.244	1.00 47.24
ATOM	620	0	ASP	1554	-13.522	15.375	18.452	1.00 48.98
ATOM	621	N	GLY	1555	-12.182	15.966	16.747	1.00 44.00
MOTA	622	CA	GLY	1555	-11.062	16.185	17.638	1.00 41.07
MOTA	623	С	GLY	1555	-9.728	15.891	16.994	1.00 40.26
ATOM	624	0	GLY	1555	-9.663	15.567	15.810	1.00 39.72
MOTA	625	N	PRO	1556	-8.635	15.987	17.759	1.00 39.21
ATOM	626	CD	PRO	1556	-8.634	16.266	19.208	1.00 39.09
MOTA	627	CA	PRO	1556	-7.271	15.740	17.294	1.00 37.84
MOTA	628	CB	PRO	1556	-6.436	15.947	18.549	1.00 39.66
ATOM	629	CG	PRO	1556	-7.269	16.842	19.389	1.00 39.53
MOTA	630	С	PRO	1556	-7.094	14.314	16.806	1.00 37.75
MOTA	631	0	PRO	1556	-7.574	13.377	17.444	1.00 37.25
ATOM	632	N	LEU	1557	-6.379	14.153	15.699	1.00 36.09
ATOM	633	CA	LEU	1557	-6.112	12.844	15.124	1.00 34.69
ATOM	634	CB	LEU	1557	-5.458	13.010	13.741	1.00 32.25
ATOM	635	CG	LEU	1557	-4.962	11.774	12.972	1.00 31.23
ATOM	636	CD1	LEU	1557	-6.080	10.763	12.715	1.00 25.69
ATOM	637	CD2	LEU	1557	-4.339	12.219	11.669	1.00 28.21
ATOM	638	C	LEU	1557	-5.190	12.057	16.060	1.00 34.59
ATOM	639	0	LEU	1557	-4.173	12.578	16.524	1.00 32.09
ATOM	640	N	TYR	1558	-5.606	10.841	16.396	1.00 32.63
ATOM	641	CA	TYR	1558	-4.796	9.993	17.237	1.00 29.66
MOTA	642	CB	TYR	1558	-5.529	9.630	18.534	1.00 33.14
ATOM	643	CG	TYR	1558	-5.588	10.754	19.539	1.00 32.87
ATOM	644	CD1	TYR	1558	-6.583	10.793	20.517	1.00 34.58
ATOM	645	CE1	TYR	1558	-6.678	11.957	21.407	1.00 34.65
ATOM	646	CD2	TYR	1558	-4.678	11.805	19.483	1.00 35.69
ATOM	647	CE2	TYR	1558	-4.760	12.878	20.367	1.00 37.01
MOTA	648	CZ	TYR	1558	-5.766	12.899	21.324	1.00 37.52
ATOM	649	OH	TYR	1558	-5.868	13.986	22.164	1.00 40.19
MOTA	650	С	TYR	1558	-4.529	8.747	16.436	1.00 28.08
MOTA	651	0	TYR	1558	-5.467	8.137	15.924	1.00 30.12
ATOM	652	N	VAL	1559	-3.254	8.444	16.225	1.00 25 89
ATOM	653	CA	VAL	1559	-2.855	7.246	15.504	1.00 23.70
ATOM	654	CB	VAL	1559	-1.729	7.528	14.485	1.00 23.78
ATOM	655	CG1	VAL	1559	-1.456	6.282	13.623	1.00 20.75
ATOM	656	CG2	VAL	1559	-2.101	8.738	13.604	1.00 22.54
ATOM	657	С	VAL	1559	-2.358	6.311	16.596	1.00 23.47
ATOM	658	0	VAL	1559	-1.328	6.572	17.220	1.00 26.84
ATOM	659	N	ILE	1560	-3.146	5.283	16.889	1.00 23.58
ATOM	660	CA	ILE	1560	-2.818	4.316	17.928	1.00 23.75
ATOM	661	СВ	ILE	1560	-4.112	3.732	18.552	1.00 22.67
ATOM	662	CG2	ILE	1560	-3.777	2.898	19.788	1.00 20.24
ATOM	663	CG1		1560	-5.063	4.884	18.904	1.00 20.09
MOTA	664	CD1		1560	-6.428	4.463	19.318	1.00 19.04
ATOM	665	C	ILE	1560	-1.954	3.181	17.356	1.00 27.39
ATOM	666	0	ILE	1560	-2.411	2.392	16.505	1.00 28.51
ATOM	667	N	VAL	1561	-0.720	3.089	17.840	1.00 26.76
ATOM	668	CA	VAL	1561	0.720	2.088	17.368	1.00 25.70
MOTA	669	CB	VAL	1561	1.445	2.801	16.653	1.00 23.51
MOTA	670		VAL	1561	0.952	3.480	15.397	1.00 24.50
WI OIL	070	-G1	A 1-7777	T 2 0 T	0.932	J. 400	10.001	T.00 T3.33

ТОМ	-	_						
ATOM			CG2 V		2.0	54 3.8	70 17.55	1 1.00 20.39
ATOM		•		AL 1561	0.6	93 1.1		
ATOM				AL 1561	0.3			
ATOM	67			LU 1562	1.3			
ATOM	67		CA GI	LU 1562				
ATOM	676		CB GI	JU 1562	2.3			
ATOM	671	7 0	G GI	U 1562	1.3			
ATOM	678	3 C	D GI	U 1562	1.89			
ATOM	679	∂ C	E1 GI	U 1562	1.28			
ATOM	680	0	E2 GL	U 1562	2.95			•
MOTA	681				2.80			
MOTA	682	2 0	GL		3.58		· -	
ATOM	683	N						
ATOM	684	C.			2.78			
MOTA	685			_	.3.67			
ATOM	686				2.90			1.00 30.34
ATOM	687		01 TY		3.74	_		1.00 33.86
ATOM	688		31 TY		4.45		3 24.915	1.00 36.58
ATOM	689			-	5.19			1.00 36.89
ATOM	690		02 TYI		3.78		26.082	1.00 34.25
ATOM	691	CE	_		4.52		27.186	1.00 34.47
ATOM		CZ			5.21			1.00 37.08
ATOM	692	OH			5.96	5 1.662		1.00 44.10
ATOM	693	C	TYF		4.884	1 -1.043	22.668	1.00 30.53
	694	0	TYF		4.74			1.00 30.66
ATOM	695	N	ALA		5.068			1.00 31.09
ATOM	696	CA		1564	7.303		-	1.00 31.09
ATOM	697	CB			8.236			
ATOM	698	, C	ALA	1564	7.940			1.00 30.82
ATOM	699	0	ALA	1564	8.703			1.00 25.32
ATOM	700	N	SER	1565	7.603			1.00 32.26
ATOM	701	CA	SER	1565	8.059		26.712	1.00 29.55
ATOM	702	CB	SER	1565	7.392		27.792	1.00 30.89
ATOM	703	OG	SER	1565	7.704		27.732	1.00 29.79
ATOM	704	C	SER	1565	9.547			1.00 30.94
ATOM	705	0	SER	1565	9.978	-0.150	26.986	1.00 31.39
ATOM	706	N	LYS	1566	10.340	-1.576	27.902	1.00 35.74
MOTA	707	CA	LYS	1566	11.756	-1.560	26.229	1.00 30.03
ATOM	708	CB	LYS	1566	12.322	-2.973	26.495	1.00 28.80
ATOM	709	CG	LYS	1566	11.756		26.447	1.00 28.98
ATOM	710	CD	LYS	1566	12.208	-3.842	27.563	1.00 25.35
ATOM	711	CE	LYS	1566		-5.279	27.459	1.00 30.93
ATOM	712	NZ	LYS	1566	11.875	-6.001	28.747	1.00 31.41
ATOM	713	C	LYS	1566	12.315	-7.421	28.716	1.00 32.83
ATOM	714	0	LYS		12.529	-0.595	25.623	1.00 29.93
ATOM		N	GLY	1566	13.756	-0.672	25.544	1.00 30.89
ATOM		CA		1567	11.799	0.322		1.00 30.67
ATOM		CA	GLY	1567	12.423	1.328		1.00 28.44
ATOM			GLY	1567	13.136	0.874		1.00 27.19
ATOM		O N	GLY	1567	12.919	-0.235		1.00 25.36
ATOM		N Cr	ASN	1568	14.011	1.731		1.00 28.39
ATOM		CA	ASN	1568	14.735	1.421		1.00 28.41
		CB	ASN	1568	15.188	2.698		1.00 28.41
ATOM	722 (CG	ASN	1568	16.396	3.352		1.00 30.32
								33.42

MOTA	723	OD1	ASN	1568	17.418	2.720	21.317	1.00	35.16
ATOM	724	ND2	ASN	1568	16.328	4.661	21.203	1.00	36.23
MOTA	725	С	ASN	1568	15.884	0.443	21.314	1.00	28.34
MOTA	726	0	ASN	1568	16.478	0.373	22.388	1.00	30.67
MOTA	727	N	LEU	1569	16.212	-0.270	20.244	1.00	27.65
MOTA	728	CA	LEU	1569	17.269	-1.270	20.247	1.00	29.10
MOTA	729	CB	LEU	1569	17.311	-1.974	18.880	1.00	27.49
MOTA	730	CG	LEU	1569	18.292	-3.130	18.657	1.00	28.82
ATOM	731	CD1	LEU	1569	18.236	-4.140	19.825	.1.00	24.68
MOTA	732	CD2	LEU	1569	17.994	-3.791	17.316	1.00	22.26
ATOM	733	С	LEU	1569	18.667	-0.790	20.676	1.00	29.37
MOTA	734	0	LEU	1569	19.389	-1.525	21.355	1.00	29.72
MOTA	735	N	ARG	1570	19.058	0.425	20.303	1.00	30.89
MOTA	736	CA	ARG	1570	20.374	0.943	20.689	1.00	33.01
MOTA	737	CB	ARG	1.570	20.591	2.353	20.121	1.00	30.95
ATOM	738	CG	ARG	1570	21.896	2.983	20.584	1.00	38.85
MOTA	739	CD	ARG	1570	21.968	4.472	20.303	1.00	43.03
MOTA	740	NE	ARG	1570 .	20.749	5.192	20.670	1.00	53.34
ATOM	741	CZ	ARG	1570.	20.404	5.573	21.905	1.00	57.49
MOTA	742	NH1	ARG	1570 .	21.184	5.310	22.955	1.00	55.59
ATOM	743	NH2	ARG	1570	19.272	6.252	22.086	1.00	59.53
ATOM	744	С	ARG	1570	20.475	0.947	22.229	1.00	33.82
ATOM	745	0	ARG	1570	21.351	0.296	22.817	1.00	33.93
MOTA	746	N	GLU	1.571	19.528	1.639	22.865	1.00	33.91
MOTA	747	CA	GLU	1571	19.435	1.746	24.317	1.00	32.59
MOTA	748	CB	GLU	1571	18.177	2.524	24.676	1.00	36.4C
MOTA	749	CG	GLU	1571 :	18.174	3.958	24.175	1.00	45.91
ATOM	750	CD	GLU	1571	16.822	4.654	24.328	1.00	52.95
ATOM	751	OE1	GLU	1571	15.793	3.959	24.529	1.00	54.50
MOTA	752	OE2	GLU	1571	16.792	5.905	24.222		55.17
ATOM	753	C	GLU	1571	19.380	0.361	24.959		31.40
MOTA	754	0	GLU	1571	20.115	0.054	25.895		31.09
MOTA	755	N	TYR	1572 .	18.503	-0.477	24.433	1.00	29.24
MOTA	756	CA	TYR	1572	18.334	-1.835	24.920	1.00	
MOTA	757	СВ	TYR	1572	17.387	-2.590	23.991	1.00	
MOTA	758	CG	TYR	1572	17.196	-4.045	24.311	1.00	
ATOM	759	CD1	TYR	1572	16.224	-4.448	25.216	1.00	28.16
ATOM	760	CE1	TYR	1572	15.983	-5.784	25.456	1.00	28.32
MOTA	761	CD2	TYR	1572	17.936	-5.024	23.665	1.00	20.00
ATOM	762	CE2		1572	17.699	-6.361	23.899		22.28
MOTA	763	CZ	TYR	1572	16.721	-6.731	24.801		26.53
ATOM	764	OH	TYR	1572	16.479	-8.058	25.055		30.25
ATOM	765	C	TYR	1572	19.671	-2.564	24.960		30.90
ATOM	766	0	TYR	1572	19.953	-3.323	25.901		30.68
MOTA	767	N	LEU	1573	20.487	-2.337	23.933		31.27
MOTA	768	CA	LEU	1573	21.776	-2.995	23.841		33.33
ATOM	769	CB	LEU	1573	22.287	-2.975	22.399		30.85
MOTA	770	CG	LEU	1573	21.643	-3.908	21.370		26.92
ATOM	771		LEU	1573	22.144	-3.546	19.980		22.76
ATOM	772		LEU	1573	21.939	-5.372	21.695		25.82
MOTA	773	C	LEU	1573	22.801	-2.390	24.791		36.07
MOTA	774	0	LEU	1573	23.544	-3.117	25.457	1.00	36.40



ATOM	827	CB	ALA	1592	20.975	-4.338	33.715	1.00	61.58
MOTA	828	С	ALA	1592	21.367	-6.350	32.252	1.00	58.15
ATOM	829	0	ALA	1592	22.543	-6.285	31.879	1.00	59.09
MOTA	830	N	ALA	1593	20.754	-7.510	32.479	1.00	55.79
MOTA	831	CA	ALA	1593	21.457	-8.775	32.324	1.00	55.06
ATOM	832	CB	ALA	1593	20.519	-9.939	32.604	1.00	57.05
MOTA	833	С	ALA	1593	22.053	-8.897	30.924	1.00	53.57
MOTA	834	0	ALA	1593	21.402	-8.598	29.926	1.00	53.85
MOTA	835	N	GLN	1594	23.303	-9.336	30.862	1.00	53.22
MOTA	836	CA	GLN	1594	24.004	-9.490	29.599	1.00	50.13
MOTA	837	CB	GLN	1594	25.400	-10.082	29.832	1.00	50.73
ATOM	838	CG	GLN	1594	26.308	-9.253	30.743	1.00	54.69
ATOM	839	CD	GLN	1594	27.550	-10.019	31.217	1.00	57.79
MOTA	840	OE1	GLN	1594	28.075	-10.900	30.524	1.00	58.82
MOTA	841	NE2	GLN	1594	28.026	-9.673	32.407	1.00	59.53
MOTA	842	C	GLN	1594	.23.210	~10.374	28.637	1.00	47.73
MOTA	843	0	GLN	1594	22.427	-11.241	29.054	1.00	47.09
MOTA	844	N	LEU	1595	23.418	-10.133	27.350	1.00	45.64
ATOM	845	CA	LEU	1595	22.758	-10.880	26.292	1.00	42.00
MOTA	846	CB	LEU	1595	22.405	-9.947	25.122	1.00	37.98
MOTA	847	CG	LEU	1595	21.345	-8.894	25.446	1.00	37.70
ATOM	848	CD1	LEU	1595	21.568	-7.611	24.660	1.00	33.34
MOTA	849	CD2	LEU	1.595	19.971	-9.479	25.222	1.00	32.84
ATOM	850	С	LEU	1595	23.729	-11.944	25.828	1.00	40.92
ATOM	851	O	LEU	1595	24.944	-11.745	25.855	1.00	41.12
MOTA	852	11	SER	1596	23.201	-13.103	25.471	1 0.0	40.09
ATOM	853	CA	SER	1596	24.044	-14.178	24.985	1.00	38.93
ATOM	854	CB	SER	1596	23.388	-15.535	25.235	1.00	37.45
ATOM	855	OG	SER	1596	22.158	-15.662	24.545	1.00	39.49
ATOM	856	C	SER	1596	24.302	-13.987	23.499	1.00	39.41
ATOM	857	0	SER	1596	23.634	-13.183	22.832	1.00	39.51
ATOM	858	N	SER	1597	25.266	-14.738	22.977	1.00	39.17
ATOM	859	CA	SER	1597	25.587	-14.667	21.563	1.00	40.23
ATOM	860	CB	SER	1597	26.740	-15.611	21.230	1.00	39.96
ATOM	861	OG	SER	1597	27.865	-15.339	22.048	1.00	46.60
ATOM	862	C	SER	1597	24.347	-15.057	20.773	1.00	39.65
ATOM	863	0	SER	1597	24.066	-14.469	19.725	1.00	41.13
MOTA	864	N	LYS	1598	23.590	-16.023	21.291	1.00	36.82
MOTA	865	CA	LYS	1598	22.390	-16.467	20.611	1.00	36.17
ATOM	866	CB	LYS	1598	21.827	-17.742	21.217	1.00	36.19
MOTA	867	CG	LYS	1598	21.030	-18.562	20.180	1.00	39.59
ATOM	868	CD	LYS	1598	20.150	-19.623	20.830	1.00	37.49
ATOM	869	CE	LYS	1598	19.769	-20.719	19.855	1.00	39.64
ATOM	870	NZ	LYS	1598	20.976	-21.437	19.380	1.00	41.43
ATOM	871	С	LYS	1598	21.340	-15.381	20.649	1.00	37.72
MOTA	872	0	LYS	1598	20.604	-15.213	19.677	1.00	39.82
ATOM	873	N	ASP	1599	21.291	-14.627	21.752	1.00	36.20
ATOM	874	CA	ASP	1599	20.331	-13.530	21.907	1.00	33.96
ATOM	875	CB	ASP	1599	20.456	-12.884	23.279	1.00	35.66
MOTA	876	CG	ASP	1599		-13.744	24.394		36.18
ATOM	877		ASP	1599		-13.565	25.544		39.14
ATOM	878	OD2	ASP	1599		-14.593	24.128		33.40



ATOM	879	C AS	P 1599	20.595 -12.471 20.857 1 00 33 53
ATOM	880	O AS	P 1599	10 660 11
ATOM	881	N LE	U 1600	21 071 20
ATOM	882	CA LE		22 204 15 15
ATOM	883	CB LE		22 904 10 000
MOTA	884	CG LET	J 1600	24 174 10 175
ATOM	885	CD1 LET		25 660 27.52
ATOM	886	CD2 LET	J 1600	23 400 24.11
ATOM	887	C LEU		27 064 77
MOTA	888	O LEU		21 205 10 50.
ATOM	889]	IAV VAI		22 271 10 -1
ATOM	890 (CA VAL		21 002 12 055
ATOM	891 (CB VAL		22 540 24 51
ATOM	892 (G1 VAL		22 402 7 2 2 2 2 2 30.47
ATOM		G2 VAL		24 156 14
MOTA	894 (. VAL	1601	24.156 -14.568 16.593 1.00 29.92
ATOM	895 C) VAL	1601	20.474 -13.353 16.399 1.00 26.23
ATOM	896 N		1602	19.991 -13.147 15.295 1.00 25.54
ATOM	8.97 C	A SER	1602	19.733 -13.590 17.478 1.00 27.43
ATOM	898 C	B SER	1602	18.277 -13.671 17.406 1.00 27.09
ATOM	899 O	G SER	1602	17.731 -14.259 18.694 1.00 29.02
ATOM	900 C	SER	1602	16.317 -14.306 18.646 1.00 35.77
ATOM	901 0	SER	1602	17.669 -12.280 17.149 1.00 26.87
ATOM	902 N		1603	16.643 -12.141 16.465 1.00 25.13
ATOM	903 C	A CYS	1603	18.289 -11.262 17.737 1.00 26.09 17.878 -9.871 17.561 1.00 26.09
ATOM	904 CI		1603	19 707
ATOM	905 S		1603	10 510
ATOM	906 C	CYS	1603	17 004
ATOM	907 O	CYS	1603	17 003
ATOM	908 N	ALA	1604	10 120
MOTA	909 CF	ALA	1604	10 400
ATOM	910 CE	ALA	1604	20 051 10 25.15
ATOM	911 C	ALA	1604	19 410 10 00-
MOTA	912 0	ALA	1604	17 004 0 700
MOTA	913 N	TYR	1605	10 120 11 120 1.00 28.81
ATOM	914 CA	TYR	1605	17 175 10 27.10
ATOM	915 CB	TYR	1605	17 104 10
ATOM	916 CG		1605	15 000 24 45
MOTA		1 TYR	1605	16 100 17 0
ATOM	918 CE	1 TYR	1605	15 000 10 10
MOTA	919 CD:	2 TYR	1605	74 000 45.27
ATOM	920 CE	2 TYR	1605	13 001 15 I I I I I I I I I I I I I I I I I I
ATOM	921 CZ	TYR	1605	13 000 11 110 20.20
ATOM	922 OH		1605	12 055 25.20
MOTA	923 C		1605	15 766 55
ATOM	924 0		1605	15 700 11
ATOM	925 N		1606	15.180 -11.635 11.578 1.00 28.40
ATOM	926 CA		1606	15.231 -11.319 13.807 1.00 27.12
MOTA	927 CB		1606	13.907 -10.699 13.892 1.00 25.32
MOTA	928 CG		1606	13.561 -10.383 15.342 1.00 24.31
ATOM	929 CD		1606	13.329 -11.608 16.210 1.00 25.05
ATOM			L606	13.052 -11.243 17.649 1.00 26.35
			-500	12.087 -10.542 17.944 1.00 26.11

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MOTA	931	NE2	GLN	1606	13.917	-11.684	18.551	1.00 27.77
MOTA	932	С	GLN	1606	13.849	-9.415	13.078	1.00 27.52
MOTA	933	0	GLN	1606	12.825	-9.089	12.455	1.00 27.87
MOTA	934	N	VAL	1607	14.943	-8.662	13.122	1.00 27.90
MOTA	935	CA	VAL	1607	15.053	-7.419	12.359	1.00 26.41
ATOM	936	CB	VAL	1607	16.337	-6.661	12.731	1.00 25.61
ATOM	937	CG1	VAL	1607	16.545	-5.457	11.800	1.00 27.37
MOTA	938	CG2	VAL	1607	16.277	-6.224	14.190	1.00 21.50
ATOM	939	C	VAL	1607	15.035	-7.718	10.860	1.00 26.09
ATOM	940	0	VAL	1607	14.337	-7.046	10.096	1.00 28.48
MOTA	941	N	ALA	1608	15.795	-8.722	10.435	1.00 23.05
ATOM	942	CA	ALA	1608	15.812	-9.079	9.027	1.00 20.32
ATOM	943	CB	ALA	1608	16.823		8.783	1.00 14.95
ATOM	944	С	ALA	1608	14.418	-9.558	8.600	1.00 23.08
ATOM	945	0	ALA	1608	14.033	-9.405	7.432	1.00 23.91
ATOM	946	N	ARG	1609	13.671	-10.169	9.530	1.00 24.57
ATOM	947	CA	ARG	1609		-10.628	9.246	1.00 24.30
MOTA	948	СВ	ARG	1609	11.822	-11.577	10.326	1.00 26.13
ATOM	949	CG	ARG	1609	12.278	-12.979	10.114	1.00 31.07
ATOM	950	CD	ARG	1609		-13.885	10.939	1.00 36.13
ATOM	951	NE	ARG	1609		-14.865	10.115	1.00 38.37
ATOM	952	CZ	ARG	1609	9.931	-15.778	10.594	1.00 37.95
MOTA	953		ARG	1609	9.674	-15.828	11.898	1.00 35.31
ATOM	954	NH2	ARG	1609	9.353	-16.649	9.776	1.00 37.85
MOTA	955	C	ARG	1609	11.318	-9.490	9.065	1.00 22.34
ATOM	956	0	ARG	1609	10.470	-9.542	8.160	1.00 24.57
ATOM	957	N	GLY	1610	11.375	-8.500	9.948	1.00 20.52
ATOM	958	CA	GLY	1610	10.497	-7.353	9.827	1.00 19.33
ATOM	959	С	GLY	1610	10.732	-6.715	8.464	1.00 20.04
ATOM	960	0	GLY	1610	9.794	-6.455	7.693	1.00 19.10
ATOM	961	N	MET	1611	12.011	-6.545	8.130	1.00 18.21
ATOM	962	CA	MET	1611	12.423	-5.970	6.851	1.00 20.32
ATOM	963	СВ	MET	1611	13.925	-5.737	6.838	1.00 19.20
ATOM	964	CG	MET	1611	14.371	-4.547	7.694	1.00 20.83
ATOM	965	SD	MET	1611	13.449	-2.960	7.422	1.00 25.39
ATOM	966	CE	MET	1611	13.869	-2.525	5.757	1.00 18.67
ATOM	967	С	MET	1611	12.024	-6.843	5.670	1.00 23.98
ATOM	968	0	MET	1611	11.608	-6.332	4.613	1.00 24.13
MOTA	969	N	GLU	1612		-8.162	5.825	
ATOM	970	CA	GLU	1612	11.759		4.743	1.00 25.49
ATOM	971	CB	GLU	1612		-10.522	5.110	1.00 26.09
ATOM	972	CG	GLU	1612		-11.468	3.968	1.00 26.56
ATOM	973	CD	GLU	1612		-12.942	4.313	1.00 29.26
ATOM	974		GLU	1612		-13.316	5.448	1.00 29.10
ATOM	975	OE2		1612		-13.725	3.443	1.00 31.11
ATOM	976	C	GLU	1612	10.283	-8.821	4.398	1.00 26.29
ATOM	977	o	GLU	1612	9.916	-8.728	3.226	1.00 28.46
ATOM	978	N	TYR	1613	9.437	-8.700	5.422	1.00 28.48
ATOM	979	CA	TYR	1613	8.003	-8.456	5.212	1.00 24.78
ATOM	980	CB	TYR	1613	7.263	-8.526	6.549	1.00 23.07
ATOM	981	CG	TYR	1613	5.785	-8.218	6.449	1.00 20.80
ATOM	982		TYR	1613	4.880	-9.213	6.062	1.00 20.80
ALON	202	CDI	111	1013	4.000	- 5.213	0.002	1.00 20.5/

3.00					
ATO		983	CE1 '	FYR 1613	3 3.517 -8.944 5.958 1.00 20 02
ATO		984		FYR 1613	3 5.330 1.00 20.03
ATO		985		TYR 1613	3 026 5 5
ATC		986		TYR 1613	3 046 5 5 5 5 5 6 6 7 6 7 7 7 7 7 7 7 7 7 7
ATC	-	987		YR 1613	1 604 7 100 24.8/
ATC		88	_	YR 1613	7 700 7
ATO	-	989		YR 1613	6 070 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
ATO ATO				EU 1614	8.436 -6.065 5.063 1.00 20.20
ATO	-			EU 1614	8.321 -4.713 4.510 7.00 7.72
ATO	_			EU 1614	9 100 20.42
ATO	_			EU 1614	9 607
ATO			CD1 L		9 504
ATO	_		CD2 L		7 220 0 70-
ATOI AOTA	-			EU 1614	0 720
ATON				EU 1614	9 073
ATOM			V AI		9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
ATOM			CA AI		10.313 -5.435 1.355 1.00 20.52
ATOM			B AI		11.625 -6.207 1.292 1.00 19.78
ATOM					9.264 -6.098 0.491 1.00 19.98
ATOM					8.945 -5.587 -0.579 1.00 20.14
ATOM					8.692 -7.205 0.972 1.00 20.65
ATOM		_	A SE		7.660 -7.919 0.207 1.00 19.59
ATOM		_			7.283 -9.217 0.912 1.00 15.96
ATOM					6.415 -8.966 2.007 1.00 16.63
ATOM	100				6.397 -7.062 -0.018 1.00 22 05
ATOM	100				5.650 -7.266 -0.975 1.00 23 63
ATOM	101				6.136 -6.135 0.895 1.00 23.39
ATOM	101			- -	4.997 -5.237 0.779 1.00 23.02
ATOM	1012				4.436 -4.881 2.160 1.00 21 50
ATOM	1013				3.709 -6.046 2.851 1.00 24.94
ATOM	1014				2.463 -6.448 2.059 1.00 26.57
ATOM	1015				1.691 -7.571 2.725 1.00 31 05
ATOM	1016		LYS		2.401 -8.852 2.601 1.00 38.73
ATOM	1017		LYS		5.346 -3.981 -0.017 1.00 24.01
ATOM	1018		LYS	1618	4.588 -3.007 -0.013 1.00 28.15
ATOM	1019			1618	0.496 - 4.002 - 0.679 1.00 23 84
ATOM	1020			1618	0.95/ -2.883 -1.528 1.00 24 05
ATOM	1021	CG	LYS	1618	$\frac{3.871}{2.513}$ -2.555 1.00 25 74
ATOM	1022	CD	LYS	1618	5.734 -3.465 -3.749 1.00 28 34
ATOM	1023	CE	LYS	1618	3.55/ -4.914 -3.328 1.00 32.45
ATOM	1024	NZ	LYS	1618	5.590 -5.850 -4.520 1.00 30.41
ATOM	1025	С	LYS	1618	4.3/3 -5.748 -5.354 1.00 31.84
ATOM	1026	0	LYS		7.404 -1.610 -0.796 1.00 23.84
MOTA	1027	N	CYS	1619	7.533 -0.548 -1.402 1.00 20 60
ATOM	1028	CA	CYS	1619	7.719 -1.744 0.489 1.00 25.11
ATOM	1029	СВ	CYS	1619	0.103 -0.614 1.312 1.00 21 68
ATOM	1030	SG	CYS	1619	7.338 -0.690 2.643 1.00 20.84
ATOM	1031	C	CYS	1619	7.916 0.427 3.957 1.00 26.69
ATOM	1032	0	CYS	1619	3.386 -0.480 1.543 1.00 23.16
ATOM	1033	N	ILE	1620	10.257 -1.435 1.958 1.00 25.60
ATOM	1034	CA	ILE	1620	10.110 0.717 1.288 1.00 23.91
					11.532 1.046 1.474 1.00 26.01

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MOTA	1035	CB	ILE	1620	12.098	1.830	0.236	1.00	22.61
MOTA	1036	CG2	ILE	1620	13.551	2.259	0.471	1.00	16.86
MOTA	1037	CG1	ILE	1620	12.014	0.977	-1.026	1.00	22.72
ATOM	1038	CD1	ILE	1620	12.096	1.804	-2.316	1.00	23.62
MOTA	1039	C	ILE	1620	11.566	1.934	2.729	1.00	26.83
ATOM	1040	0	ILE	1620	10.900	2.965	2.772	1.00	28.92
ATOM	1041	N	HIS	1621	12.293	1.500	3.758	1.00	26.44
ATOM	1042	CA	HIS	1621	12.386	2.245	5.007	1.00	23.61
MOTA	1043	CB	HIS	1621	13.142	1.429	6.065	1.00	20.98
ATOM	1044	CG	HIS	1621	12.940	1.917	7.463	1.00	21.57
ATOM	1045	CD2	HIS	1621	12.321	1.346	8.528	1.00	20.74
ATOM	1046	ND1	HIS	1621	13.382	3.151	7.897	1.00	21.08
ATOM	1047	CE1	HIS	1621	13.035	3.321	9.162	1.00	21.00
ATOM	1048		HIS	1621	12.396	2.237	9.572	1.00	21.97
ATOM	1049	С	HIS	1621	13.054	3.582	4.841	1.00	24.83
MOTA	1050	0	HIS	1621	12.560	4.585	5.310	1.00	25.76
ATOM	1051	N	ARG	1622	14.247	3.565	4.269	1.00	27.57
MOTA	1052	CA	ARG	1622	15.056	4.776	4.066	1.00	26.47
MOTA	1053	CB	ARG	1622	14.233	5.918	3.460		20.08
MOTA	1054	CG	ARG	1622	13.762	5.634	2.077	1.00	15.87
ATOM	1055	CD	ARG	1622	12.998	6.791	1.501	0.50	11.86
ATOM	1056	NE	ARG	1622	12.613	6.458	0.144	0.50	12.46
MOTA	1057	CZ	ARG	1622	11.537	5.748	-0.178	0.50	11.18
MOTA	1058		ARG	1622	10.711	5.304	0.767	0.50	7.16
ATOM .	1059	NH2		1622	11.340	5.398	-1.442	0.50	9.57
MOTA	1060	С	ARG	1622	15.813	5.250	5.325	1.00	26.18
MOTA	1061	0	ARG	1622	16.645	6.150	5.250	1.00	26.90
MOTA	1062	N	ASP	1623	15.544	4.650	6.480	1.00	27.26
MOTA	1063	CA	ASP	1623	16.268	5.042	7.684		29.80
ATOM	1064	CB	ASP	1623	15.714	6.330	8.292		32.13
ATOM	1065	CG	ASP	1623	16.690	6.940	9.298		37.87
ATOM	1066		ASP	1623	16.237	7.671	10.202		42.95
ATOM	1067		ASP	1623	17.907	6.684	9.191		41.09
MOTA	1068	C	ASP	1623	16.364	3.943	8.738		29.10
MOTA	1069	0	ASP	1623	16.164	4.168	9.939		27.69
ATOM	1070	N	LEU	1624	16.723	2.755	8.270		28.23
MOTA	1071	CA	LEU	1624	16.874	1.599	9.129		26.00
MOTA	1072	CB	LEU	1624	16.944	0.351	8.245		22.14
ATOM	1073	CG	LEU	1624	17.036	-0.998	8.941		22.32
MOTA	1074		LEU	1624	15.853	-1.196	9.932		17.01
ATOM	1075		LEU	1624	17.068	-2.064	7.848		20.50
ATOM	1076	С	LEU	1624	18.129	1.757	10.003		25.89
ATOM	1077	0	LEU	1624	19.247	1.917	9.499		26.11
ATOM	1078	N	ALA	1625	17.930	1.706	11.316		25.58
ATOM	1079	CA	ALA	1625	19.006	1.864	12.292		23.16
ATOM	1080	CB	ALA	1625	19.323	3.340	12.493		19.06
ATOM	1081	C	ALA	1625	18.475	1.286	13.584		24.12
MOTA	1082	0	ALA	1625	17.269	1.083	13.721		27.40
ATOM	1083	N	ALA	1626	19.357	1.041	14.543		24.67
ATOM	1084	CA	ALA	1626	18.929	0.491	15.827		25.07
ATOM	1085	CB	ALA	1626	20.148	0.145	16.691		26.06
ATOM	1086	С	ALA	1626	18.015	1.474	16.560	1.00	25.13

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ATC	M 108	7 0	ALA	1626	17.1	0.4			
ATO	M 108	8 N	ARG	1627	17.1		069 17.3	66 1.00 26.38	8
ATO	M 108	9 CA	ARG	1627	18.1		770 16.3	08 1.00 23.08	8
ATO		0 CB	ARG	1627	17.3		784 16.9	39 1.00 24.05	5
ATO	M 109	l CG	ARG	1627	17.8			65 1.00 28.09	5
ATO	M 109	2 CD	ARG	1627	17.7		0	78 1.00 37.58	
ATO	M 1093		ARG	1627	18.1			40 1.00 42.10	
ATO	M 1094		ARG	1627	18.4		85 13.3	10 1.00 42.67	
ATOM	M 1095		ARG	1627	19.66			34 1.00 43.58	
ATON	1 1096			1627	20.7			1.00 46.17	
ATOM			ARG	1627	19.84			2 1.00 43.78	
ATOM	1 1098		ARG		15.92			12 1.00 23.04	
ATOM			ASN	1627	15.01		79 17.21		
ATOM			ASN	1628	15.72				
ATOM			ASN	1628	14.38	2 2.93	34 14.72		
ATOM			ASN ASN	1628	14.35		7 13.26		
ATOM		OD1		1628	14.50		18 13.14		
ATOM		ND2		1628	13.87	6 5.68	36 13.86		
ATOM	1105	_		1628	15.36		8 12.22	0 1.00 31.50	
ATOM	1106		ASN	1628	13.78		4 14.83		
ATOM	1107		ASN	1628	12.896	5 1.16			
ATOM	1108			1629	14.30				
ATOM	1109			1629	13.778		0 16.036		
ATOM	1110	CG1 V		1629	14.829	-1.72			
ATOM	1111			1629	14.346		4 16.462		
ATOM	1112			1629	15.068	-1.962			
ATOM	1113			1629	13.411		5 17.520		
ATOM	1114	-		L629	14.237	-0.204			
ATOM	1115			L630	12.181		17.850	1.00 24.34	
ATOM	1116			-630	11.751	-0.919		1.00 24.34	
ATOM	1117		_	.630	10.447	-0.129	19.359	1.00 26.19	
ATOM	1118	CD1 L		630	10.522	1.293		1.00 24.33	
ATOM	1119	CD2 Li		630	9.149	1.870		1.00 20.51	
ATOM	1120			630	11.339	2.196		1.00 19.77	
ATOM	1121			630	11.641	-2.327	19.835	1.00 28.14	
ATOM		N A		630	11.475	-3.320	19.108	1.00 28.31	
ATOM				631	11.792	-2.418	21.153	1.00 28.21	
ATOM			_	631	11.741	-3.694	21.866	1.00 26.96	
ATOM		CB VA CG1 VA		531	13.068	-3.930	22.624	1.00 25.71	
ATOM		CG2 VA		531	13.113	-5.345	23.222	1.00 20.40	
ATOM		CGZ VA C VA		531	14.240	-3.688	21.680	1.00 19.88	
ATOM	_	O VA		31	10.560	-3.758	22.836	1.00 29.84	
ATOM				31	10.419	-2.918	23.738	1.00 32.46	
ATOM				32	9.703	-4.756	22.641	1.00 30.90	
ATOM				32	8.530	-4.939	23.487	1.00 31.16	
ATOM	_			32	7.476	-5.800	22.793	1.00 29.58	
ATOM		G1 TH		32	7.948	-7.152	22.708	1.00 29.17	
ATOM		G2 TH		32	7.186	-5.262	21.414	1.00 22.23	
ATOM					8.882	-5.603	24.809	1.00 22.23	
ATOM					9.950	-6.185		1.00 32.23	
ATOM	_				7.946	-5.589		1 00 24 20	
ATOM		A GLU			8.165	-6.193		1.00 34.38	
V.1	1138 C	B GLU	16:	33	6.881	-6.114	and the second second	1.00 35.51	
						-	· · · · · · · · · · ·	1.00 35.48	

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ATOM	1139	CG	GLU	1633	7.004	-6.685	29.309	1.00 45.16
ATOM	1140	CD	GLU	1633	8.070	-5.999	30.183	1.00 50.45
MOTA	1141			1633	8.174	-4.750	30.163	1.00 52.70
ATOM	1142		GLU	1633	8.789	-6.723	30.919	1.00 53.59
ATOM	1143	С	GLU	1633	8.624	-7.635	26.930	1.00 35.40
ATOM	1144	0	GLU	1633	9.387	-8.119	27.758	1.00 36.57
ATOM	1145	N	ASP	1634	8.204	-8.308	25.861	1.00 36.76
ATOM	1146	CA	ASP	1634	8.573	-9.709	25.662	1.00 37.95
ATOM	1147	CB	ASP	1634		-10.491	24.991	1.00 42.90
MOTA	1148	CG	ASP	1634	6.100	-10.315	25.706	1.00 49.06
ATOM	1149		ASP	1634	5.885	-10.957	26.759	1.00 50.95
ATOM	1150		ASP	1634	5.256	-9.544	25.197	1.00 53.92
MOTA	1151	С	ASP	1634	9.842	-9.882	24.840	1.00 36.05
ATOM	1152	0	ASP	1634	10.148	-10.988	24.414	1.00 34.95
MOTA	1153	N	ASN	1635	10.582	-8.787	24.655	1.00 36.53
MOTA	1154	CA	ASN	1635	11.833	-8.763	23.868	1.00 36.21
ATOM	1155	CB	ASN	1635	12.893	-9.692	24.471	1.00 37.91
MOTA	1156	CG	ASN	1635	13.335	-9.244	25.840	1.00 37.60
MOTA	1157		ASN	1635	13.496	-8.057	26.088	1.00 42.72
MOTA	1158	ND2	ASN	1635	13.525	-10.191	26.743	1.00 38.03
MOTA	1159	C	ASN	1635	11.641	-9.073	22.372	1.00 34.59
MOTA	1160	0	ASN	1635	12.431	-9.799	21.754	1.00 33.52
MOTA	1161	N	VAL	1636	10.557	-8.541	21.819	1.00 31.95
ATOM	1162	CA	VAL	1636	10.260	-8.722	20.415	1.00 28.92
ATOM	1163	CB	VAL	1636	8.743	-8.945	20.177	1.00 31.00
MOTA	1164	CG1	VAL	1636	8.451	-9.066	18.678	1.00 29.52
MOTA	1165		VAL	1636	8.289	-10.220	20.884	1.00 29.03
MOTA	1166	С	VAL	1636	10.725	-7.461	19.721	1.00 28.05
MOTA	1167	0	VAL	1636	10.432	-6.355	20.179	1.00 25.21
MOTA	1168	N	MET	1637	11.567	-7.637	18.707	1.00 28.78
ATOM	1169	CA	MET	1637	12.107	-6.539	17.927	1.00 27.29
MOTA	1170	CB	MET	1637	13.325	-7.008	17.138	1.00 27.97
ATOM	1171	CG	MET	1637	14.446	-7.576	17.982	1.00 29.31
MOTA	1172	SD	MET	1637	15.051	-6.440	19.245	1.00 29.58
MOTA	1173	CE	MET	1637	15.163	-7.542	20.648	1.00 23.51
MOTA	1174	С	MET	1637	11.033	-6.108	16.951	1.00 26.60
MOTA	1175	0	MET	1637	10.479	-6.951	16.244	1.00 26.60
ATOM	1176	N	LYS	1638	10.758	-4.805	16.893	1.00 24.35
MOTA	1177	CA	LYS	1638	9.745	-4.255	16.006	1.00 20.79
MOTA	1178	CB	LYS	1638	8.495	-3.883	16.793	1.00 18.95
MOTA	1179	CG	LYS	1638	7.723	-5.087	17.268	1.00 22.82
MOTA	1180	CD	LYS	1638	6.442	~4.699	17.969	1.00 25.49
MOTA	1181	CE	LYS	1638	5.560	-5.934	18.189	1.00 24.36
MOTA	1182	NZ	LYS	1638	4.892	-6.414	16.941	1.00 22.23
MOTA	1183	C	LYS	1638	10.254	-3.034	15.257	1.00 22.79
MOTA	1184	0	LYS	1638	10.613	-2.041	15.868	1.00 24.60
MOTA	1185	N	ILE	1639	10.259	-3.101	13.934	1.00 23.92
ATOM	1186	CA	ILE	1639	10.707	-1.984	13.113	1.00 24.22
MOTA	1187	CB	ILE	1639	10.925	-2.439	11.648	1.00 23.18
MOTA	1188	CG2	ILE	1639	11.270	-1.262	10.766	1.00 17.17
ATOM	1189	CG1	ILE	1639	12.068	-3.454	11.604	1.00 19.97
ATOM	1190	CD1	ILE	1639	11.975	-4.369	10.461	1.00 26.92



ATO	M 11.	^-		_						
				LE	1639	9.68	86	-0.84	6 13.1°	73 1.00 25.63
ATO		_ :		LE	1639	8.4	73	-1.079		
ATO			N A	LA	1640	10.20	00	0.364		20.20
ATO				LΑ	1640	9.39	94	1.577		27.31
ATO				LΑ	1640	9.62	23	2.211		
ATON		96 (C A	LΑ	1640	9.72		2.595		
ATON) Ai	ĹA	1640	10.76		2.522		
ATON	1 119	8 1	V AS	SP	1641	8.81		3.551		
ATOM	1 119	9 (CA AS	SP	1641	8.95		4.631		
ATOM	1 120	0 0	B AS	SP	1641	10.09				
ATOM	1 120	1 0	G AS	ъ	1641	9.71		5.581		
ATOM	1 120	2 0	D1 AS	P	1641	10.47		6.551		
ATOM	120		D2 AS		1641			7.524		
ATOM	120				1641	8.68		6.355	13.47	
ATOM	120				1641	9.08		4.228	9.79	
ATOM					1642	9.52		5.022	8.96	
ATOM					1642	8.61		3.032	9.47	7 1.00 30.38
ATOM						8.664		2.528	8.114	
ATOM					1642	8.459		1.009	8.100	1.00 25.46
ATOM			D1 PH		1642	7.167		0.555	8.697	1.00 20.44
ATOM	1211		D2 PH		1642	6.002		0.547	7.942	
ATOM	1212		22 PH		1642	7.119		0.112	10.007	1.00 18.52
ATOM	1213				1642	4.796		0.094	8.485	1.00 25.55
ATOM	1214		E2 PHI		642	5.926		0.341	10.559	1.00 21.76
ATOM	1214				642	4.760	-	0.352	9.802	
ATOM			PHI		642	7.686		3.242	7.163	
ATOM	1216		PHI		642	7.946	-	3.330	5.975	
	1217		GL)		643	6.600		3.791	7.693	
ATOM ATOM	1218				643	5.640		4.476	6.845	1.00 28.27
	1219		GLY		643	5.736		5.991	6.874	1.00 28.46
ATOM	1220		GLY		643	4.896	(5.707	6.332	1.00 24.29
ATOM	1221	N	LEU		644	6.816		5.471	7.458	1.00 31.65
ATOM	1222	CA			644	7.077		7.890	7.601	1.00 36.03
ATOM	1223	CB			644	8.363		3.058	8.389	1.00 38.03
ATOM	1224	CG			544	8.321		9.137	9.446	1.00 32.41
ATOM	1225		l LEU	1	544	7.161		8.827	10.384	
ATOM	1226		2 LEU	16	544	9.663		186	10.190	1.00 37.60
ATOM	1227	C	LEU	16	544	7.178		708	6.293	1.00 36.62
ATOM	1228	0	LEU	16	544	7.770		.267		1.00 40.21
ATOM	1229	N	ALA	16	45	6.553		.881	6.293	1.00 40.65
ATOM	1230	CA	ALA	16	45	6.591		.786		1.00 44.50
MOTA	1231	CB	ALA		45	5.432		.762	5.148	1.00 48.66
ATOM	1232	С	ALA		45	7.935		. 545	5.241	1.00 45.63
ATOM	1233	0	ALA		45	8.254		.200	5.173	1.00 51.32
MOTA	1234	N	ALA		46	8.727			6.163	1.00 52.68
ATOM	1235	CA	ALA		46	10.023		.444	4.107	1.00 52.77
MOTA	1236	CB	ALA		46			.121	4.077	1.00 54.73
ATOM	1237	С	ALA	16		11.108		.194	4.646	1.00 55.34
MOTA	1238	0	ALA	16		10.446		.601	2.692	1.00 56.41
ATOM	1239	N	ASP			10.430		.823	1.740	1.00 57.76
ATOM	1240	CA	ASP	16		10.811		. 876	2.567	1.00 58.20
ATOM	1241	CB	ASP	16		11.280		394	1.283	1.00 59.39
ATOM	1242	CG	ASP	16		10.898		861	1.083	1.00 59.29
-			ADP	16	± /	11.128	16.	339 -	-0.356	1.00 60.67
										· - ·

ATOM	1243	OD1	ASP	1647	12.110	15.908	-1.009	1.00	61.21
ATOM	1244	OD2	ASP	1647	10.337	17.173	-0.835	1.00	61.34
ATOM	1245	С	ASP	1647	12.793	14.236	1.273	1.00	60.16
MOTA	1246	0	ASP	1647.	13.523	15.023	1.889	1.00	58.16
ATOM	1247	N	ILE	1648	13.248	13.209	0.562	1.00	61.28
ATOM	1248	CA	ILE	1648	14.658	12.878	0.439	1.00	62.12
ATOM	1249	CB	ILE	1648	14.848	11.626	-0.444	1.00	59.97
ATOM	1250	CG2	ILE	1648	14.023	10.469	0.131	1.00	58.26
ATOM	1251	CG1	ILE	1648	14.429	11.922	-1.883	1.00	55.69
MOTA	1252	CD1	ILE	1648	15.005	10.976	-2.890	1.00	54.38
ATOM	1253	C	ILE	1648	15.470	14.047	-0.127	1.00	65.02
MOTA	1254	0	ILE	1648	16.633	14.245	0.233	1.00	66.85
ATOM	1255	N	HIS	1649	14.844	14.839	-0.995	1.00	65.85
ATOM	1256	CA	HIS	1649	15.505	15.992	-1.589	1.00	66.73
ATOM	1257	CB	HIS	1649	14.859	16.358	-2.934	1.00	65.67
ATOM	1258	CG	HIS	1649	15.142	15.388	-4.038	1.00	66.47
ATOM	1259	CD2	HIS	1649	16.253	14.686	-4.355	1.00	67.11
MOTA	1260	ND1	HIS	1649	14.210	15.064	-4.999	1.00	
ATOM	1261	CE1	HIS	1649	14.733	14.216	-5.867	1.00	66.52
ATOM	1262	NE2	HIS	1649	15.974	13.966	-5.494	1.00	66.25
ATOM	1263	С	HIS	1649	15.505	17.200	-0.663	1.00	68.55
MOTA	1264	0	HIS	1649	15.636	18.341	-1.116	1.00	69.35
ATOM	1265	N	HIS	1650 .	15.273	16.963	0.629	1.00	71.25
MOTA	1266	CA	HIS	1650	15.262	18.026	1.633	1.00	73.53
MOTA	1267	СВ	HIS	1650	13.849	18.551	1.860	1.00	76.79
MOTA	1268	CG	HIS	1650	13.342	19.448	0.765	1.00	83.36
MOTA	1269	CD2	HIS	1650	13.509	20.772	0.537	1.00	86.47
MOTA	1270	ND1	HIS	1650	12.571	18.984	-0.270	1.00	87.02
MOTA	1271	CE1	HIS	1650	12.279	19.983	-1.076	1.00	88.66
MOTA	1272	NE2	HIS	1650	12.840	21.080	-0.609	1.00	88.34
MOTA	1273	С	HIS	1650	15.872	17.580	2.965	1.00	73.11
MOTA	1274	0	HIS	1650	15.686	18.241	3.977	1.00	73.23
MOTA	1275	N	ILE	1651	16.599	16.464	2.949	1.00	72.64
ATOM	1276	CA	ILE	1651	17.234	15.937	4.143	1.00	72.54
MOTA	1277	CB	ILE	1651	17.660	14.472	3.942	1.00	74.59
MOTA	1278	CG2	ILE	1651	18.463	13.966	5.142	1.00	75.52
MOTA	1279	CG1	ILE	1651	16.426	13.591	3.752	1.00	77.59
ATOM	1280	CD1	ILE	1651	16.747	12.141	3.472	1.00	80.12
MOTA	1281	C	ILE	1651	18.463	16.769	4.523	1.00	71.47
MOTA	1282	0	ILE	1651	19.326	17.022	3.688	1.00	72.40
ATOM	1283	N	ASP	1652	18.529	17.197	5.784	1.00	70.34
MOTA	1284	CA	ASP	1652	19.678	17.976	6.235	1.00	68.57
MOTA	1285	CB	ASP	1652	19.272	18.878	7.411	1.00	72.80
ATOM	1286	CG	ASP	1652	20.456	19.640	7.982	1.00	76.90
MOTA	1287	OD1	ASP	1652	21.463	19.888	7.287	1.00	79.62
MOTA	1288	OD2	ASP	1652	20.369	20.030	9.170	1.00	80.36
ATOM	1289	С	ASP	1652	20.771	17.007	6.652		66.01
MOTA	1290	0	ASP	1652	20.709	16.421	7.735		64.75
MOTA	1291	N	TYR	1653	21.778	16.868	5.808		64.05
MOTA	1292	CA	TYR	1653	22.906	15.978	6.074		63.55
ATOM	1293	СВ	TYR	1653	23.829	15.913	4.855		63.81
MOTA	1294	CG	TYR	1653	23.316	14.993	3.771		65.65

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ATC		295	CD1			24.0	82	14.71	10 2.6	43 1	00	CF 20
ATC		296	CE1			23.6	38	13.81				65.32
ATO		297	CD2		1653	22.0		14.35		_		68.40
ATO		98	CE2	ryr	1653	21.6		13.45				66.72
ATO		99	CZ ?	ryr	1653	22.4		13.18				69.93
ATO		00	OH :	ΓYR	1653	21.9		12.27	_			70.13
ATO		01	C 7	YR	1653	23.7						72.73
ATO	M 13	02	0 7	YR	1653	24.3		16.33	_			62.96
ATO	M 13	03	N 7	'YR	1654	23.6		15.47	_			63.31
ATO	M 13	04		'YR	1654			17.59		7 1.	00	63.02
ATOM	1 13	05		YR	1654	24.3		18.06				63.89
ATOM	1 13	06 (YR	1654	24.89		19.49				60.37
ATOM	1 130		_	YR	1654	26.03		19.56				59.33
ATOM				YR	1654	25.73		19.673				59.29
ATOM				YR		26.75		19.687				61.50
ATOM				YR	1654	27.34		19.480	8.06			50.05
ATOM					1654	28.38		19.498	7.11			51.35
ATOM		_		YR	1654	28.08		19.598				52.41
ATOM				/R	1654	29.09	8	19.589				50.57
ATOM		_		/R	1654	23.58		17.984				55.65
ATOM					1654	24.10		18.321				7.31
ATOM		_	_		1655	22.34	_	17.504				
ATOM					1655	21.49		17.390				7.52
	131	_			1655	20.02		17.445	10.893			9.54
ATOM	131		_		1655	19.05		17.518	12.049			1.09
MOTA	131		D LY	S	1655	17.648	_	17.713	11.531			3.08
ATOM	132		E LY	S	1655	16.624		17.320				6.73
MOTA	132		Z LY	S	1655	15.232		17.521	12.568			1.94
ATOM	1322	_	LY	s	1655	21.783		16.102	12.072			4.53
ATOM	1323	3 0	LY	S	1655	21.952		15.032	12.076			0.33
ATOM	1324	ı n	LY	S :	1656	21.825		6.218	11.478			0.43
ATOM	1325	C.P	LY:	S :	1656	22.093			13.403			0.11
ATOM	1326	CE	LY:	_	1656	23.049		5.079	14.274	1.00		
ATOM	1327	' CG	LYS		1656	24.473		5.481	15.394	1.00		
ATOM	1328	CD	LYS		L656	25.326		5.716	14.947	1.00	66	.34
ATOM	1329	CE			1656			6.124	16.136	1.00	66	.60
ATOM	1330				.656	26.801		5.839	15.905	1.00		
ATOM	1331		LYS		.656	27.612		6.059	17.138	1.00		
ATOM	1332	0	LYS		.656	20.823		4.480	14.881	1.00		
ATOM	1333	N	THR			19.759		5.104	14.864	1.00		
ATOM	1334	CA	THR		657	20.941		3.265	15.412	1.00		
ATOM	1335	CB	THR		657	19.818		2.586	16.035	1.00		
ATOM	1336		THR L THR		657	20.052		1.051	16.101	1.00	69	30
ATOM	1337	CG2			657	21.179	10	0.757	16.941	1.00	68	20
ATOM	1338				657	20.310	10	.479	14.713	1.00	69	71
ATOM	1339	C	THR		657	19.706	13	3.145	17.445	1.00		
ATOM		0	THR		657	20.521			17.846	1.00	67	. 60
	1340	N	ALA		558	18.715			18.206			
ATOM	1341	CA	ALA		558	18.564			19.582	1.00		
ATOM	1342	CB	ALA		558	17.345			20.234	1.00		
ATOM	1343	C	ALA	16	558	19.833				1.00		
ATOM	1344	0	ALA	,	558	20.368		-	20.364	1.00		
ATOM	1345	N	ASN		59	20.343		_	21.115	1.00	66.	33
ATOM	1346	CA	ASN		59	21.545			20.129	1.00	65.	38
						~ 4.545	T T	.143	20.801	1.00	62.	65



MOTA	1347	CB	ASN	1659	21.702	9.638	20.616	1.00 63.61
ATOM	1348	CG	ASN	1659	22.548	9.009	21.697	1.00 64.09
ATOM	1349		ASN	1659	22.526	9.451	22.850	1.00 63.69
MOTA	1350	ND2		1659	23.279	7.959	21.345	1.00 64.10
MOTA	1351	С	ASN	1659	22.808	11.844	20.321	1.00 60.46
ATOM	1352	0	ASN	1659	23.882	11.601	20.856	1.00 60.78
MOTA	1353	N	GLY	1660	22.671	12.675	19.285	1.00 58.84
MOTA	1354	CA	GLY	1660	23.803	13.407	18.735	1.00 56.69
MOTA	1355	С	GLY	1660	24.570	12.721	17.616	1.00 56.40
ATOM	1356	0	GLY	1660	25.738	13.028	17.377	1.00 56.43
MOTA	1357	N	ARG	1661	23.929	11.779	16.937	1.00 56.00
ATOM	1358	CA	ARG	1661	24.585	11.048	15.849	1.00 53.80
MOTA	1359	CB	ARG	1661	24.312	9.540	15.952	1.00 54.52
MOTA	1360	CG	ARG	1661	24.876	8.879	17.218	1.00 55.28
MOTA	1361	CD	ARG	1661	24.556	7.395	17.226	1.00 58.01
MOTA	1362	NE	ARG	1661	25.051	6.670	18.396	1.00 58.41
MOTA	1363	CZ	ARG	1661	24.918	5.355	18.559	1.00 59.08
MOTA	1364	NHl	ARG	1661	24.306	4.637	17.623	1.00 55.82
MOTA	1365	NH2	ARG	1661	25.394	4.762	19.652	1.00 57.53
MOTA	1366	С	ARG	1661	24.139	11.581	14.491	1.00 51.03
ATOM	1367	0	ARG	1661	23.160	12.323	14.401	1.00 48.69
ATOM	1368	N	LEU	1662	24.859	11.189	13.440	1.00 48.33
MOTA	1369	CA	LEU	1662	24.565	11.647	12.087	1.00 45.87
MOTA	1370	CB	LEU	1662	25.839	12.199	11.426	1.00 46.18
MOTA	1371	CG	LEU	1662	26.374	13.511	12.016	1.00 45.78
ATOM	1372	CD1	LEU	1662	27.856	13.681	11.722	1.00 45.92
MOTA	1373	CD2	LEU	1662	25.576	14.698	11.489	1.00 44.92
MOTA	1374	C	LEU	1662	23.961	10.542	11.230	1.00 43.02
MOTA	1375	0	LEU	1662	24.647	9.607	10.811	1.00 42.04
MOTA	1376	N	PRO	1663	22.648	10.640	10.968	1.00 41.48
MOTA	1377	CD	PRO	1663	21.769	11.718	11.468	1.00 40.54
MOTA	1378	CA	PRO	1663	21.886	9.680	10.161	1.00 39.60
MOTA	1379	CB	PRO	1663	20.582	10.424	9.889	1.00 38.77
MOTA	1380	CG	PRO	1663	20.386	11.183	11.151	1.00 40.83
ATOM	1381	С	PRO	1663	22.578	9.273	8.860	1.00 35.90
MOTA	1382	0	PRO	1663	22.448	8.124	8.427	1.00 36.85
ATOM	1383	N	VAL	1664	23.356	10.180	8.276	1.00 33.16
ATOM	1384	CA	VAL	1664	24.053	9.880	7.024	1.00 32.51
ATOM	1385	CB	VAL	1664	24.851	11.106	6.439	1.00 32.44
ATOM	1386	CG1	VAL	1664	23.917	12.213	6.065	1.00 26.99
MOTA	1387	CG2	VAL	1664	25.897	11.607	7.421	1.00 29.84
MOTA	1388	С	VAL	1664	24.989	8.675	7.158	1.00 30.30
MOTA	1389	0	VAL	1664	25.400	8.091	6.161	1.00 30.16
ATOM	1390	N	LYS	1665	25.278	8.276	8.393	1.00 27.72
ATOM	1391	CA	LYS	1665	26.170	7.151	8.649	1.00 27.96
ATOM	1392	СВ	LYS	1665	26.808	7.276	10.025	1.00 26.42
MOTA	1393	CG	LYS	1665	27.857	8.351	10.061	1.00 28.20
ATOM	1394	CD	LYS	1665	28.221	8.754	11.478	1.00 32.47
ATOM	1395	CE	LYS	1665	29.398	9.720	11.468	1.00 32.33
ATOM	1396	NZ	LYS	1665	29.713	10.231	12.819	1.00 30.38
ATOM	1397	C	LYS	1665	25.522	5.794	8.486	1.00 25.81
ATOM	1398	0	LYS	1665	26.159	4.769	8.691	1.00 27.53
		•		_005	20.100	1.705	0.001	~.00 27.33



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ATON ACTOR	-				24.24	7 5.793	8.120	1.00 26.13
ATON			A TR		23.49	9 4.554		
MOTA			B TR		22.25	9 4.537		
ATOM			G TR	P 1666	22.54	7 4.067		
ATOM		_	D2 TR	P 1666	23.02			
ATOM		4 C	E2 TR	P 1666	23.15			
ATOM		5 C	E3 TR	P 1666	23.34			
ATOM	140	6 C	D1 TR	P 1666	22.40			
ATOM	140	7 N	E1 TR	P 1666	22.77			
ATOM		B C	Z2 TR	P 1666	23.60			1.00 22.55
ATOM	1409	9 C:	Z3 TRI	P 1666	23.79	_	13.684	1.00 25.32
ATOM	1410	O CI	H2 TRI		23.920		12.712	1.00 21.72
ATOM	1411	l C	TRI		23.092		13.798	1.00 23.77
ATOM	1412	2 0	TRI			_	6.425	1.00 24.79
ATOM			MET		22.662		5.971	1.00 25.26
ATOM	1414				23.350		5.664	1.00 24.21
ATOM	1415				22.963		4.252	1.00 23.79
ATOM	1416				22.796		3.809	1.00 25.08
ATOM	1417				21.793		4.564	1.00 32.58
ATOM	1418				21.778		3.910	1.00 41.43
ATOM	1419				21.011		2.387	1.00 40.85
ATOM	1420		MET		23.938		3.279	1.00 22.52
ATOM	1421		MET		25.139		3.362	1.00 23.63
ATOM			ALA		23.406	4.195	2.324	1.00 22.77
	1422				24.218	3.576.	1.278	1.00 24.91
ATOM	1423				23.342	2.672	0.396	1.00 24.41
ATOM	1424		ALA		24.800		0.438	1.00 26.66
ATOM	1425	0	ALA	1668	24.163	5.748	0.251	1.00 24.54
MOTA	1426	N	PRO	1669	26.011	4.511	-0.101	1.00 26.97
ATOM	1427	CD	PRO	1669	26.935	3.374	0.066	1.00 26.23
ATOM	1428	CA	PRO	1669	26.614	5.563	-0.919	1.00 26.05
ATOM	1429	CB	PRO	1669	27.855	4.876	-1.482	1.00 24.03
ATOM	1430	CG	PRO	1669	28.259	3.946	-0.358	1.00 24.03
ATOM	1431	C	PRO	1669	25.687	6.048	-2.030	1.00 26.27
ATOM	1432	0	PRO	1669	25.576	7.250	-2.263	
ATOM	1433	N	GLU	1670	24.971	5.137	-2.685	1.00 27.72
ATOM	1434	CA	GLU	1670	24.093	5.553	-3.769	1.00 27.16
ATOM	1435	CB	GLU	1670	23.613	4.365		1.00 27.63
ATOM	1436	CG	GLU	1670	22.545	3.492	-4.614	1.00 29.35
MOTA	1437	CD	GLU	1670	23.089	2.238	-3.980	1.00 29.16
ATOM	1438	OE1	GLU	1670	22.248	1.430	-3.310	1.00 28.03
ATOM	1439		GLU	1670	24.325		-2.874	1.00 24.12
ATOM	1440	С	GLU	1670	22.931	2.040		1.00 26.07
ATOM	1441	0	GLU	1670		6.407		1.00 25.52
ATOM	1442	N	ALA	1671	22.477	7.281		1.00 24.12
ATOM	1443	CA	ALA	1671	22.452			1.00 27.74
ATOM	1444	CB	ALA	1671	21.337			1.00 27.65
ATOM	1445	C	ALA		20.729		-0.319	1.00 23.18
ATOM	1446	0		1671	21.860	8.283	-1.065	1.00 28.22
ATOM	1447	N	ALA	1671	21.234		-1.305	1.00 28.51
ATOM	1448		LEU	1672	23.011			1.00 30.60
ATOM	1448	CA	LEU	1672	23.647	9.484		1.00 32.67
ATOM		CB	LEU	1672	24.831	9.127		1.00 32.05
ATOM	1450	CG	LEU	1672	25.662	10.264		1.00 34.00

ATOM	1451	CD1	LEU	1672	24.874	10.981	2.577	1.00	38.85
MOTA	1452	CD2	LEU	1672	26.910	9.667	2.149	1.00	35.22
MOTA	1453	С	LEU	1672	24.121	10.398	-1.067	1.00	37.10
MOTA	1454	0	LEU	1672	23.799	11.580	-1.086	1.00	37.19
MOTA	1455	N	PHE	1673	24.905	9.858	-1.997	1.00	37.60
MOTA	1456	CA	PHE	1673	25.403	10.664	-3.102	1.00	37.11
MOTA	1457	CB	PHE	1673	26.692	10.061	-3.667	1.00	35.24
MOTA	1458	CG	PHE	1673	27.782	9.857	-2.644	1.00	33.54
MOTA	1459	CD1	PHE	1673	28.456	8.633	-2.566	1.00	31.54
MOTA	1460	CD2	PHE	1673	28.143	10.874	-1.762	1.00	33.10
MOTA	1461	CE1	PHE	1673	29.467	8.421	-1.623	1.00	34.66
ATOM	1462	CE2	PHE	1673	29.156	10.678	-0.816	1.00	35.41
MOTA	1463	CZ	PHE	1673	29.819	9.444	-0.748	1.00	34.81
MOTA	1464	C	PHE	1673	24.406	10.890	-4.245	1.00	39.03
MOTA	1465	0	PHE	1673	24.276	11.997	-4.734	1.00	39.02
MOTA	1466	N	ASP	1674	23.693	9.844	-4.651	1.00	42.35
MOTA	1467	CA	ASP	1674	22.757	9.931	-5.762	1.00	41.59
MOTA	1468	CB	ASP	1674	22.957	8.736	-6.700	1.00	46.08
MOTA	1469	CG	ASP	1674	24.384	8.617	-7.201	1.00	51.20
MOTA	1470	OD1	ASP	1674	25.057	9.663	-7.333	1.00	53.97
ATOM	1471	OD2	ASP	1674	24.822	7.470	-7.469	1.00	50.65
ATOM	1472	C	ASP	1674	21.263	9.999	-5.418	1.00	42.89
ATOM	1473	0	ASP	1674	20.427	10.079	-6.317	1.00	41.95
ATOM	1474	N	ARG	1675	20.923	9.899	-4.134	1.00	42.82
MOTA	1475	CA	ARG	1675	19.521	9.944	-3.706	1.00	42.64
ATOM	1476	CB	ARG	1675	18.890	11.300	-4.028	1.00	48.80
ATOM	1477	CG	ARG	1675	19.480	12.449	-3.252	1.00	61.19
MOTA	1478	CD	ARG	1675	19.407	13.727	-4.068	1.00	72.90
ATOM	1479	NE	ARG	1675	20.025	14.854	-3.381	1.00	83.15
MOTA	1480	CZ	ARG	1675	19.652	16.123	-3.539	1.00	88.21
MOTA	1481	NH1	ARG	1675	18.662	16.439	-4.365	1.00	89.58
MOTA	1482	NH2	ARG	1675	20.265	17.085	-2.860	1.00	92.07
MOTA	1483	C	ARG	1675	18.674	8.825	-4.299	1.00	38.05
ATOM	1484	0	ARG	1675	17.495	9.005	-4.588	1.00	38.87
MOTA	1485	N	ILE	1676	19.281	7.658	-4.479	1.00	34.44
MOTA	1486	CA	ILE	1676	18.576	6.514	-5.012	1.00	30.11
ATOM	1487	CB	ILE	1676	19.378	5.825	-6.096	1.00	29.58
ATOM	1488	CG2	ILE	1676	18.509	4.850	-6.797	1.00	30.72
MOTA	1489	CG1	ILE	1676	19.835	6.868	-7.116	1.00	34.29
ATOM	1490		ILE	1676	20.798	6.348	-8.145	1.00	41.15
MOTA	1491	C	ILE	1676	18.315	5.541	-3.874	1.00	26.90
MOTA	1492	0	ILE	1676	19.236	4.898	-3.364		22.06
ATOM	1493	N	TYR	1677	17.056	5.465	-3.454	1.00	28.17
ATOM	1494	CA	TYR	1677	16.677	4.589	-2.350		26.80
ATOM	1495	CB	TYR	1677	15.742	5.310	-1.398	1.00	26.05
ATOM	1496	CG	TYR	1677	16.442	6.367	-0.580	1.00	26.92
MOTA	1497	CD1		1677	16.510	7.693	-1.018	1.00	23.98
ATOM	1498	CE1	TYR	1677	17.129	8.665	-0.250	1.00	23.90
MOTA	1499	CD2	TYR	1677	17.022	6.048	0.644	1.00	26.99
MOTA	1500	CE2	TYR	1677	17.642	7.017	1.414	1.00	24.87
MOTA	1501	CZ	TYR	1677	17.685	8.315	0.968	1.00	26.44
MOTA	1502	OH	TYR	1677	18.227	9.273	1.783	1.00	30.89



3 000		_						
ATO				·-	16.00	6 3.350	-2.894	1 1.00 26.30
ATON					15.08	0 3.445	-3.703	
ATON					16.48	9 2.197		
ATON			A TH		15.97			
ATOM			B TH		16.90	4 0.336		
ATOM			G1 TH	_	18.18	0.095		
ATOM			G2 TH		17.068	3 1.305	-5.174	
ATOM					15.987	7 -0.049	-1.758	
ATOM					16.476		-0.693	
ATOM				· · · -	15.500	-1.260	-1.974	
ATOM					15.496		-0.933	
ATOM				_	14.747	-3.520	-1.411	
ATOM					13.297		-1.695	
ATOM			D2 HI		12.552		-2.812	
ATOM			O1 HIS		12.423		-0.741	1.00 27.21
ATOM			El HIS		11.206		-1.255	1.00 22.60
ATOM	1519		E2 HIS		11.255		-2.515	1.00 23.66
ATOM	1520		HIS		16.976		-0.665	1.00 20.81
ATOM	1521	_	HIS		17.358		0.451	1.00 22.50
ATOM	1522		GLN		17.799	-2.382	-1.695	1.00 19.58
MOTA	1523				19.248	-2.587	-1.657	1.00 20.89
ATOM	1524				19.860	-2.400	-3.038	1.00 23.76
ATOM	1525	_			19.896	-3.651	-3.877	1.00 34.08
ATOM	1526				19.015		-5.096	1.00 37.77
ATOM	1527				18.069	-2.780	-5.122	1.00.43.23
MOTA	1528	NE			19.321	-4.356	-6.113	1.00 37.02
ATOM	1529	C	GLN		19.913	-1.609	-0.724	1.00 20.72
ATOM	1530	0	GLN		20.814	-1.981	0.021	1.00 21.53
ATOM	1531		SER		19.514	-0.350	-0.773	1.00 21.01
ATOM ATOM	1532	CA	SER	1681	20.128	0.606	0.135	1.00 23.86
ATOM	1533	CB	SER	1681	19.841	2.065	-0.248	1.00 21.10
ATOM	1534	OG	SER	1681	18.473	2.290	-0.506	1.00 23.18
ATOM	1535	C	SER	1681	19.695	0.292	1.564	1.00 23.91
ATOM	1536	0	SER	1681	20.457	0.542	2.495	1.00 26.70
ATOM	1537	N	ASP	1682	18.511	-0.303	1.739	1.00 21.71
ATOM	1538	CA	ASP	1682	18.044	-0.662	3.080	1.00 21.28
ATOM	1539	CB	ASP	1682	16.595	-1.149	3.070	1.00 23.22
ATOM	1540	CG	ASP	1682	15.569	-0.016	3.198	1.00 23.08
ATOM	1541		ASP	1682	14.363	-0.282	3.017	1.00 21.99
ATOM	1542		ASP	1682	15.948	1.135	3.498	1.00 24.42
ATOM	1543	C	ASP	1682	18.955	-1.756	3.611	1.00 20.86
ATOM	1544	0	ASP	1682	19.289	-1.770		1.00 21.62
	1545	N	VAL	1683	19.398	-2.649		1.00 21.60
ATOM	1546	CA	VAL	1683	20.307	-3.732		1.00 22.27
ATOM	1547	СВ	VAL	1683	20.515	-4.740		1.00 22.22
ATOM	1548		VAL	1683	21.587	-5.777		1.00 22.22
ATOM	1549		VAL	1683	19.187	-5.437		1.00 20.89
ATOM	1550	C	VAL	1683	21.618	-3.150		1.00 20.89
ATOM	1551	0	VAL	1683	22.107	-3.577		1.00 21.36
ATOM	1552	N	TRP	1684	22.172	-2.160		1.00 24.39
ATOM	1553	CA	TRP	1684	23.375	-1.489		1.00 22.01
ATOM	1554	CB	TRP	1684	23.685	-0.273		1.00 23.06
								00 20.25

MOTA	1555	CG	TRP	1684	24.808	0.549	3.069	1.00 22.35
ATOM	1556	CD2	TRP	1684	26.118	0.644	2.503	1.00 24.14
ATOM	1557	CE2	TRP	1684	26.879	1.500	3.334	1.00 23.68
MOTA	1558	CE3	TRP	1684	26.728	0.091	1.370	1.00 25.09
MOTA	1559	CD1	TRP	1684	24.825	1.346	4.193	1.00 22.52
ATOM	1560	NE1	TRP	1684	26.066	1.915	4.355	1.00 21.48
ATOM	1561	CZ2	TRP	1684	28.216	1.815	3.061	1.00 20.56
MOTA	1562	CZ3	TRP	1684	28.059	0.405	1.095	1.00 23.92
MOTA	1563	CH2	TRP	1684	28.785	1.257	1.942	1.00 23.18
MOTA	1564	C	TRP	1684	23.105	-1.025	4.903	1.00 23.96
MOTA	1565	0	TRP	1684	23.889	-1.308	5.815	1.00 25.98
ATOM	1566	N	SER	1685	21.992	-0.332	5.118	1.00 24.68
MOTA	1567	CA	SER	1685	21.615	0.144	6.447	1.00 22.75
MOTA	1568	CB	SER	1685	20.266	0.870	6.376	1.00 21.11
ATOM	1569	OG	SER	1685	20.276	1.950	5.452	1.00 21.98
ATOM	1570	C	SER	1685	21.516	-1.011	7.457	1.00 23.06
ATOM	1571	0	SER	1685	21.865	-0.850	8.638	1.00 22.55
ATOM	1572	N	PHE	1686	21.041	-2.168	6.998	1.00 21.83
MOTA	1573	CA	PHE	1686	20.915	-3.340	7.854	1.00 21.92
MOTA	1574	CB	PHE	1686	20.153	-4.457	7.129	1.00 18.02
MOTA	1575	CG	PHE	1686	19.965	-5.683	7.971	1.00 20.86
MOTA	1576	CD1	PHE	1686	19.142	-5.641	9.108	1.00 18.76
ATOM	1577	CD2	PHE	1686	20.669	-6.853	7.688	1.00 18.96
MOTA	1578	CE1	PHE	1686	19.023	-6.743	9.947	1.00 19.29
MOTA	1579	CE2	PHE	1686	20.554	-7.965	8.514	1.00 19.27
ATOM	1580	CZ	PHE	1686	19.732	-7.908	9.653	1.00 21.91
MOTA	1581	С	PHE	1686	22.304	-3.845	8.316	1.00 22.11
MOTA	1582	0	PHE	1686	22.473	-4.378	9.436	1.00 21.35
MOTA	1583	N	GLY	1687	23.294	-3.691	7.436	1.00 20.48
MOTA	1584	CA	GLY	1687	24.653	-4.079	7.769	1.00 20.41
MOTA	1585	С	GLY	1687	25.185	-3.211	8.899	1.00 19.03
MOTA	1586	0	GLY	1687	25.857	-3.714	9.808	1.00 20.27
MOTA	1587	N	VAL	1688	24.893	-1.906	8.829	1.00 20.57
MOTA	1588	CA	VAL	1688	25.296	-0.937	9.860	1.00 21.14
MOTA	1589	CB	VAL	1688	24.974	0.548	9.467	1.00 20.78
MOTA	1590	CG1	VAL	1688	25.440	1.493	10.564	1.00 21.51
MOTA	1591	CG2	VAL	1688	25.681	0.923	8.186	1.00 19.70
ATOM	1592	C	VAL	1688	24.547	-1.297	11.142	1.00 23.16
ATOM	1593	0	VAL	1688	25.126	-1.271	12.225	1.00 24.14
ATOM	1594	N	LEU	1689	23.264	-1.648	11.021	1.00 24.50
MOTA	1595	CA	LEU	1689	22.465	-2.058	12.187	1.00 25.93
MOTA	1596	CB	LEU	1689	21.008	-2.316	11.776	1.00 25.42
MOTA	1597	CG	LEU	1689	19.933	-2.392	12.874	1.00 26.29
ATOM	1598	CD1	LEU	1689	18.572	-2.053	12.272	1.00 23.43
MOTA	1599	CD2	LEU	1689	19.885	-3.768	13.543	1.00 25.66
MOTA	1600	C	LEU	1689	23.080	-3.330	12.797	1.00 28.01
MOTA	1601	0	LEU	1689	23.203	-3.426	14.016	1.00 30.06
MOTA	1602	N	LEU	1690	23.487	-4.287	11.956	1.00 27.19
MOTA	1603	CA	LEU	1690	24.111	-5.520	12.457	1.00 25.29
ATOM	1604	CB	LEU	1690	24.556	-6.446	11.315	1.00 24.98
ATOM	1605	CG	LEU	1690	23.594	-7.390	10.589	1.00 24.85
ATOM	1606	CD1	LEU	1690	24.385	-8.132	9.538	1.00 24.22

ATC		507	CD2	LEU	1690	22.9	960 -	0 434			
ATC		808	C]	LEU	1690	25.3		8.434			0 19.10
ATO		09	0 1	EU	1690	25.5		5.123 5.624			0 24.70
ATO		10	N 7	RP	1691	26.1					0 23.57
ATO		11	CA 1	RP	1691	27.3		4.197			23.68
ATO:	M 16	12	св т	'RP	1691			3.693			24.83
ATO	M 16	13		'RP	1691	27.9		2.621	12.56	7 1.00	20.94
ATO	M 16	14		RP	1691	29.3		2.173	13.10	5 1.00	24.80
ATO	У 16			RP	1691	29.5		.082	14.00		23.71
ATON	4 16			RP	1691	30.9		.996	14.20		23.81
ATON			D1 T			28.7		.167	14.65		22.20
ATOM				RP	1691	30.5		.702	12.81		24.44
ATOM				RP	1691	31.5		.995	13.47		25.38
ATOM			223 TI		1691	31.54		.022	15.03		24.39
ATOM					1691	29.30		.799	15.484	_	21.99
ATOM					1691	30.70		.862	15.669		25.57
ATOM		_			1691	26.99	8 -3	.131	14.823		25.87
ATOM					1691	27.77		.301	15.750	•	23.87
ATOM		_			1692	25.86		.448	14.956		27.39
ATOM		_	A GI		1692	25.45		869	16.238		26.45
ATOM	-			-	1692	24.25		933	16.068		25.13
ATOM	162	_			1692	24.36		091	14.962		23.56
	162				1692	23.11		935	14.880		18.73
ATOM	162		E1 GL		1692	22.30		722		_	23.79
ATOM	163		E2 GL	U :	1692	22.91		819	13.962	-	22.70
ATOM	163		GL	נ ע	L692	25.072		963	15.738	1.00	
ATOM	1632	_	GL	ָן ל	692	25.278			17.225	1.00	
ATOM	1633	3 N	ILI	3 1	693	24.484			18.422	1.00	
ATOM	1634		ILI	3 1	.693	24.080			16.720	1.00	26.23
ATOM	1635		ILE		693	23.177			17.565	1.00	
ATOM	1636			1	693	22.966			16.787	1.00 2	
ATOM	1637		1 ILE		693	21.820			17.637	1.00 2	
ATOM	1638	CD	1 ILE	1	693	20.964			16.416	1.00 2	
ATOM	1639	С	ILE	1	693	25.322			15.435	1.00 1	
ATOM	1640	0	ILE		693	25.401			18.133	1.00 2	
MOTA	1641	N	PHE		694	26.329			19.324	1.00 2	
ATOM	1642	CA	PHE		594	27.503			L7.304	1.00 2	7.59
MOTA	1643	CB	PHE		594		-6.7		L7.827	1.00 2	9.42
ATOM	1644	CG	PHE		594	28.122	-7.6		.6.771	1.00 2	9.37
ATOM	1645	CD:	PHE		94	27.142	-8.6		.6.263	1.00 2	7.99
ATOM	1646		PHE		94	26.522	-8.4		5.034	1.00 2	
ATOM	1647		PHE		94	26.751	-9.7		7.074	1.00 2	7.86
ATOM	1648		PHE		94	25.525	-9.3		4.625	1.00 3	0.12
ATOM	1649	CZ	PHE			25.751	-10.5	86 1	6.674	1.00 25	5.78
ATOM	1650	C	PHE		94	25.136			5.453	1.00 26	5.17
ATOM	1651	ō	PHE	16		28.495	-5.82		8.578	1.00 29	9 83
ATOM	1652	N		16		29.485	-6.30		9.126	1.00 32	9 81
ATOM	1653	CA	THR	16		28.217	-4.51			1.00 28	
ATOM	1654		THR	16		29.044	-3.59			1.00 25	
ATOM	1655	CB	THR	16		29.540	-2.37			1.00 23	01
ATOM	1656		THR	16		28.422	-1.62			1.00 21	· O T
ATOM		CG2		169		30.457	-2.81			1.00 21 1.00 16	. 54
ATOM ATOM	1657	C	THR	169		28.198	-3.12			1 00 20	. 33
	1658	0	THR	169	95	28.620	-2.26	_		1.00 26	· TP
							0	- 41		1.00 26	.77

ATOM	1659	N	LEU	1696	27.023	-3.747	20.747	1.00	26.87
MOTA	1660	CA	LEU	1696	26.069	-3.446	21.813	1.00	27.64
MOTA	1661	CB	LEU	1696	26.572	-3.977	23.156	1.00	30.54
ATOM	1662	CG	LEU	1696	26.903	-5.456	23.182	1.00	29.75
MOTA	1663	CD1	LEU	1696	27.448	-5.821	24.546	1.00	32.53
ATOM	1664	CD2	LEU	1696	25.658	-6.234	22.882	1.00	33.79
ATOM	1665	С	LEU	1696	25.727	-1.984	21.946	1.00	25.51
ATOM	1666	0	LEU	1696	25.824	-1.410	23.025	1.00	27.90
MOTA	1667	N	GLY	1697	25.265	-1.395	20.857	1.00	26.48
ATOM	1668	CA	GLY	1697	24.899	0.007	20.859	1.00	25.81
ATOM	1669	С	GLY	1697	26.040	0.900	20.452		26.40
MOTA	1670	0	GLY	1697	26.055	2.090	20.760	1.00	29.69
MOTA	1671	N	GLY	1698	27.008	0.330	19.748	1.00	
ATOM	1672	CA	GLY	1698	28.150	1.110	19.314		28.38
ATOM	1673	С	GLY	1698	27.795	2.186	18.310		30.13
ATOM	1674	0	GLY	1698	26.896	2.028	17.496		32.55
ATOM	1675	N	SER	1699	28.520	3.295	18.375		30.56
ATOM	1676	CA	SER	1699	28.304	4.420	17.491		32.11
ATOM	1677	CB	SER	1699	28.622	5.714	18.246	1.00	
ATOM	1678	OG	SER	1699	28.578	6.863	17.407		38.87
ATOM	1679	С	SER	1699	29.203	4.269	16.268		32.10
ATOM	1680	0	SER	1699	30.408	4.073	16.403	1.00	
ATOM	1681	N	PRO	1700	28.629	4.324	15.062		32.70
MOTA	1682	CD	PRO	1700	27.204	4.482	14.745		34.35
ATOM	1683	CA	PRO	1700	29.427	4.192	13.837		32.25
ATOM	1684	CB	PRO	1700	28.358	4.096	12.736		32.85
ATOM	1685	CG	PRO	1700	27.101	3.713	13.461		35.54
ATOM	1686	C	PRO	1700	30.258	5.456	13.651	1.00	
ATOM	1687	0	PRO	1700	29.792	6.550	13.983	1.00	31.56
ATOM	1688	N	TYR	1701	31.487	5.306	13.170	1.00	
ATOM	1689	CA	TYR	1701	32.372	6.441	12.910		32.41
ATOM	1690	CB	TYR	1701	32.039	7.055	11.537		32.39
ATOM	1691	CG	TYR	1701	32.088	6.092	10.378		35.63
ATOM	1692	CD1	TYR	1701	30.936	5.807	9.638	1.00	37.94
ATOM	1693	CE1	TYR	1701	30.977	4.955	8.535		40.79
ATOM	1694	CD2	TYR	1701	33.293	5.495	9.990		37.49
ATOM	1695	CE2	TYR	1701	33.351	4.646	8.886		41.82
ATOM	1696	CZ	TYR	1701	32.190	4.382	8.160	1.00	45.96
MOTA	1697	OH	TYR	1701	32.251	3.572	7.039		55.61
ATOM	1698	C	TYR	1701	32.377	7.559	13.970		32.85
ATOM	1699	0	TYR	1701			13.570		
	1700	N	PRO		32.066	8.711			32.41
ATOM				1702	32.753	7.229	15.215		34.48
ATOM	1701	CD	PRO	1702	33.288	5.946	15.695		35.64
ATOM	1702	CA	PRO	1702	32.775	8.258	16.270		33.68
MOTA	1703	CB	PRO	1702	33.321	7.499	17.482		32.52
ATOM	1704	CG	PRO	1702	33.063	6.061	17.166		38.81
ATOM	1705	C	PRO	1702	33.736	9.388	15.919		33.47
MOTA	1706	0	PRO	1702	34.875	9.145	15.522		34.66
ATOM	1707	N	GLY	1703	33.275	10.625	16.089		35.31
ATOM	1708	CA	GLY	1703	34.101	11.792	15.802		32.51
ATOM	1709	C	GLY	1703	34.232	12.166	14.339		33.68
MOTA	1710	0	GLY	1703	34.904	13.146	14.005	1.00	31.22

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ATOM			31 VA					
MOTA			32 VA	L 1706				
ATOM	1730		VA:	L 1706	30.69		6.155	1.00 32.74
ATOM	1731		VA]	1706			5.463	1.00 36.20
ATOM	1732		GLī	J 1707			6.020	1.00 38.16
ATOM	1733		GLU	J 1707			4.987	1.00 34.38
ATOM	1734		GLU	1707			5.083	1.00 33.75
ATOM	1735	С	GLU	1707			4,982	1.00 35.79
ATOM	1736		GLU	1707	34.036		3.923	1.00 31.97
ATOM	1737		GLU	1708	33.964		6.160	1.00 32.84
ATOM	1738			1708	34.987		6.249	1.00 29.57
ATOM	1739			1708	35.567		7.664	1.00 31.32
ATOM	1740	CG	GLU	1708	36.189		8.144	1.00 36.11
ATOM	1741	CD	GLU		37.444		7.383	1.00 44.10
ATOM	1742		1 GLU	1708	38.059		6.681	1.00 55.58
ATOM	1743	OE:	2 GLU	1708	37.830		7.517	1.00 61.47
ATOM	1744	С	GLU	1708	34.365	11.906	5.889	1.00 60.54
ATOM	1745	0	GLU	1708	35.013	11.041	5.294	1.00 32.20
ATOM	1746	N	LEU	1709	33.094	11.749	6.245	1.00 32.39
ATOM	1747	CA	LEU	1709	32.378	10.522	5.961	1.00 31.43
ATOM	1748	CB	LEU	1709	30.973	10.548	6.565	1.00 31.71 1.00 28.84
ATOM	1749	CG	LEU	1709	30.136	9.357	6.081	1.00 28.84
ATOM	1750		. LEU	1709	30.662	8.059	6.679	1.00 28.28
ATOM	1751		LEU	1709	28.705	9.556	6.437	1.00 27.34
ATOM	1752	С	LEU	1709	32.306	10.317	4.454	1.00 29.71
ATOM	1753	0	LEU	1709	32.489	9.202	3.970	
ATOM	1754	N	PHE	1710	32.043	11.399	3.727	1.00 31.79
ATOM	1755	CA	PHE	1710	31.945	11.366	2.279	1.00 30.99
ATOM	1756	CB	PHE	1710	31.680	12.768	1.737	1.00 32.80
ATOM	1757	CG	PHE	1710	30.310	13.261		1.00 34.22
ATOM	1758		PHE	1710	29.337	12.393		1.00 37.65
ATOM	1759		PHE	1710	29.984	14.596		1.00 43.43
ATOM	1760		PHE	1710	28.054	12.834		1.00 42.87
ATOM	1761		PHE	1710	28.698	15.053		1.00 46.00
MOTA	1762	CZ	PHE	1710	27.733	14.169		1.00 46.30
							2.005	1.00 46.49

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ATOM	1763	C	PHE	1710	33.196	10.802	1.667	1.00 34.25
MOTA	1764	0	PHE	1710	33.133	9.948	0.785	1.00 36.09
ATOM	1765	N	LYS	1711	34.324	11.249	2.209	1.00 34.37
MOTA	1766	CA	LYS	1711	35.664	10.840	1.789	1.00 34.11
ATOM	1767	CB	LYS	1711	36.672	11.768	2.476	1.00 37.74
ATOM	1768	CG	LYS	1711	38.114	11.567	2.119	1.00 43.59
MOTA	1769	CD	LYS	1711	38.978	12.573	2.857	1.00 46.97
MOTA	1770	CE	LYS	1711	40.386	12.575	2.304	1.00 51.53
MOTA	1771	NZ	LYS	1711	41.074	11.291	2.603	1.00 58.84
ATOM	1772	C	LYS	1711	35.948	9.354	2.103	1.00 33.25
ATOM	1773	0	LYS	1711	36.512	8.641	1.274	1.00 32.22
ATOM	1774	N	LEU	1712	35.537	8.894	3.285	1.00 32.62
ATOM	1775	CA	LEU	1712	35.718	7.496	3.667	1.00 31.41
ATOM	1776	СВ	LEU	1712	35.223	7.237	5.106	1.00 29.80
ATOM	1777	CG	LEU	1712	36.020	7.889	6.244	1.00 29.22
ATOM	1778	CD1	LEU	1712	35.385	7.643	7.608	1.00 24.09
ATOM	1779	CD2	LEU	1712	37.437	7.356	6.234	1.00 28.36
ATOM	1780	С	LEU	1712	34.939	6.638	2.674	1.00 31.88
ATOM	1781	0	LEU	1712	35.452	5.654	2.143	1.00 34.08
ATOM	1782	N	LEU	1713	33.700	7.029	2.413	1.00 32.28
ATOM	1783	CA	LEU	1713	32.850	6.305	1.482	1.00 35.36
ATOM	1784	CB	LEU	1713	31.433	6.887	1.485	1.00 38.97
MOTA	1785	CG	LEU	1713	30.629	6.494	2.730	1.00 39.56
ATOM	1786	CD1	LEU	1713	29.308	7.228	2.768	1.00 37.14
MOTA	1787	CD2	LEU	1713	30.424	4.988	2.748	1.00 37.73
ATOM	1788	С	LEU	1713	33.430	6.296	0.070	1.00 36.47
ATOM	1789	0	LEU	1713	33.502	5.244	-0.563	1.00 39.32
ATOM	1790	N	LYS	1714	33.855	7.455	-0.413	1.00 35.21
MOTA	1791	CA	LYS	1714	34.437	7.544	-1.743	1.00 34.55
MOTA	1792	CB	LYS	1714	34.812	8.984	-2.075	1.00 34.81
MOTA	1793	CG	LYS	1714	33.624	9.903	-2.290	1.00 36.55
MOTA	1794	$^{\rm CD}$	LYS	1714	32.681	9.372	-3.353	1.00 40.68
MOTA	1795	CE	LYS	1714	31,488	10.310	-3.577	1.00 44.87
MOTA	1796	NZ	LYS	1714	30.611	9.853	-4.701	1.00 50.99
MOTA	1797	С	LYS	1714	35.671	6.649	-1.856	1.00 35.97
MOTA	1798	0	LYS	1714	35.948	6.084	-2.920	1.00 38.11
MOTA	1799	N	GLU	1715	36.385	6.490	-0.749	1.00 33.65
MOTA	1800	CA	GLU	1715	37.582	5.663	-0.729	1.00 34.34
MOTA	1801	CB	GLU	1715	38.574	6.221	0.288	1.00 34.90
MOTA	1802	CG	GLU	1715	39.032	7.613	-0.110	1.00 42.07
MOTA	1803	CD	GLU	1715	39.729	8.405	0.989	1.00 47.94
MOTA	1804	OE1	GLU	1715	39.977	7.870	2.098	1.00 45.03
MOTA	1805	OE2	GLU	1715	40.026	9.596	0.709	1.00 51.48
MOTA	1806	C	GLU	1715	37.285	4.191	-0.466	1.00 34.76
ATOM	1807	0	GLU	1715	38.205	3.384	-0.411	1.00 37.36
MOTA	1808	N	GLY	1716	36.002	3.848	-0.347	1.00 32.00
MOTA	1809	CA	\mathtt{GLY}	1716	35.604	2.474	-0.122	1.00 30.49
ATOM	1810	С	GLY	1716	35.932	1.937	1.251	1.00 31.32
ATOM	1811	0	GLY	1716	36.134	0.738	1.430	1.00 31.83
ATOM	1812	N	HIS	1717	35.957	2.822	2.233	1.00 31.55
ATOM	1813	CA	HIS	1717	36.265	2.416	3.595	1.00 33.20
MOTA	1814	CB	HIS	1717	36.494	3.661	4.452	1.00 37.67



ATC	NA 10					•				
		15		IS 171		36.7	86	3.36	5.8	95 1.00 42.42
ATO			CD2 H		.7	37.9	57	3.25		
ATO			ND1 H		.7	35.7	89	3.14		
ATO			CE1 H			. 36.3	33	2.91		
ATO			NE2 H		7	37.6		2.97		
ATO				IS 171	7	35.1		1.56		
ATO				IS 171	7	33.9		1.81		
IOTA				RG 171	8	35.52		0.58		
ATO				RG 171	8 .	34.58		-0.28		
ATON			CB AI		8	34.53		-1.66		
ATON			CG AF		8	34.04		-1.65		
ATON			CD AF			32.57		-1.26		
ATOM			IE AR			32.03		-1.320		- · · · · · · · · · · · · · · · · · · ·
ATOM			Z AR		3 .	3,2.10	_	-0.324		
ATOM			TH1 AR		3	32.70		0.819		
ATOM			TH2 AR	G 1718	3	31.46		-0.444		22.00
ATOM			AR	G 1718	3	35.04		-0.438		
ATOM			AR	G 1718	:	36.23		-0.596		
ATOM			ME	T 1719	•	34.08		-0.372		
ATOM		_	A ME	T 1719		34.38		0.466		
ATOM				T 1719		33.11		0.246		
ATOM	1836	_		Γ 1719		32.51		1.155		
ATOM	1837			Ր 1719		31.082		1.526	11.251	
ATOM	1838					29.906		0.373	10.618	- 100 37, 43
ATOM	1839		MET			35.033		1.799	9.844	0 07.02
MOTA	1840		MET			34.900		2.772	9.098	
ATOM ATOM	1841		ASI			35.77€		1.825	10.945	
ATOM	1842					36.466		3.038	11.388	1.00 35.49
ATOM	1843 1844					37.585		2.694	12.376	1.00 41.64
ATOM	1845		_			38.688	- :	1.859	11.754	1.00 46.44
ATOM	1846		1 ASP			38.507	_	1.410	10.604	1.00 52.86
ATOM	1847	C	2 ASP			39.740		L.650	12.422	1.00 46.76
ATOM	1848	0	ASP			35.516		1.005	12.053	1.00 34.70
ATOM	1849	N	ASP	1720		34.459		3.603	12.548	1.00 34.31
ATOM	1850	CA	LYS LYS	1721		35.937		.265	12.132	1.00 33.39
ATOM	1851	CB	LYS	1721		35.119		.297	12.755	1.00 32.68
ATOM	1852	CG	LYS	1721		35.692		.690	12.500	1.00 33.55
ATOM	1853	CD	LYS	1721		34.834		.791	13.119	1.00 33.62
ATOM	1854	CE	LYS	1721 1721		35.336	-10	.158	12.771	1.00 35.77
ATOM	1855	NZ	LYS			36.082	-10	.747	13.931	1.00 38.73
ATOM	1856	C	LYS	1721		36.325			13.711	1.00 43.86
ATOM	1857	0	LYS	1721		35.034		.107	14.240	1.00 34.61
ATOM	1858	N	PRO	1721 1722		36.057		.944	14.905	1.00 37.05
ATOM	1859	CD	PRO			33.808		.092	14.781	1.00 36.16
ATOM	1860	CA	PRO	1722		32.518		.062	14.066	1.00 34.73
ATOM	1861	СВ	PRO	1722 1722		33.611		.926	16.222	1.00 37.84
ATOM	1862	CG	PRO	1722		32.095			16.360	1.00 37.19
ATOM	1863	C	PRO	1722		31.607			15.073	1.00 36.00
ATOM	1864	0	PRO	1722		34.266			16.950	1.00 39.95
ATOM	1865	N	SER	1723		34.340			16.406	1.00 38.82
ATOM	1866	CA	SER	1723		34.783			18.150	1.00 42.36
						35.359	-7.	995	18.890	1.00 45.70

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MOTA	1867	CB	SER	1723	36.170	-7.511	20.093	1.00 47.50
ATOM	1868	OG	SER	1723	35.341	-6.964	21.100	1.00 55.28
MOTA	1869	С	SER	1723	34.136	-8.784	19.346	1.00 46.70
ATOM	1870	0	SER	1723	33.037	-8.224	19.477	1.00 47.27
ATOM	1871	N	ASN	1724	34.296	-10.081	19.559	1.00 47.84
ATOM	1872	CA	ASN	1724	33.174	-10.900	19.992	1.00 51.26
MOTA	1873	СВ	ASN	1724	32.620	-10.361	21.330	1.00 57.15
MOTA	1874	CG	ASN	1724	33.732	-10.088	22.365	1.00 61.53
ATOM	1875	OD1	ASN	1724	34.565	-10.955	22.646	1.00 64.13
MOTA	1876	ND2		1724	33.763	-8.867	22.912	1.00 61.69
MOTA	1877	С	ASN	1724	32.101	-10.916	18.873	1.00 50.72
ATOM	1878	0	ASN	1724	30.925	-10.617	19.089	1.00 52.63
ATOM	1879	N	CYS	1725	32.564	-11.193	17.663	1.00 48.01
ATOM	1880	CA	CYS	1725		-11.295	16.478	1.00 45.16
ATOM	1881	CB	CYS	1725	31.603	-9.929	15.788	1.00 44.77
ATOM	1882	SG	CYS	1725	30.605	-9.929	14.272	1.00 40.74
ATOM	1883	C	CYS	1725	32.421	-12.308	15.570	1.00 41.51
ATOM	1884	0	CYS	1725		-12.236	15.370	1.00 42.47
ATOM	1885	N	THR	1726		-12.236	15.064	1.00 42.47
ATOM	1886	CA	THR	1726	32.268		14.202	1.00 35.03
ATOM	1887	CB	THR	1726		-14.313	13.993	1.00 35.03
		OG1	THR	1726	31.308	-15.500		
ATOM	1888	CG2			30.074	-15.042	13.406	1.00 32.84
ATOM	1889		THR	1726	31.017	-16.160	15.306	1.00 29.78
ATOM	1890	C	THR	1726	32.678	-13.770	12.845	1.00 34.76
ATOM	1891	0	THR	1726	32.180	-12.729	12.415	1.00 38.22
ATOM	1892	N	ASN	1727	33.596	-14.450	12.175	1.00 32.47
ATOM	1893	CA	ASN	1727	34.009	-14.024	10.842	1.00 34.75
ATOM	1894	CB .	ASN	1727	35.167	-14.872	10.308	1.00 39.77
ATOM	1895	CG	ASN	1727	36.464	-14.591	11.026	1.00 46.09
ATOM	1896		ASN	1727	37.019	-13.495	10.933	1.00 49.54
ATOM	1897	ND2	ASN	1727	36.961	-15.585	11.749	1.00 50.04
ATOM	1898	C	ASN	1727	32.825	-14.147	9.905	1.00 33.38
ATOM	1899	0	ASN	1727		-13.405	8.929	1.00 34.10
ATOM	1900	N	GLU	1728	31.916	-15.065	10.224	1.00 32.01
ATOM	1901	CA	GLU	1728	30.707	-15.310	9.418	1.00 30.41
ATOM	1902	CB	GLU	1728	30.010	-16.580	9.917	1.00 32.27
ATOM	1903	CG	GLU	1728	28.811	-17.034	9.094	1.00 31.55
ATOM	1904	CD	GLU	1728	28.251	-18.369	9.577	1.00 36.38
ATOM	1905	OE1	GLU	1728		-18.694	10.777	1.00 38.35
ATOM	1906		GLU	1728			8.758	1.00 36.34
ATOM	1907	C	GLU	1728			9.468	1.00 29.40
ATOM	1908	0	GLU	1728		-13.679	8.438	1.00 26.23
MOTA	1909	N	LEU	1729		-13.610	10.672	1.00 29.19
MOTA	1910	CA	LEU	1729		-12.462	10.849	1.00 30.26
MOTA	1911	CB	LEU	1729		-12.343	12.310	1.00 30.74
MOTA	1912	CG	LEU	1729	27.198	-13.410	12.721	1.00 31.27
MOTA	1913		LEU	1729	27.013	-13.377	14.226	1.00 33.65
ATOM	1914	CD2	LEU	1729	25.865	-13.161	12.010	1.00 26.16
MOTA	1915	С	LEU	1729	29.269	-11.161	10.335	1.00 28.79
ATOM	1916	0	LEU	1729	28.548	-10.255	9.914	1.00 30.60
ATOM	1917	N	TYR	1730	30.594	-11.069	10.363	1.00 26.64
MOTA	1918	CA	TYR	1730	31.281	-9.881	9.844	1.00 26.47

ATC	OM 19	919	CB :	ryr	1720						
ATC	_	920		TYR	1730	32.			9 10.2	98 1.00 24.31	3
ATO		21			1730	33.			0 9.8	05 1.00 25.61	
ATO	_	22	CD1 7		1730	33.0					
ATO		23	CE1 7		1730	33.6					
ATO	_		CD2 1		1730	34.6	88	-8.82	-		
ATO				YR	1730	35.3	61	-7.71			
	_			YR	1730	34.8					
ATO					1730	35.4		-5.35			
ATO			C T	YR	1730	31.1		-9.90		= 1 4 4 21.37	
ATO			ОТ	YR	1730	30.9		-8.88			
ATO			N M	ET :	1731			-11.084			
ATON			CA M	ET :	1731	31.2	47	-11.27	_		
ATOM		31 (CB M	ET :	1731	31 4	75	-12.740		45.50	
ATOM	1 193	32 (CG MI		1731	31 0	76	-13.157			
ATOM	1 193	33 5	SD MI	er 1	1731	31 6	10	-13.15,			
ATOM	1 193	34 (CE ME		1731	32.6	- 2	-14.831			
ATOM	193	5 C	: ME		731			-14.506			
ATOM	193	6 C			731			-10.819			
ATOM	193	7 N		_	.732			-10.194		1 1.00 30.94	
ATOM	193		A ME		732			-11.134		3 1.00 29.40	
ATOM	193		В МЕ		732	27.47	5	-10.743	6.32	8 1.00 26.97	
ATOM		_			732	26.53	7	-11.293	7.398	8 1.00 25.73	
ATOM								-10.984	7.156		
ATOM	194				732			-11.637	8.407	7 1.00 26.97	
ATOM	194			_	732	23.77	3 -	-13.354	7.798		
ATOM	194	_		_	732	27.38		-9.220	6.271	1.00 27.49	
ATOM	194	_	ME'		732	26.77		-8.661	5.361		
ATOM	1946		ME'		733	27.98		-8.550	7.259		
ATOM	1947				733	28.00	1	-7.090	7.293		
ATOM					733	28.79	7	-6.587	8.484	1.00 27.41	
ATOM	1948				733	28.15	3	-6.761	9.829		
ATOM	1949				733	29.300		-6.248	11.127		
ATOM	1950				733	28.850		-7.423	12.399		
ATOM	1951		MEI		33	28.711		-6.599	6.035	05	
	1952		MET	17	33	28.250		-5.680	5.357	1.00 28.54	
ATOM	1953		ARG		34	29.865		-7.194	5.751	1.00 30.69	
ATOM	1954	_		17	34	30.650		-6.831		1.00 28.59	
ATOM	1955	CB	ARG	17	34	31.970		-7.609	4.571	1.00 29.53	
ATOM	1956	CG	ARG	17	34	32.944		-7.245	4.531	1.00 28.74	
ATOM	1957	CD	ARG	17	34	33.158		-5.755	5.638	1.00 26.75	
ATOM	1958	NE	ARG	17	34	33.825			5.702	1.00 26.58	
ATOM	1959	CZ	ARG	17:	34	35.139		·5.288 ·5.360	4.499	1.00 34.72	
ATOM.	1960	NH	L ARG	173	34	35.927			4.306	1.00 37.67	
ATOM	1961	NH2	ARG	173		35.663		5.867	5.251	1.00 40.46	
ATOM	1962	C	ARG	173		29.855		4.986	3.147	1.00 38.11	
ATOM	1963	0	ARG	173				7.051	3.294	1.00 28.03	
ATOM	1964	N	ASP	173		29.958		6.260	2.359	1.00 27.22	
ATOM	1965	CA	ASP	173		29.071		8.130	3.260	1.00 27.81	
ATOM	1966	CB	ASP	173		28.212		8.436	2.103	1.00 27.27	
ATOM	1967	CG	ASP			27.608	-	9.835	2.216	1.00 28.62	
ATOM	1968		ASP	173		28.638	-1	0.932	2.075	1.00 30.15	
ATOM	1969		ASP	173		29.745	-1	0.663	1.553	1.00 31.23	
ATOM	1970	C C		173		28.354	-12	2.070	2.501	1.00 32.00	
	-270	_	ASP	173	5	27.099	- 7	7.400	1.971	1.00 24.78	
									-	44 44,70	

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ATOM	1971	0	ASP	1735	26.714	-7.068	0.852	1.00	24.52
MOTA	1972	N	CYS	1736	26.590	-6.908	3.104	1.00	24.10
MOTA	1973	CA	CYS	1736	25.530	-5.871	3.140	1.00	25.20
MOTA	1974	CB	CYS	1736	24.965	-5.679	4.569	1.00	23.85
MOTA	1975	SG	CYS	1736	23.898	-7.030	5.143		18.77
ATOM	1976	C	CYS	1736	26.042	-4.520	2.611		23.39
MOTA	1977	0	CYS	1736	25.276	-3.718	2.070	1.00	21.76
MOTA	1978	N	TRP	1737	27.348	-4.303	2.743	1.00	23.53
ATOM	1979	CA	TRP	1737	27.988	-3.072	2.302	1.00	21.57
MOTA	1980	CB	TRP	1737	29.026	-2.631	3.314	1.00	18.82
MOTA	1981	CG	TRP	1737	28.485	-2.418	4.686	1.00	19.89
MOTA	1982		TRP	1737	29.194	-2.609	5.913		22.39
MOTA	1983		TRP	1737	28.329	-2.213	6.959	1.00	21.78
ATOM	1984		TRP	1737	30.478	-3.083	6.238		23.52
MOTA	1985		TRP	1737	27.248	-1.932	5.022		19.40
MOTA	1986	NE1	TRP	1737	27.147	-1.805	6.383		21.52
ATOM	1987		TRP	1737	28.705	-2.270	8.319		21.85
ATOM	1988		TRP	1737	30.857	-3.134	7.583		25.30
ATOM	1989	CH2	TRP	1737	29.972	-2.728	8.604		26.17
ATOM	1990	С	TRP	1737	28.673	-3.226	0.956		24.49
ATOM	1991	0	TRP	1737	29.648	-2.519	0.670		25.09
MOTA	1992	N	HIS	1738	28.203	-4.170	0.136		25.12
ATOM	1993	CA	HIS	1738	28.808	-4.341	-1.172		22.90
MOTA	1994	CB	HIS	1738	28.163	-5.497	-1.928		23.14
ATOM	1995	CG	HIS	1738	29.017	-6.013	-3.051		23.26
ATOM	1996	CD2		1738	29.550	-5.380	-4.129		23.78
ATOM	1997	ND1		1738	29.492	-7.308	-3.104		24.91
ATOM	1998	CE1		1738	30.286	-7.445	-4.156		25.29
ATOM	1999	NE2		1738	30.341	-6.288	-4.794		26.99
ATOM	2000	C	HIS	1738	28.670	-3.024	-1.958		22.92
ATOM	2001	0	HIS	1738	27.615	-2.381	-1.933		20.27
ATOM	2002	N	ALA	1739	29.752	-2.608	-2.607		24.30
ATOM	2003 2004	CA CB	ALA ALA	1739	29.762	-1.378	-3.385		23.70
ATOM ATOM	2004	CB	ALA	1739 1739	31.079	-1.234	-4.076 -4.416		25.24
ATOM	2005	0	ALA	1739	28.645 27.955	-1.391 -0.391	-4.416		25.37 27.86
ATOM	2007	N	VAL	1740	28.507	-2.521	-5.102		23.97
ATOM	2007	CA	VAL	1740	27.481	-2.700	-6.121		24.64
ATOM	2009	CB	VAL	1740	27.966	-3.698	-7.206		26.39
ATOM	2010	_	VAL	1740	27.013	-3.757	-8.360		22.65
ATOM	2011		VAL	1740	29.308	-3.757	-7.720		27.43
ATOM	2012	C	VAL	1740	26.170	-3.209	-5.481		23.97
ATOM	2012	0	VAL	1740	26.176	-4.347	-4.978		24.14
ATOM	2014	N	PRO	1741	25.090	-2.397	-5.545		22.77
ATOM	2015	CD	PRO	1741	25.074	-1.093	-6.237		17.82
ATOM	2016	CA	PRO	1741	23.763	-2.695	-4.980		23.22
ATOM	2017	CB	PRO	1741	22.891	-1.554	-5.526		18.19
ATOM	2017	CG	PRO	1741	23.866	-0.419	-5.647		15.09
ATOM	2019	C	PRO	1741	23.189	-4.074	-5.343		23.26
ATOM	2020	0	PRO	1741	22.700	-4.788	-4.462		22.42
ATOM	2021	N	SER	1742	23.335	-4.473	-6.615		23.49
ATOM	2021	CA	SER	1742	22.826	-5.754	-7.119		23.49
.11011		C. 3		~ / 34	22.020	5.754	, , , , ,	1.00	23.11

ATON	1 202	3 C	B SE	R 1742	22.056			
ATOM					22.956	-5.808	-8.641	1.00 23.67
ATOM			SE		24.324	-5.891	-9.023	
ATOM		_		_	23.524	-6.984	-6.545	1.00 23.09
ATOM			SE	· - -	22.993	-8.104	-6.603	
ATOM	_		GL		24.719	~6.782	-5.997	
ATOM					25.466	-7.895	~5.416	
					26.953	-7.754	-5.702	
ATOM					27.255	-7.828	-7.170	
ATOM		-	-		26.684	-9.076	-7.810	1.00 24.83
ATOM			:1 GLI		27.176	-10.178	-7.584	
MOTA			2 GLI	N 1743	25.647	-8.907	-8.625	1.00 21.07
MOTA	2034	f C	GL1	V 1743	25.227	-8.121	-3.927	
ATOM	2035	5 0	GL1	V 1743	25.744	-9.083	-3.366	1.00 23.85
ATOM	2036	N	ARC	3 1744	24.458	-7.240	-3.290	1.00 25.36
ATOM	2037	' CA	ARC	3 1744	24.155	-7.395		1.00 22.69
MOTA	2038	СВ	ARÇ		23.635		-1.868	1.00 21.65
ATOM	2039	CG			24.623	-6.087	-1.277	1.00 21.22
ATOM	2040	CD	ARG			-4.962	-1.342	1.00 21.63
ATOM	2041		ARG	· · · - •	24.013	-3.656	-0.863	1.00 19.06
ATOM	2042		ARG	·	24.869	-2.563	-1.318	1.00 24.44
ATOM	2043		l ARG		24.461	-1.322	-1.564	1.00 22.49
ATOM	2044		2 ARG		23.184	-0.972	-1.378	1.00 18.95
ATOM	2045		ARG		25.337	-0.438	-2.034	1.00 22.19
ATOM	2046	0		- -	23.095	-8.470	-1.712	1.00 22.45
ATOM	2047	N	ARG		22.363	-8.772	-2.654	1.00 25.62
ATOM	2047		PRO		23.065	-9.139	-0.559	1.00 21.78
ATOM		CD	PRO		24.025	-9.114	0.563	1.00 21.02
ATOM	2049	CA	PRO		22.057 -		-0.362	1.00 20.99
ATOM	2050	CB	PRO	1745	22.532 -	10.879	0.919	1.00 21.12
ATOM	2051	CG	PRO	1745	23.240	-9.777	1.676	1.00 19.86
	2052	C	PRO	1745	20.726	-9.485	-0.146	1.00 22.18
MOTA	2053	0	PRO	1745	20.680	-8.281	0.128	1.00 23.04
ATOM	2054	N	THR	1746	19.646 -	10.236	-0.297	1.00 19.31
ATOM	2055	CA	THR	1746			-0.085	1.00 19.12
ATOM	2056	CB	THR	1746	17.307 -		-1.045	1.00 19.12
ATOM	2057	OG1	THR	1746	17.299 -		-0.886	1.00 19.88
ATOM	2058	CG2	THR	1746	17.668 -		-2.479	
ATOM	2059	C	THR	1746		-9.975	1.367	1.00 22.97
ATOM	2060	0	THR	1746	18.676 -:		2.058	1.00 19.91
MOTA	2061	N	PHE	1747		-9.381		1.00 19.93
MOTA	2062	CA	PHE	1747		-9.678	1.855	1.00 21.80
ATOM	2063	CB	PHE	1747		-8.720	3.224	1.00 23.46
ATOM	2064	CG	PHE	1747				1.00 21.84
ATOM	2065	CD1	PHE	1747		7.368		1.00 24.84
ATOM	2066	CD2		1747		7.207		1.00 22.23
ATOM	2067	CE1		1747		6.248		1.00 22.97
ATOM	2068	CE2		1747		5.944		1.00 19.42
ATOM	2069	CZ	PHE			4.991	3.646	1.00 17.14
ATOM	2070	C		1747		4.846		1.00 18.02
ATOM	2070		PHE	1747	15.992 -1			1.00 22.28
ATOM	2071		PHE	1747	16.189 -1			1.00 23.76
ATOM			LYS	1748	15.430 -1			1.00 23.46
	2073		LYS	1748	14.971 -1	3.014		1.00 25.84
ATOM	2074	CB	LYS	1748	14.344 -1	_		L.00 26.89
								30 40.09

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MOTA	2075	CG	LYS	1748	14.061	-14.793	0.583	1.00	31.07
MOTA	2076	CD	LYS	1748	13.714	-15.064	-0.861	1.00	37.82
MOTA	2077	CE	LYS	1748	13.231	-16.493	-1.068	1.00	44.36
MOTA	2078	NZ	LYS	1748	12.027	-16.782	-0.235	1.00	50.16
ATOM	2079	C	LYS	1748	16.160	-13.949	2.393	1.00	27.27
MOTA	2080	0	LYS	1748	16.067	-14.877	3.202	1.00	27.87
ATOM	2081	N	GLN	1749	17.288	-13.674	1.730	1.00	25.64
MOTA	2082	CA	GLN	1749	18.507	-14.457	1.903	1.00	24.32
MOTA	2083	CB	GLN	1749	19.608	-13.938	0.983	1.00	28.87
MOTA	2084	CG	GLN	1749	19.343	-14.049	-0.496	1.00	36.24
MOTA	2085	CD	GLN	1749	20.437	-13.374	-1.318	1.00	41.30
MOTA	2086	OE1	GLN	1749	20.173	-12.422	-2.044	1.00	38.35
MOTA	2087	NE2	GLN	1749	21.683	-13.861	-1.190	1.00	45.38
MOTA	2088	С	GLN	1749	19.002	-14.310	3.346	1.00	22.89
MOTA	2089	0	GLN	1749	19.302	-15.305	4.008	1.00	22.55
MOTA	2090	N	LEU	1750	19.114	-13.064	3.813	1.00	20.89
MOTA	2091	CA	LEU	1750	19.570	-12.776	5.167	1.00	21.44
ATOM	2092	CB	LEU	1750	19.471	-11.282	5.462	1.00	19.53
ATOM	2093	CG	LEU	1750	20.432	-10.400	4.663	1.00	19.14
MOTA	2094	CD1	LEU	1750	20.069	-8.919	4.816	1.00	14.53
MOTA	2095	CD2	LEU	1750	21.863	-10.685	5.106	1.00	16.18
MOTA	2096	C	LEU	1750	18.776	-13.538	6.208	1.00	22.98
ATOM	2097	0	LEU	1750	19.335	-14.057	7.183	1.00	23.12
ATOM	2098	N	VAL	1751	17.465	-13.586	6.020	1.00	23.48
MOTA	2099	CA	VAL	1751	16.610	-14.292	6.945	1.00	23.21
MOTA	2100	CB	VAL	1751	15.132	-14.075	6.590	1.00	20.94
MOTA	2101	CG1	VAL	1751	14.268	-15.008	7.375	1.00	21.67
ATOM	2102	CG2	VAL	1751	14.730	-12.649	6.929	1.00	20.32
ATOM	2103	С	VAL	1751	16.974	-15.774	6.990	1.00	26.13
ATOM	2104	0	VAL	1751	17.030	-16.379	8.058	1.00	26.35
MOTA	2105	N	GLU	1752	17.260	-16.348	5.831	1.00	30.05
MOTA	2106	CA	GLU	1752	17.632	-17.747	5.778	1.00	32.54
MOTA	2107	CB	GLU	1752	17.695	-18.221	4.338	1.00	38.54
ATOM	2108	CG	GLU	1752	16.322	-18.226	3.673	1.00	50.06
MOTA	2109	CD	GLU	1752	16.333	-18.759	2.247	1.00	56.55
MOTA	2110	OE1	GLU	1752	15.365	-18.480	1.507	1.00	61.63
MOTA	2111	OE2	GLU	1752	17.303	-19.466	1.875	1.00	59.57
MOTA	2112	C	GLU	1752	18.974	-17.965	6.486	1.00	31.62
ATOM	2113	0	GLU	1752	19.113	-18.858	7.322	1.00	29.63
ATOM	2114	N	ASP	1753		-17.103	6.193		30.74
MOTA	2115	CA	ASP	1753	21.246	-17.211	6.807	1.00	31.00
MOTA	2116	CB	ASP	1753	22.209	-16.181	6.203	1.00	31.47
ATOM	2117	CG	ASP	1753	22.445	-16.390	4.710	1.00	35.82
MOTA	2118	OD1	ASP	1753		-17.549	4.248		36.78
ATOM	2119	OD2	ASP	1753		-15.396	3.992		41.04
ATOM	2120	С	ASP	1753		-17.058	8.314		28.94
ATOM	2121	0	ASP	1753		-17.933	9.059		29.91
ATOM	2122	N	LEU	1754		-15.984	8.764		28.33
ATOM	2123	CA	LEU	1754		-15.731	10.199		26.88
ATOM	2124	СВ	LEU	1754		-14.372	10.457		19.82
ATOM	2125	CG	LEU	1754		-13.269	10.154		20.90
ATOM	2126		LEU	1754		-11.886	9.995		14.83



ATO	OM ⊃	7 7 7	G D 0		
ATO	_	127	CD2		4 21.831 -13.308 11.240 1.00 16 39
ATO	_	128	_	LEU 175	4 19 645 16 55
ATO		129		LEU 175	4 20 020 17 010
		130		ASP 175	5 18.638 ~17.421 10.220 1.00 50.33
ATO		131		ASP 175	5 17 993 10 755
ATC		132		ASP 1759	16 722 10 000
ATC		133		ASP 1755	15 076 10 00-
ATO		L34	OD1 A		15 410 70 000
ATO			OD2 A	SP 1755	15 600 01 000
ATO			C A	SP 1755	19 901 10 71
ATO			O A	SP 1755	18 665 20 100
ATO			A N	RG 1756	19 739 10 000
ATO			CA A	RG 1756	20 700 01 01
ATO		40	CB A	RG 1756	21 477 21
ATO			CG A	RG 1756	22 522 22 53.41
ATON	_		CD A	RG 1756	23 101 22 222
ATOM			IE AI	RG 1756	23 676 20 24.00
ATOM		44 (Z AI	RG 1756	24 705 20 205
ATOM		45 N	IH1 AF		25 556 20 00-
ATOM		16 N	H2 AF	RG 1756	25 165 10 165
ATOM		17 C	AR		21 710 00
ATOM		8 C	AR		22 000 23 53.01
ATOM		9 N	IL		22 244 10 77
ATOM		0 C	A IL		23 242 10 155
ATOM		1 C	B IL		22 045
ATOM		2 C	G2 IL		23.847 -17.753 11.984 1.00 34.59
ATOM	215	3 C	G1 IL	E 1757	24.915 -17.401 12.995 1.00 32.98
ATOM	215		01 IL		24.481 -17.757 10.586 1.00 33.64
ATOM	215	5 C	IL		24.812 -16.387 10.032 1.00 28.79
MOTA	215	6 0	IL		22.673 -19.182 13.716 1.00 36.74
ATOM	215	7 N	VAI		23.283 -19.764 14.601 1.00 36.60
ATOM	2158	3 CF	VAI		21.489 -18.608 13.917 1.00 39.16
ATOM	2159) CE	VAL		20.854 -18.589 15.243 1.00 41.06
ATOM	2160) CG	1 VAI	1758	19.378 -18.104 15.165 1.00 38.77
ATOM	2161		2 VAL		18.715 -18.183 16.530 1.00 38.72
ATOM	2162	C	VAL		19.309 -16.670 14.651 1.00 39.49
ATOM	2163	0	VAL		20.885 -19.986 15.850 1.00 43.92
ATOM	2164		ALA		21.403 -20.182 16.954 1.00 46.90
MOTA	2165	CA	ALA		20.370 -20.957 15.098 1.00 43.96
MOTA	2166	CB	ALA	1759	20.325 -22.354 15.528 1.00 43.47
ATOM	2167	C	ALA		19.653 -23.197 14.460 1.00 42.26
ATOM	2168	0	ALA	1759	21.693 -22.953 15.890 1.00 44.02
ATOM	2169	N	LEU	1760	21.780 -23.872 16.697 1.00 45.94
ATOM	2170	CA	LEU	1760	22.750 -22.465 15.255 1.00 45.07
ATOM	2171	CB	LEU	1760	24.095 -22.949 15.514 1.00 46.72
ATOM	2172	CG	LEU	1760	24.899 -22.900 14.225 1.00 48.22
ATOM	2173		LEU	1760	24.279 -23.645 13.053 1.00 51.98
ATOM	2174		LEU	1760	25.016 -23.279 11.778 1.00 56.19
ATOM	2175	C	LEU	1760	24.32/ -25.136 13.313 1.00 52.82
ATOM	2176	0	LEU	1760	24.811 -22.118 16.578 1 00 47 50
ATOM	2177	N	THR	1761	25.935 -22.432 16.986 1 00 44 63
ATOM	2178	CA	THR	1761	24.181 -21.031 17.004 1 00 40 33
				T 10T	24.791 -20.166 17.987 1.00 50.15
					- 3 - 3

ATOM	2179	CB	THR	1761	24.309	-18.707	17.811	1.00 49.78
MOTA	2180	OG1	THR	1761	24.650	-18.262	16.489	1.00 49.83
ATOM	2181	CG2	THR	1761	24.997	-17.793	18.809	1.00 49.37
MOTA	2182	С	THR	1761		-20.655	19.426	1.00 51.84
ATOM	2183	0	THR	1761	23.565	-21.064	19.866	1.00 51.38
ATOM	2184	N	SER	1762		-20.622	20.143	1.00 53.45
ATOM	2185	CA	SER	1762		-21.042	21.533	1.00 53.79
MOTA	2186	CB	SER	1762	27.301	-21.039	21.969	1.00 58.33
MOTA	2187	OG	SER	1762	27.502	-21.759	23.173	1.00 63.27
MOTA	2188	С	SER	1762	25.033	-20.081	22.403	1.00 50.43
MOTA	2189	0	SER	1762		-18.856	22.301	1.00 48.42
MOTA	2190	N	ALA	461	79.680	25.808	14.502	1.00 57.40
MOTA	2191	CA	ALA	461	79.609	24.651	13.610	1.00 53.47
ATOM	2192	CB	ALA	461	78.307	23.875	13.860	1.00 54.34
MOTA	2193	C	ALA	461	79.707	25.105	12.151	1.00 49.53
ATOM	2194	0	ALA	461	79.739	24.289	11.243	1.00 48.04
MOTA	2195	N	ALA	462		-26.417	11.957	1.00 46.57
ATOM	2196	CA	ALA	462	79.919	27.014	10.634	1.00 43.66
MOTA	2197	CB	ALA	462	80.034	28.532	10.750	1.00 43.87
MOTA	2198	С	ALA	462	81.074	26.461 ·	9.806	1.00 39.75
ATOM	2199	0	ALA	462	80.869	26.036	8.673	1.00 36.18
MOTA	2200	N	TYR	463	82.279	26.449	10.383	1.00 37.82
MOTA	2201	CA	TYR	463	83.477	25.959	9.686	1.00 36.88
MOTA	2202	CB	TYR	463	84.615	26.968	9.765	1.00 39.12
ATOM	2203	CG	TYR	463	84.372	28.176	8.894	1.00 45.68
ATOM	2204	CD1	TYR	463	84.071	29.422	9.456	1.00 46.07
ATOM	2205	CE1	TYR	463	83.783	30.518	8.652	1.00 48.07
ATOM	2206	CD2	TYR	463	84.384	28.064	7.501	1.00 47.80
ATOM	2207	CE2	TYR	463	84.096	29.154	6.690	1.00 45.55
ATOM	2208	CZ	TYR	463	83.796	30.372	7.271	1.00 47.44
ATOM	2209	OH	TYR	463	83.491	31.442	6.476	1.00 49.77
ATOM	2210	C	TYR	463	83.988	24.579	10.024	1.00 34.97
ATOM	2211	0	TYR	463	84.605	23.947	9.175	1.00 35.48
ATOM	2212	N	GLU	464	83.761	24.109	11.244	1.00 34.33
ATOM	2213	CA	GLU	464	84.224	22.769	11.630	1.00 36.96
ATOM ATOM	2214 2215	CB CG	GLU GLU	464 464	85.725	22.790	11.901	1.00 41.01
ATOM	2215	CD	GLU	464	86.123	23.764	12.991	1.00 45.91
ATOM	2217	OE1	GLU	464	87.619	24.009	13.075	1.00 53.97
ATOM	2218		GLU	464	88.013 88.400	24.922	13.835	1.00 58.84
ATOM	2219	C	GLU	464	83.517	23.311	12.383	1.00 56.78
ATOM	2220	0	GLU	464		22.294 23.106	12.875	1.00 34.98 1.00 35.30
ATOM	2221	N	LEU	465	83.252		13.763 12.939	
ATOM	2222	CA	LEU	465	83.193 82.527	21.003 20.449		1.00 33.52
	2223	CB					14.121	1.00 35.65
ATOM ATOM	2224	CG	LEU LEU	465 465	81.520	19.348	13.762 12.651	1.00 32.97 1.00 33.16
ATOM	2224		LEU	465	80.488	19.538		
ATOM	2225	CD2		465	79.356 79.983	18.544 20.981	12.911	1.00 27.30 1.00 29.96
ATOM	2227	CD2	LEU	465			12.596	1.00 29.96
ATOM	2228	0	LEU	465	83.572 84.707	19.862 19.573	15.058	
ATOM	2229	N	PRO	466		19.573	14.642	1.00 35.58
	2229	CD	PRO	466	83.215	19.684	16.338	1.00 39.91
MOTA	2230	\mathcal{L}	FRU	400	81.929	20.073	16.942	1.00 42.38



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ATO		231	CA	PRO	466	84.11	8 19.1	26 27 5	
ATO		232	CB	PRO	466	83.26		~	00 40.02
ATC		233	CG	PRO	466	82.32			02
ATC		234	C	PRO	466	84.47			
ATC		35	0	PRO	466	83.68			
ATO	M 22	36	N	GLU	467	85.66			
ATO	M 22	37	CA	GLU	467	86.10			
ATO	M 22	38	CB	GLU	467	87.56			
ATO	M 22	39		GLU	467		_		
ATO	M 22	40		GLU	467	88.00			
ATO	M 22	41 (OE1		467	89.37		_	4 1.00 63.95
ATO				GLU	467	90.12	_		8 1.00 62.08
ATO	M 224			GLU	467	89.69			5 1.00 66.76
ATO				GLU	467	85.892			3 1.00 44.81
ATOM				ASP		85.988		6 19.39	7 1.00 45.53
ATOM				ASP	468	85.572			1.00 43.85
ATOM				ASP	468	85.357			1.00 43.44
ATOM			_	ASP	468	83.872		2 19.247	
ATOM		-	D1 <i>F</i>		468	83.611		20.420	
ATOM			D2 A		468	82.452		20.888	1.00 48.19
ATOM					468	84.557			
ATOM				SP	468	85.887	11.411	18.299	
ATOM				SP	468	85.158	10.644		
ATOM			_	RO	469	87.194	11.182	18.433	1.00 40.72
ATOM		_		RO	469	88.167	12.102		1.00 40.72
ATOM	225	_	_	RO	469	87.861	9.992		1.00 39.00
ATOM				RO	469	89.228	10.078		1.00 39.00
ATOM	225° 2258			RO	469	89.484	11.564	18.551	1.00 39.03
ATOM		_		RO	469	87.173	8.663	18.229	1.00 38.11
ATOM	2259			RO	469	87.235	7.718	17.442	1.00 39.37
ATOM	2260 2261		AI		470	86.497	8.596	19.371	1.00 39.27
ATOM					470	85.814	7.374	19.770	1.00 42.32
ATOM	2262				470	85.030	7.614	21.062	
ATOM	2263				470	85.766	8.370	22.149	1.00 46.12
ATOM	2264				470	84.839	8.592	23.344	1.00 50.76
ATOM	2265				470	83.649	9.362	22.991	1.00 52.76
	2266				470	82.770	9.823	23.873	1.00 54.47
ATOM	2267		1 AR		470	82.945	9.597	25.169	1.00 59.36
ATOM	2268		2 AR		470	81.712	10.508	23.455	1.00 61.19
ATOM	2269	C	AR	G	470	84.814	6.896	18.721	1.00 62.88
ATOM	2270	0	AR	G	470	84.670	5.700		1.00 42.79
ATOM	2271	N	TR	₽	471	84.139	7.844	18.504	1.00 45.63
ATOM	2272	CA	TR	Ρ.	471	83.100	7.542	18.078	1.00 41.98
ATOM	2273	CB	TRI	, د	471	81.844	8.307	17.093	1.00 38.34
ATOM	2274	CG	TRI	,	471	81.195		17.451	1.00 35.68
ATOM	2275	CD2	TRI		171	80.388	7.794	18.670	1.00 37.42
ATOM	2276	CE2	TRE		171	79.961	6.614	18.772	1.00 37.19
ATOM	2277	CE3	TRE		171	79.987	6.513	20.112	1.00 36.99
ATOM	2278		TRE		171	81.223	5.626		1.00 37.80
ATOM	2279		TRP		71		8.350		1.00 33.34
ATOM	2280		TRP		71	80.486	7.583	20.794	1.00 34.46
ATOM	2281		TRP		71	79.150	5.464	20.559	1.00 38.31
ATOM	2282		TRP		71	79.180		18.303	1.00 36.97
				-		78.772	4.506	19.638	1.00 36.14

MOTA	2283	С	TRP	471	83.409	7.830	15.641	1.00	38.26
MOTA	2284	0	TRP	471	82.655	7.430	14.749	1.00	38.72
ATOM	2285	N	GLU	472	84.478	8.569	15.397	1.00	37.71
MOTA	2286	CA	GLU	472	84.839	8.951	14.041	1.00	38.43
MOTA	2287	CB	GLU	472	86.014	9.924	14.087	1.00	37.56
MOTA	2288	CG	GLU	472	86.146	10.835	12.871	1.00	37.26
MOTA	2289	CD	GLU	472	84.930	11.728	12.625	1.00	39.02
ATOM	2290	OE1	GLU	472	84.361	12.301	13.571	1.00	40.26
MOTA	2291	OE2	GLU	472	84.568	11.879	11.445	1.00	39.35
MOTA	2292	С	GLU	472	85.135	7.806	13.069	1.00	38.32
MOTA	2293	0	GLU	472	85.872	6.875	13.386	1.00	38.11
MOTA	2294	N	LEU	473	84.535	7.884	11.883	1.00	38.44
ATOM	2295	CA	LEU	473	84.775	6.893	10.848	1.00	37.19
MOTA	2296	CB	LEU	473	83.505	6.112	10.511	1.00	35.38
ATOM	2297	CG	LEU	473	83.805	4.910	9.599	1.00	36.49
ATOM	2298	CD1	LEU	473	84.365	3.748	10.406	1.00	34.47
ATOM	2299	CD2	LEU	473	82.556	4.452	8.859	1.00	37.55
ATOM	2300	C	LEU	473	85.283	7.623	9.601	1.00	38.21
ATOM	2301	0	LEU	473	84.696	8.631	9.187	1.00	38.52
ATOM	2302	N	PRO	474	86.412	7.156	9.025	1.00	37.74
ATOM	2303	CD	PRO	474	87.292	6.107	9.568	1.00	36.38
ATOM	2304	CA	PRO	474	87.010	7.753	7.824	1.00	36.91
ATOM	2305	CB	PRO	474	88.233	6.865	7.587	1.00	34.65
ATOM	2306	CG	PRO	474	88.620	6.477	8.967	1.00	32.99
ATOM	2307	C	PRO	474	86.036	7.663	6.660	1.00	38.15
ATOM	2308	0	PRO	474	85.536	6.578	6.362	1.00	38.24
ATOM	2309	N	ARG	475	85.793	8.784	5.981	1.00	38.90
ATOM	2310	CA	ARG	475	84.846	8.802	4.863	1.00	41.23
ATOM	2311	CB	ARG	475	84.743	10.206	4.258	1.00	38.36
MOTA	2312	CG	ARG	475	84.311	11.271	5.267	1.00	35.30
ATOM	2313	CD	ARG	475	84.282	12.691	4.679	1.00	35.23
MOTA	2314	NE	ARG	475	83.850	13.658	5.679	1.00	27.27
MOTA	2315	CZ	ARG	475	82.585	13.859	6.011	1.00	25.77
MOTA	2316	NHl	ARG	475	81.630	13.181	5.402	1.00	25.09
ATOM	2317	NH2	ARG	475	82.286	14.639	7.047	1.00	25.24
MOTA	2318	C	ARG	475	85.101	7.745	3.791	1.00	42.43
MOTA	2319	0	ARG	475	84.160	7.212	3.204	1.00	44.06
ATOM	2320	N	ASP	476	86.359	7.381	3.594	1.00	44.69
MOTA	2321	CA	ASP	476	86.690	6.384	2.583	1.00	48.37
MOTA	2322	CB	ASP	476	88.197	6.371	2.319	1.00	52.12
ATOM	2323	CG	ASP	476	88.988	5.925	3.521	1.00	56.56
ATOM	2324	OD1	ASP	476	89.299	4.718	3.613	1.00	59.72
ATOM	2325	OD2	ASP	476	89.294	6.779	4.376	1.00	61.19
ATOM	2326	C	ASP	476	86.210	4.988	2.973	1.00	49.50
MOTA	2327	0	ASP	476	86.204	4.074	2.145	1.00	51.61
ATOM	2328	N	ARG	477	85.852	4.814	4.241	1.00	48.26
ATOM	2329	CA	ARG	477	85.357	3.525	4.732	1.00	47.16
MOTA	2330	CB	ARG	477	85.909	3.252	6.126	1.00	49.76
MOTA	2331	CG	ARG	477	87.325	2.723	6.088		53.26
MOTA	2332	CD	ARG	477	88.043	2.898	7.406	1.00	58.02
MOTA	2333	NE	ARG	477	87.394	2.213	8.517	1.00	61.16
ATOM	2334	CZ	ARG	477	87.810	2.297	9.776	1.00	63.35



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ATO			NH1 AR		88.87	5 3.032	2 10.083	1.00 64.92
ATO			NH2 AR		87.13	9 1.675		
ATO			C ARO		83.822			
ATO			O ARO		83.239			
ATO			N LEU		83.175			
ATO			CA LEU		81.721			12.05
ATO			CB LEU		81.198			/ -
ATO			CG LEU		79.673			
ATON			CD1 LEU		79.146			
ATON			D2 LEU		79.313			
ATOM	_	_			81.329			1.00 34.82
ATOM		_			81.818		1.935	
ATOM					80.477		1.925	1.00 40.60
ATOM			'A VAL	479	80.020	4.058	0.544	1.00 38.78
ATOM			B VAL	479	80.353	2.845	-0.360	1.00 37.97
ATOM			G1 VAL	479	79.837	3.090	-1.759	1.00 36.36
ATOM			G2 VAL	479	81.868	2.626	-0.405	1.00 33.55
ATOM		2 C	VAL	479	78.523	4.298		1.00 33.76
ATOM			VAL	479	77.750	3.383	0.562 0.820	1.00 37.83
ATOM			LEU	480	78.127	5.542	0.820	1.00 37.70
ATOM	235	5 C	A LEU	480	76.723	5.942	0.333	1.00 39.32
ATOM	2356		3 LEU	480	76.630	7.458	0.224	1.00 38.41
ATOM	2357			480	77.287	8.226	1.377	1.00 38.29
ATOM	2358		O1 LEU	480	77.098	9.730	1.159	1.00 37.99
ATOM	2359		2 LEU	480	76.666	7.785	2.703	1.00 34.00
ATOM	2360		LEU	480	75.893	5.287	-0.753	1.00 32.79
ATOM	2361	. 0	LEU	480	76.315	5.205	-1.903	1.00 38.24
ATOM	2362		\mathtt{GLY}	481	74.672	4.896		1.00 39.11
ATOM	2363		GLY	481	73.811	4.223	-0.394	1.00 36.70
ATOM	2364		\mathtt{GLY}	481	72.417	4.782	-1.357	1.00 36.53
ATOM	2365	0	${ t GLY}$	481	72.159	5.961	-1.524 -1.277	1.00 37.61
ATOM	2366	N	LYS	482	71.484	3.913		1.00 40.02
ATOM	2367	CA	LYS	482	70.099	4.313	-1.911 -2.153	1.00 37.52
ATOM	2368	CB	LYS	482	69.243	3.104		1.00 39.89
ATOM	2369	C	LYS	482	69.447		-2.551 -0.984	1.00 42.44
ATOM	2370	. 0	LYS	482	69.538	4.589		1.00 41.25
ATOM	2371	N	PRO	483	68.779			1.00 42.22
ATOM	2372	CD	PRO	483	68.643			1.00 41.71
ATOM	2373	CA	PRO	483	68.118	-		1.00 41.01
ATOM	2374	CB	PRO	483	67.606			1.00 42.72
ATOM	2375	CG	PRO	483	67.425			1.00 41.26
ATOM	2376	C	PRO	483	66.999	6.061		1.00 40.16
MOTA	2377	0	PRO	483	66.306			1.00 44.69
MOTA	2378	N	LEU	484	66.883	6.163		1.00 45.26
MOTA	2379	CA	LEU	484	65.872	5.450		1.00 45.34
ATOM	2380	CB	LEU	484	66.494	4.793		1.00 47.34
ATOM	2381	CG	LEU	484	67.517	3.668		1.00 42.40
ATOM	2382		LEU	484	68.208	3.337		.00 39.50
ATOM	2383	CD2	LEU	484	66.861			.00 33.64
ATOM	2384	C	LEU	484	64.733	2.419 6.391		.00 33.44
MOTA	2385	0	LEU	484	63.611			.00 52.14
ATOM	2386	N	GLY	485	65.013			.00 53.64
					-2.013	7.697	3.025 1	.00 55.25



ATOM	2387	CA	GLY	485	63.982	8.653	3.427	1.00	58.76
MOTA	2388	C	GLY	485	64.441	10.104	3.503	1.00	60.58
MOTA	2389	0	GLY	485	65.640	10.376	3.600	1.00	61.49
ATOM	2390	N	ALA	486	63.490	11.032	3.489	1.00	61.46
ATOM	2391	CA	ALA	486	63.791	12.458	3.545	1.00	63.24
MOTA	2392	CB	ALA	486	63.847	13.035	2.126	1.00	64.42
ATOM	2393	С	ALA	486	62.730	13.179	4.355	1.00	63.86
ATOM	2394	0	ALA	486	61.655	12.633	4.599	1.00	65.24
ATOM	2395	N	GLY	487	63.022	14.404	4.768		63.89
ATOM	2396	CA	GLY	487	62.054	15.158	5.538	1.00	64.30
ATOM	2397	С	GLY	487	62.431	16.617	5.623	1.00	65.34
MOTA	2398	0	GLY	487	63.071	17.154	4.718	1.00	65.98
ATOM	2399	N	ALA	488	62.023	17.259	6.711	1.00	66.16
MOTA	2400	CA	ALA	488	62.317	18.666	6.934	1.00	66.71
ATOM	2401	CB	ALA	488	61.647	19.132	8.219	1.00	70.05
ATOM	2402	С	ALA	488	63.828	18.844	7.027		66.55
ATOM	2403	0	ALA	488	64.432	18.547	8.063		65.59
ATOM	2404	N	PHE	489	64.430	19.228	5.904		65.54
ATOM	2405	CA	PHE	489	65.875	19.457	5.807	1.00	65.40
ATOM	2406	CB	PHE	489	66.244	20.775	6.498	1.00	
ATOM	2407	С	PHE	489	66.773	18.296	6.311		64.01
ATOM	2408	0	PHE	489	67.942	18.502	6.651		62.51
MOTA	2409	N	GLY	490	66.234	17.075	6.288		61.41
ATOM	2410	CA	GLY	490	66.974	15.901	6.724	1.00	
ATOM	2411	С	GLY	490	66.858	14.821	5.667	1.00	53.58
ATOM	2412	0	GLY	490	65.825	14.703	5.000	1.00	54.22
ATOM	2413	N	GLN	491	67.899	14.006	5.543	1.00	51.23
ATOM	2414	CA	GLN	491	67.966	12.934	4.556	1.00	47.90
MOTA	2415	CB	GLN	491	68.823	13.445	3.387	1.00	50.09
ATOM	2416	CG	GLN	491	68.979	12.529	2.183	1.00	56.77
ATOM	2417	CD	GLN	491	69.945	13.115	1.161	1.00	60.83
MOTA	2418	OE1	GLN	491	70.283	14.292	1.218	1.00	65.11
MOTA	2419	NE2	GLN	491	70.411	12.284	0.232	1.00	63.81
MOTA	2420	С	GLN	491	68.597	11.673	5.190	1.00	45.27
MOTA	2421	0	GLN	491	69.507	11.758	6.014	1.00	45.41
ATOM	2422	N	VAL	492	68.112	10.503	4.805	1.00	41.69
MOTA	2423	CA	VAL	492	68.624	9.245	5.325	1.00	39.95
ATOM	2424	CB	VAL	492	67.583	8.528	6.230	1.00	41.77
MOTA	2425	CG1	VAL	492	68.117	7.168	6.701	1.00	39.86
ATOM	2426	CG2	VAL	492	67.226	9.399	7.421	1.00	42.87
ATOM	2427	C	VAL	492	68.911	8.348	4.126	1.00	38.86
ATOM	2428	0	VAL	492	68.025	8.114	3.301	1.00	37.55
MOTA	2429	N	VAL	493	70.141	7.862	4.010	1.00	36.01
MOTA	2430	CA	VAL	493	70.481	6.994	2.895	1.00	37.55
MOTA	2431	CB	VAL	493	71.471	7674	1.889	1.00	38.65
MOTA	2432	CG1	VAL	493	71.128	9.137	1.709	1.00	37.08
ATOM	2433		VAL	493	72.929	7.498	2.318	1.00	39.03
MOTA	2434	С	VAL	493	71.071	5.678	3.371		38.61
ATOM	2435	0	VAL	493	71.645	5.599	4.456		39.75
MOTA	2436	N	LEU	494	70.899	4.637	2.572		39.68
ATOM	2437	CA	LEU	494	71.460	3.345	2.910		40.98
ATOM	2438	CB	LEU	494	70.748	2.241	2.123		42.14



3.50								
ATON	-		G LEU		71.25	0 0.80	8 2.309	1.00 40.33
ATON			D1 LEU		71.18	6 0.42		
ATOM	_		D2 LEU		70.41	1 -0.11		
ATOM	_				72.91			
ATOM			_		73.24	9 4.163		
ATOM		_			73.798	3 2.725		
ATOM					75.202	2.768		
ATOM					75.858	3.999		
MOTA			ALA	495	75.887	1.497		
ATOM			ALA	495	75.271			
ATOM			GLU	496	77.140	1.314		
ATOM			-	496	77.910	0.154		
ATOM				496	. 78.282			
ATOM				496	77.062			1.00 56.98
ATOM				496	77.316			1.00 60.32
ATOM			El GLU	496	76.448			1.00 62.17
ATOM	2455	-	_	496	78.371		-0.103	1.00 60.48
ATOM	2456		GLU	496	79.151	0.658	3.987	1.00 43.27
ATOM	2457		GLU	496	79.957	1.366	3.387	1.00 44.49
ATOM	2458		ALA	497	79.232	0.385	5.282	1.00 43.29
ATOM	2459			497	80.374	0.799	6.086	1.00 44.01
ATOM	2460			497	79.910	1.182	7.471	1.00 42.35
ATOM	2461		ALA	497	81.381	-0.351	6.150	1.00 45.60
ATOM	2462		ALA	497	80.997	-1.512	6.107	1.00 43.35
ATOM	2463		ILE	498	82.666	-0.025	6.206	1.00 48.78
ATOM	2464		ILE	498	83.709	-1.042	6.262	1.00 49.43
ATOM	2465	CB	ILE	498	84.611	-0.977	5.014	1.00 50.66
ATOM	2466	CG:		498	85.681	-2.054	5.082	1.00 51.85
ATOM	2467	CG:		498	83.780	-1.150	3.741	1.00 50.27
ATOM	2468	CD:		498	83.073	0.112	3.255	1.00 54.24
ATOM	2469	C	ILE	498	84.572	-0.878	7.510	1.00 50.32
MOTA	2470	0	ILE	498	85.055	0.219	7.801	1.00 49.08
ATOM ATOM	2471	N	GLY	499	84.713	-1.964	8.270	1.00 51.88
		CA	GLY	499	85.526	-1.958	9.480	1.00 55.86
ATOM	2473	C	GLY	499	85.061	-1.111	10.661	1.00 59.72
ATOM	2474	0	GLY	499	85.885	-0.545	11.393	1.00 61.66
ATOM ATOM	2475	N	LEU	500	83.747	-1.058	10.878	1.00 59.88
ATOM	2476	CA	LEU	500	83.167	-0.275	11.974	1.00 58.62
ATOM	2477	CB	LEU	500	81.663	-0.556	12.086	1.00 57.41
ATOM	2478	CG	LEU	500	80.764	-0.090	10.937	1.00 55.24
	2479		LEU	500	79.331	-0.536	11.168	1.00 51.91
ATOM	2480		LEU	500	80.845	1.426		1.00 54.93
ATOM	2481	C	LEU	500	83.849	-0.565		1.00 58.51
ATOM	2482	0	LEU	500	84.226	~1.710		1.00 60.71
ATOM	2483	N	PRO	505	87.501	-6.102		1.00 82.25
ATOM	2484	CD	PRO	505	88.578	-6.722		1.00 82.69
ATOM	2485	CA	PRO	505	87.860	-4.730		1.00 80.47
ATOM	2486	CB	PRO	505	89.257	-4.557		1.00 80.88
MOTA	2487	CG	PRO	505	89.782			1.00 81.84
ATOM	2488	C	PRO	505	87.850	-4.508		1.00 31.84
ATOM	2489	0	PRO	505	88.038	-3.391		1.00 76.83
ATOM	2490	N	ASN	506	87.632	-5.584		1.00 74.91
								



MOTA	2491	CA	ASN	506	87.572	-5.502	6.375	1.00 73.04
ATOM	2492	CB	ASN	506	88.632	-6.406	5.749	1.00 73.39
ATOM	2493	С	ASN	506	86.180	-5.938	5.929	1.00 71.75
ATOM	2494	0	ASN	506	85.918	-6.094	4.739	1.00 71.33
ATOM	2495	N	ARG	507	85.294	-6.124	6.905	1.00 69.66
ATOM	2496	CA	ARG	507	83.924	-6.534	6.638	1.00 66.59
ATOM	2497	CB	ARG	507	83.369	-7.329	7.819	1.00 69.86
MOTA	2498	C	ARG	507	83.048	-5.321	6.409	1.00 63.59
MOTA	2499	0	ARG	507	83.225	-4.291	7.070	1.00 64.09
MOTA	2500	N	VAL	508	82.126	-5.429	5.462	1.00 59.52
MOTA	2501	CA	VAL	508	81.217	-4.334	5.187	1.00 57.28
ATOM	2502	CB	VAL	508	80.905	-4.178	3.686	1.00 55.73
ATOM	2503		VAL	508	82.163	-3.952	2.922	1.00 57.01
MOTA	2504		VAL	508	80.184	-5.390	3.149	1.00 58.06
MOTA	2505	C	VAL	508	79.928	-4.614	5.935	1.00 57.10
MOTA	2506	0	VAL	508	79.483	-5.759	6.018	1.00 57.35
ATOM	2507	N	THR	509	79.345	-3.555	6.482	1.00 55.31
MOTA	2508	CA	THR	509	78.107	-3.652	7.227	1.00 50.14
ATOM	2509	CB	THR	509	78.329	-3.192	8.686	1.00 50.91
ATOM	2510	OG1		509	79.476	-3.851	9.227	1.00 49.20
MOTA	2511	CG2	THR	509	77.123	-3.524	9.559	1.00 51.96
ATOM	2512	С	THR	509	77.140	-2.705	6.528	1.00 47.53
ATOM	2513	0	THR	509	77.485	-1.558	6.242	1.00 47.22
ATOM	2514	N	LYS	510	75.958	-3.191	6.191	1.00 45.64
ATOM	2515	CA	LYS	510	74.975	-2.333	5.551	1.00 44.44
ATOM	2516	CB	LYS	510	73.861	-3.175	4.948	1.00 46.74
ATOM	2517	CG	LYS	510	73.008	-2.420	3.950	1.00 54.51
ATOM	2518	CD	LYS	510	73.463	-2.645	2.513	1.00 54.97
ATOM	2519	CE	LYS	510	72.846	-3.917	1.934	1.00 58.25
MOTA	2520	NZ	LYS	510	73.112	-5.150	2.740	1.00 58.33
MOTA	2521	С	LYS	510	74.430	-1.470	6.696	1.00 42.75
MOTA	2522	0	LYS	510	74.053	-2.006	7.742	1.00 43.14
ATOM	2523	N	VAL	511	74.443	-0.149	6.531	1.00 38.63
ATOM	2524	CA	VAL	511	73.975	0.757	7.576	1.00 34.16
MOTA	2525	CB	VAL	511	75.161	1.399	8.333	1.00 35.66
ATOM	2526		VAL	511	75.922	0.340	9.100	1.00 31.46
ATOM	2527		VAL	511	76.098	2.100	7.357	1.00 35.08
ATOM	2528	C	VAL	511	73.116	1.873	7.024	1.00 31.58
ATOM	2529	0	VAL	511	72.962	1.984	5.818	1.00 33.18
ATOM	2530	N	ALA	512	72.542	2.687	7.906	1.00 30.77
ATOM	2531	CA	ALA	512	71.724	3.818	7.484	1.00 28.58
ATOM	2532	CB	ALA	512	70.382	3.774	8.145	
MOTA	2533	С	ALA	512	72.487	5.075	7.905	1.00 29.94
MOTA	2534	0	ALA	512	72.996	5.151	9.031	1.00 29.90
MOTA	2535	N	VAL	513	72.556	6.057	7.012	1.00 28.68
ATOM	2536	CA	VAL	513	73.286	7.290	7.280	1.00 28.26
ATOM	2537	CB	VAL	513	74.439	7.503	6.269	1.00 26.92
MOTA	2538		VAL	513	75.213	8.730	6.618	1.00 25.26
MOTA	2539		VAL	513	75.353	6.308	6.238	1.00 25.10
MOTA	2540	С	VAL	513	72.383	8.526	7.230	1.00 29.54
MOTA	2541	0	VAL	513	71.745	8.799	6.200	1.00 28.56
MOTA	2542	N	LYS	514	72.304	9.228	8.359	1.00 28.94



ATOM	2543			514	71.519	10.450	8.48]	1.00 28.60
MOTA	2544		LYS	514	70.942	10.611	9.893	
ATOM	2545	5 CG	LYS	514	69.988	9.542	10.328	
ATOM	2546	CI.	LYS	514	69.454	9.922	11.690	
ATOM	2547	CE	LYS	514	68.484	8.892	12.222	
MOTA	2548	NZ	LYS	514	67.198	8.861	11.475	
MOTA	2549	C	LYS	514	72.430	11.636	8.196	
ATOM	2550	0	LYS	514	73.544	11.714	8.722	
MOTA	2551	N	MET	515	71.928	12.576	7.407	
ATOM	2552	CA	MET	515	72.676	13.762	7.008	
MOTA	2553	CB	MET	515	73.425	13.487	5.693	
ATOM	2554	CG	MET	515	72.502	13.026	4.556	
ATOM	2555	SD	MET	515	73.377	12.418	3.113	1.00 28.70
ATOM	2556	CE	MET	515	73.949	10.803	3.715	1.00 32.30
ATOM	2557	С	MET	515	71.683	14.880	6.779	1.00 24.88
ATOM	2558	0	MET	515	70.472	14.685	6.889	1.00 28.41
ATOM	2559	N	LEU	516	72.202	16.056	6.466	1.00 32.15
ATOM	2560	CA	LEU	516	71.383	17.220	6.180	1.00 29.12
ATOM	2561	CB	LEU	516	72.110	18.512	6.593	1.00 29.98
ATOM	2562	CG	LEU	516	72.455	18.767	8.067	1.00 25.32
ATOM	2563	CDI	LEU	516	73.210	20.057	8.190	1.00 26.60
ATOM	2564	CD2	LEU	516	71.217	18.844	8.900	1.00 24.56 1.00 22.75
ATOM	2565	C	LEU	516	71.092	17.274	4.674	1.00 22.75
ATOM	2566	0	LEU	516	71.763	16.636	3.873	1.00 31.30
ATOM	2567	N	LYS	517	70.069	18.018	4.293	
ATOM	2568	CA	LYS	517	69.755	18.187	2.890	1.00 33.29 1.00 32.20
ATOM	2569	CB	LYS	517	68.246	18.363	2.699	1.00 32.20
ATOM	2570	CG	LYS	517	67.432	17.182	3.192	1.00 43.49
ATOM	2571	CD	LYS	517	66.172	16.940	2.356	1.00 53.91
A'TOM	2572	CE	LYS	517	65.088	17.984	2.581	1.00 58.71
ATOM	2573	NZ	LYS	517	63.902	17.740	1.704	1.00 59.37
ATOM	2574	C	LYS	517	70.520	19.455	2.507	1.00 31.31
ATOM	2575	0	LYS	517	70.917	20.217	3.383	1.00 28.74
ATOM	2576	N	SER	518	70.744	19.672	1.213	1.00 32.48
ATOM	2577	CA	SER	518	71.486	20.840	0.714	1.00 33.52
ATOM	2578	CB	SER	518	71.611	20.772	-0.809	1.00 32.98
ATOM	2579	OG	SER	518	70.375	20.407	-1.396	1.00 36.75
ATOM	2580	C	SER	518	70.896	22.189	1.110	1.00 34.62
ATOM	2581	0	SER	518	71.580	23.214	1.058	1.00 34.57
ATOM	2582	N	ASP	519	69.624	22.193	1.485	1.00 35.47
ATOM	2583	CA	ASP	519	68.943	23.422	1.885	1.00 36.10
ATOM	2584	CB	ASP	519	67.529	23.480	1.268	1.00 38.11
ATOM	2585	CG	ASP	519	66.668	22.258	1.608	1.00 41.64
ATOM	2586	OD1		519	67.150	21.309	2.253	1.00 41.70
ATOM	2587	OD2		519	65.478	22.250	1.220	1.00 49.25
ATOM	2588	C	ASP	519	68.881	23.645	3.395	1.00 34.66
ATOM	2589	0	ASP	519	68.266	24.602	3.860	1.00 33.39
ATOM	2590		ALA	520	69.551	22.784	4.150	1.00 33.52
ATOM	2591		ALA	520	69.561	22.895	5.605	1.00 32.12
ATOM	2592		ALA	520	70.253	21.687	6.207	1.00 32.08
MOTA	2593		ALA	520	70.242	24.163	6.076	1.00 30.91
MOTA	2594	0	ALA	520	71.014 2	24.778		1.00 30.57
								- -

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MOTA 2595 N THR 521 69.943 24.555 7.311 1.00 30.80 ATOM 2596 CA THR 521 70.546 25.738 7.921 1.00 32.33 MOTA 2597 CB THR 521 69.493 26.763 8.440 1.00 34.30 68.817 MOTA 2598 OG1 THR 521 26.242 9.598 1.00 35.14 MOTA 2599 CG2 THR 68.484 7.366 521 27.109 1.00 37.70 ATOM 2600 C THR 521 71.418 25.312 9.098 1.00 33.11 ATOM 2601 0 THR 521 71.518 24.125 9.426 1.00 31.39 ATOM 2602 GLU 522 72.022 26.293 9.753 1.00 34.91 N MOTA 2603 CA GLU 522 72.882 26.048 10.901 1.00 39.44 **ATOM** 2604 CB GLU 522 73.516 27.357 11.360 1.00 46.96 2605 CG GLU 74.550 27.220 12.488 ATOM 522 1.00 59.20 **ATOM** 2606 CDGLU 522 75.919 26.740 12.011 1.00 64.70 2607 MOTA OE1 GLU 522 76.910 27.478 12.219 1.00 63.87 2608 76.006 25.627 MOTA OE2 GLU 522 11.445 1.00 71.55 ATOM 2609 C GLU 522 72.083 25.428 12.044 1.00 39.61 72.587 24.554 12.757 ATOM 2610 0 GLU 522 1.00 36.74 MOTA 2611 LYS 70.827 25.849 12.193 N 523 1.00 38.60 69.970 25.327 MOTA 2612 CA LYS 523 13.252 1.00 37.77 2613 68.628 26.053 13.273 ATOM CB LYS 523 1.00 44.52 1.00 51.14 ATOM 2614 CG LYS 523 67.665 25.562 14.355 2615 CD66.380 24.983 13.756 ATOM LYS 523 1.00 57.39 14.852 ATOM 2616 CE LYS 523 65.499 24.376 1.00 59.17 64.365 23.553 ATOM 2617 NZ LYS 14.327 523 1.00 62.68 **ATOM** 2618 C LYS 523 69.751 23.849 13.002 1.00 34.63 ATOM 2619 0 LYS 523 69.817 23.041 13.931 1.00 35.00 **ATOM** 2620 N ASP 524 69.496 23.495 11.746 1.00 31.60 **ATOM** 2621 CA ASP 524 69.293 22.100 11.367 1.00 29.05 ATOM 2622 CB ASP 524 69.002 21.975 9.871 1.00 29.60 ATOM 2623 CG ASP 524 67.695 22.626 9.472 1.00 31.90 OD1 ASP 66.666 22.368 **ATOM** 2624 524 10.130 1.00 38.83 ATOM 2625 OD2 ASP 67.687 23.383 8.485 524 1.00 29.79 MOTA 2626 С ASP 524 70.558 21.317 11.696 1.00 28.02 2627 ATOM 0 ASP 524 70.494 20.201 12.212 1.00 28.12 MOTA 2628 N LEU 525 71.709 21.899 11.378 1.00 28.32 MOTA 2629 CA LEU 525 72.971 21.231 11.677 1.00 27.71 ATOM 2630 CB LEU 525 74.173 22.085 11.257 1.00 22.53 ATOM 2631 CG LEU 525 75.548 21.490 11.602 1.00 22.13 **ATOM** 2632 CD1 LEU 525 75.677 20.082 11.019 1.00 19.92 MOTA 2633 CD2 LEU 525 76.673 22.401 11.147 1.00 18.60 73.007 20.952 ATOM 2634 С LEU 525 13.162 1.00 27.44 ATOM 2635 0 LEU 525 73.227 19.817 13.577 1.00 29.73 ATOM 2636 N SER 526 72.689 21.976 13.947 1.00 29.09 SER 72.672 21.891 MOTA 2637 CA 526 15.412 1.00 30.83 ATOM 2638 CB SER 526 72.222 23.230 16.006 1.00 34.25 ATOM 2639 OG: SER 526 71.966 23.147 17.397 1.00 40.67 MOTA 2640 C SER 526 71.765 20.777 15.931 1.00 29.32 MOTA 2641 SER 526 72.055 20.133 16.954 0 1.00 28.94 ASP **ATOM** 2642 N 527 70.644 20.587 15.242 1.00 26.54 CA ASP MOTA 2643 527 69.681 19.558 15.601 1.00 27.00 ASP MOTA 2644 CB 527 68.392 19.798 14.829 1.00 25.91 MOTA 2645 CG ASP 527 67.640 21.052 15.290 1.00 29.22 MOTA 2646 OD1 ASP 527 68.016 21.662 16.320 1.00 26.80

Δ	TOM	2647										
		2647			527	66.	660	21.	425	• • • •		
		2648	_		527		231	18.		14.605		33.85
		2649	-	ASP 5	527		058			15.325		8.34
		2650	N	LEU 5	28		884	17.2		16.130	1.00 2	8.36
		2651	CA	LEU 5	28		448	17.9		14.177	1.00 2	9.50
		2652	CB :		28			16.6		13.830	1.00 3	0.48
	rom 2	2653	CG j	·	28		915	16.6		2.366	1.00 2	7.89
		2654	CD1 1		28	72.		15.3		1.832	1.00 2	5.48
		655	CD2 I		28	71.4		14.1		2.148	1.00 2	1 52
		656	_		28	72.		15.3	83 1	0.333	1.00 20	1 22
AT	_	657	_		28	72.5		16.3	08 1	4.804	1.00 3	.23
AT		658				72.6		15.1	45 1	5.222	1.00 30	
ATO	OM 2	659			29	73.3		17.29		5.195	1.00 30	7.09
ATO		660				74.5		17.08		5.140	1.00 30	. 79
ATC		561				75.3	98	18.31		5.278	1.00 28	.88
ATC		662	CG1 I			76.5		18.00		7.217	1.00 25	.69
ATO		63	CD1 T			75.9		18.72		.941	1.00 20	.54
ATO		64	CD1 II			76.9		19.83		.035	1.00 23	.71
ATO		65		_		73.9		16.76			1.00 24	.21
ATO			O II			74.43		5.85		.533	1.00 31	. 52
ATO			N SE		0	72.9		7.50		.213	1.00 30	66
ATO			CA SE	,)	72.31		7.25		.947	1.00 29.	79
ATON			CB SE)	71.17		8.23		.244	1.00 32.	03 .
ATON			OG SE			70.26		8.23		.492	1.00 38.	91
ATOM	_	`	C SE	R 530)	71.79				412	1.00 49.	86
ATOM		`	SE	R 530		71.92		5.819		316	1.00 30.	10
ATOM		_	J GL	J 531		71.18		5.154		353	L.00 31.	31
	_		A GLU	J 531		70.67		5.350		231 1	.00 27.	18
ATOM			B GLU	531		69.92		3.989		180 1	.00 27.	39
ATOM			G GLU	531		69.434		3.744		881 1	.00 31.2	29
ATOM		_	D GLU			68.717		324		769 <u>1</u>	.00 30.4	13
ATOM		-	E1 GLU	531		68.293		.040		486 <u>1</u>	.00 30.6	7
ATOM			E2 GLU	531		68.571		.892	15.	317 1	.00 37.7	9
ATOM	267	_	GLU					.941	14.6	543 1	.00 34.2	0
ATOM	268	_	GLU	531		71.765		.929	18.3	348 1	.00 26.6	7
ATOM	2683	N	MET	532		71.604		. 986	19.1	.19 1	.00 24.3	, マ
ATOM	2682	C.	MET	532		72.851		.074	17.5	95 1.	00 28.9	3
ATOM	2683	CE		532		74.000		.156	17.6	44 1.	00 28.3	=
ATOM	2684	CG		532		75.073		637	16.6		00 29.48	, ,
ATOM	2685	SD		532		76.458		034	16.8		00 25.84) I
ATOM	2686	CE		532		77.650	12.	692	15.5		00 30.60	
ATOM	2687	C	MET	532		77.831		373	16.1		00 20.10	,
ATOM	2688	0	MET	532		74.571	12.	120	19.0		00 29.06	ı
ATOM	2689	N	GLU			74.876	11.	053	19.58		00 29.06 00 28.22	
ATOM	2690	CA	GLU	533		74.640	13.	289	19.68		00 28.22	
ATOM	2691	CB		533		75.150	13.		21.04		00 28.61	
ATOM	2692	CG	GLU	533		75.340	14.8		21.42		00 28.40	
ATOM	2693	CD	GLU	533		76.449	15.5		20.64		00 29.34	
ATOM	2694		GLU	533		77.822	14.9		20.89		0 31.87	
ATOM	2695		GLU	533		78.242	14.8				0 35.10	
ATOM	2696		GLU	533		78.490	14.5		22.06		0 37.36	
ATOM		C	GLU	533		74.211	12.6	_	19.91		0 37.71	
ATOM	2697	0	GLυ	533		74.651	11.9		22.02		0 31.03	
*** OI1	2698	N	MET	534			12.9		22.906	5 1.0	0 30.76	
							±2.3	02 2	21.860	1.0	0 31.71	



ATOM	2699	CA	MET	534	71.940	12.256	22.727	1.00	30.58
MOTA	2700	CB	MET	534	70.510	12.620	22.315		33.53
MOTA	2701	CG	MET	534	69.538	12.624	23.509	0.50	32.45
MOTA	2702	SD	MET	534	67.778	12.682	23.150	0.50	30.95
MOTA	2703	CE	MET	534	67.523	14.422	22.895	0.50	30.50
MOTA	2704	C	MET	534	72.158	10.752	22.616	1.00	28.44
MOTA	2705	0	MET	534	72.304	10.077	23.614	1.00	27.63
MOTA	2706	N	MET	535	72.216	10.232	21.395	1.00	30.00
ATOM	2707	CA	MET	535	72.448	8.800	21.176		29.38
MOTA	2708	CB	MET	535	72.626	8.483	19.690	1.00	25.41
MOTA	2709	CG	MET	535	71.395	8.753	18.893	1.00	25.06
ATOM	2710	SD	MET	535	71.468	7.917	17.344	1.00	27.17
MOTA	2711	CE	MET	535	71.439	9.227	16.247	1.00	33.70
MOTA	2712	С	MET	535	73.675	8.345	21.938	1.00	30.77
MOTA	2713	0	MET	535	73.681	7.254	22.534	1.00	27.49
MOTA	2714	N	LYS	536	74.710	9.183	21.916	1.00	32.72
MOTA	2715	CA	LYS	536	75.937	8.889	22.649	1.00	34.05
MOTA	2716	CB	LYS	536	76.995	9.964	22.401	1.00	32.69
MOTA	2717	CG	LYS	536	77.719	9.838	21.073	1.00	28.00
MOTA	2718	CD	LYS	536	78.732	10.956	20.941	1.00	29.61
MOTA	2719	CE	LYS	536	79.242	11.124	19.514	1.00	26.58
ATOM	2720	NZ	LYS	536	80.020	12.389	19.460	1.00	22.22
MOTA	2721	С	LYS	536	75.652	8.769	24.145	1.00	34.80
MOTA	2722	0	LYS	536	76.004	7.763	24.750	1.00	34.44
ATOM	2723	N	MET	537	74.958	9.749	24.716	1.00	34.66
ATOM	2724	CA	MET	537	74.634	9.724	26.131	1.00	37.25
MOTA	2725	CB	MET	537	73.951	11.034	26.549	1.00	46.08
MOTA	2726	CG	MET	537	74.862	12.272	26.619	1.00	57.95
MOTA	2727	SD	MET	537	76.159	12.203	27.919	1.00	66.50
MOTA	2728	CE	MET	537	75.287	12.873	29.377		64.52
MOTA	2729	C	MET	537	73.749	8.537	26.523	1.00	36.05
MOTA	2730	0	MET	537	74.021	7.865	27.514		36.71
ATOM	2731	N	ILE	538	72.730	8.255	25.719	1.00	33.77
MOTA	2732	CA	ILE	538	71.804	7.160	26.007	1.00	30.52
MOTA	2733	CB	ILE	538	70.616	7.172	25.012		28.15
ATOM	2734	CG2	ILE	538	69.780	5.899	25.122		26.08
ATOM	2735	CG1	ILE	538	69.729	8.377	25.289		26.24
ATOM	2736	CD1	ILE	538	68.644	8.558	24.256		26.87
ATOM	2737	C	ILE	538	72.399	5.750	26.100		30.05
MOTA	2738	0	ILE	538	71.984	4.950	26.941		31.57
MOTA	2739	N	GLY	539	73.320	5.424	25.211		30.34
ATOM	2740	CA	GLY	539	73.910	4.103	25.249		28.22
MOTA	2741	C	GLY	539	73.158	3.094	24.408		31.25
ATOM	2742	0	GLY	539	72.050	3.359	23.935		32.88
MOTA	2743	N	LYS	540	73.781	1.933	24.221		31.96
ATOM	2744	CA	LYS	540	73.222	0.845	23.416		33.40
MOTA	2745	CB	LYS	540	74.342	-0.023	22.878		31.53
ATOM	2746	CG	LYS	540	75.177	0.645	21.846		37.05
MOTA	2747	CD	LYS	540	76.273	-0.266	21.361		40.15
MOTA	2748	CE	LYS	540	77.143	0.480	20.363		46.84
MOTA	2749	NZ	LYS	540	76.374	0.920	19.152		48.60
MOTA	2750	С	LYS	540	72.183	-0.090	24.023	1.00	36.22

	OM 275	_	YS 540	72.237 -0.430 25 215 1 00 45 25
AT		52 N H	IS 541	71 254 0 500 25.215 1.00 40.10
AT			IS 541	70.234 20.521 23.175 1.00 34.86
ATO		4 CB H	IS 541	60.223 -1.486 23.535 1.00 33.96
ATO		5 CG H	IS 541	03.064 -0.860 24.293 1.00 31.57
ATO		6 CD2 H	IS 541	50.127 -1.862 24.890 1.00 32.28
ATO	DM 275			67 006 -2.482 26.093 1.00 32.39
ATC	M 275			57.000 -2.411 24.177 1.00 30 10
ATC	M 275	9 NE2 H]		67 202 24.911 1.00 33.35
ATO	M 276			-3.384 26.081 1.00 30 46
ATO	M 276			03.720 -2.206 22.275 1.00 35 33
ATO	M 2762			03.040 -1.614 21.200 1.00 34 97
ATO	M 2763			03.348 = 3.478 22.430 1.00 35 42
ATO	M 2764			68.908 -4.311 21.306 1.00 32 03
ATO	M 2765		_	68.715 -5.766 21.753 1.00 30 96
ATO				67.652 -3.848 20.614 1.00 30.03
ATON				67.474 -4.058 19.417 7 00 30 70
ATON				66.778 -3.212 21.369 1.00 20.54
ATOM				65.529 -2.754 20.803 1 00 20 20
ATOM		CG ASI		64.372 -3.241 21.660 1 00 20 70
ATOM		OD1 ASN	•	64.387 -4.739 21.840 1.00 30 74
ATOM		ND2 ASN		64.732 -5.242 22.909 1 00 32 05
ATOM				64.053 -5.462 20.787 1.00 20.50
ATOM		C ASN O ASN		65.426 -1.257 20.529 1 00 20 25
ATOM		N ILE		64.342 -0.679 20.647 7 00 20 25
ATOM	2776			66.546 -0.635 20.168 1 00 36 70
ATOM	2777		544	66.582 0.794 19.833 1.00 26.70
ATOM	2778		544	67.052 1.721 21.019 1.00 24.75
ATOM	2779		544	66.338 1.353 22.306 1.00 20.00
ATOM	2780		544	68.568 1.614 21.234 1.00 23.73
ATOM	2781	-	544	69.105 2.531 22.332 1.00 21 64
ATOM	2782		544	67.582 0.901 18.680 1 00 27 0-
ATOM	2783		544	68.388 -0.008 18.480 1 00 36 22
ATOM	2784		545	67.449 1.940 17.849 1.00 20.80
ATOM	2785		545	68.376 2.163 16.745 1 00 27 74
ATOM	2786		545	67 824 2 764
ATOM	2787		545	68 920 2 555
ATOM	2788		545	66.625 2.568 14.955 1.00 23.70
ATOM			545	66 900 1 300
ATOM			545	69 623
ATOM			545	69 500 3 777
ATOM		N ASN	546	70 740 2 0 0 0
ATOM		CA ASN	546	72 004 2 222
ATOM		CB ASN	546	72 709 1 100 28.49
ATOM		CG ASN	546	71 956 0 15 1.00 27.05
ATOM		OD1 ASN	546	71 702 1 002
ATOM		ND2 ASN	546	71 472 0 71
ATOM	2797 (546	72 992 2 22
	2798 (546	73 045 2 221 10.941 1.00 28.39
ATOM	2799 N		547	73 774 2 22 23.732 1.00 29.62
ATOM		'A LEU	547	74 939 4 775
ATOM	0000	B LEU	547	75 207 5 202 10.325 1.00 30.68
ATOM	2802 C	G LEU	547	76 367 6 25.28
				76.367 6.828 17.267 1.00 24.81

ATOM	2803	CD1	LEU	547	75.868	7.524	15.990	1.00	22.25
MOTA	2804	CD2	LEU	547	76.716	7.853	18.313	1.00	24.17
MOTA	2805	C	LEU	547	76.016	3.812	16.629	1.00	31.67
ATOM	2806	0	LEU	547	76.481	3.090	17.509	1.00	31.34
ATOM	2807	N	LEU	548	7 6.47 5	3.823	15.380	1.00	30.60
ATOM	2808	CA	LEU	548	77.594	2.995	14.955	1.00	29.31
ATOM	2809	CB	LEU	548	77.197	2.165	13.729	1.00	25.94
ATOM	2810	CG	LEU	548	75.968	1.247	13.883	1.00	28.78
ATOM	2811	CD1	LEU	548	75.848	0.360	12.659	1.00	27.14
ATOM	2812	CD2	LEU	548	76.049	0.392	15.149	1.00	23.72
ATOM	2813	С	LEU	548	78.850	3.821	14.644	1.00	31.60
ATOM	2814	0	LEU	548	79.967	3.330	14.753	1.00	32.65
ATOM	2815	N	GLY	549	78.665	5.076	14.248	1.00	32.22
MOTA	2816	CA	GLY	549	79.795	5.928	13.937	1.00	31.40
ATOM	2817	C	GLY	549	79.344	7.267	13.391	1.00	30.78
MOTA	2818	0	GLY	549	78.140	7.536	13.291	1.00	29.84
ATOM	2819	N	ALA	550	80.320	8.099	13.045	1.00	31.88
MOTA	2820	CA	ALA	550	80.073	9.416	12.485	1.00	30.14
ATOM	2821	CB	ALA	550	79.634	10.382	13.590	1.00	31.08
MOTA	2822	C	ALA	550	81.291	9.978	11.742	1.00	28.78
MOTA	2823	0	ALA	550	82.447	9.705	12.102	1.00	26.39
ATOM	2824	N	CYS	551	81.011	10.690	10.651	1.00	28.48
ATOM	2825	CA	CYS	551	82.012	11.391	9.846	1.00	23.69
MOTA	2826	СВ	CYS	551	81.825	11.128	8.352		24.18
ATOM	2827	SG	CYS	551	81.870	9.395	7.840	1.00	28.40
ATOM	2828	C	CYS	551	81.612	12.847	10.127	1.00	20.99
ATOM	2829	0	CYS	551	80.561	13.282	9.684	1.00	22.11
MOTA	2830	N	THR	552	82.357	13.524	10.996	1.00	20.18
ATOM	2831	CA	THR	552	82.073	14.914	11.349	1.00	22.79
ATOM	2832	CB	THR	552	82.090	15.080	12.874	1.00	23.16
ATOM	2833	OG1	THR	552	83.408	14.803	13.363	1.00	23.52
ATOM	2834	CG2	THR	552	81.125	14.112	13.529	1.00	25.31
MOTA	2835	C	THR	552	83.138	15.886	10.824	1.00	24.74
MOTA	2836	0	THR	552	82.939	17.103	10.782	1.00	22.75
MOTA	2837	N	GLN	553	84.276	15.334	10.431	1.00	26.82
MOTA	2838	CA	GLN	553	85.387	16.153	9.980	1.00	26.99
MOTA	2839	CB	GLN	553	86.686	15.627	10.602	1.00	26.40
MOTA	2840	CG	GLN	553	86.632	15.494	12.141	1.00	22.69
MOTA	2841	CD	GLN	553	86.438	16.836	12.823	1.00	25.90
MOTA	2842	OE1	GLN	553	87.259	17.729	12.656	1.00	29.03
MOTA	2843	NE2	GLN	553	85.351	16.994	13.566	1.00	23.53
MOTA	2844	C	GLN	553	85.502	16.216	8.466	1.00	26.23
ATOM	2845	0	GLN	553	85.177	15.259	7.779	1.00	30.00
ATOM	2846	N	ASP	554	85.863	17.394	7.968	1.00	26.54
ATOM	2847	CA	ASP	554	86.084	17.631	6.531	1.00	28.38
ATOM	2848	CB	ASP	554	87.410	17.031	6.105		26.78
ATOM	2849	CG	ASP	554	88.538	17.570	6.912		31.53
ATOM	2850		ASP	554	88.789	18.795	6.823		35.18
ATOM	2851		ASP	554	89.141	16.795	7.665		29.04
ATOM	2852	С	ASP	554	85.011	17.221	5.545		29.14
ATOM	2853	0	ASP	554	85.278	16.468	4.610		31.22
MOTA	2854	N	GLY	555	83.824	17.793	5.709		31.20

ATO	M 28	55	CA	GLY	555					
ATO			C	GLY		82.72		490	4.8	11 1.00 28.83
ATO			0	GLY		81.44		413	5.6	
ATON			N	PRO		81.44		647	6.8	14 1.00 21.78
ATOM			CD	PRO	556 556	80.31		093	4.9	
ATOM			CA	PRO		80.21		781	3.53	1.00 19.37
ATOM		_	CB	PRO	556 556	79.01		973	5.61	
ATOM			CG	PRO	556 556	78.107		497	4.47	77 1.00 22.88
ATOM	_			PRO	556	79.077			3.48	15 1.00 23.50
ATOM				PRO	556 556	79.006		982	6.77	
ATOM				LEU	556	79.676			6.73	6 1.00 27.13
ATOM				LEU	557	78.253			7.82	
ATOM				LEU	557	78.164			8.97	
ATOM				LEU	557 557	77.583			10.18	8 1.00 29.94
ATOM		-	D1 ;		557	77.019			11.32	3 1.00 26.87
ATOM			D2 1		557	78.131			12.06	2 1.00 23.83
ATOM				LEU	557	76.237			12.27	
ATOM		-		LEU	557 557	77.291	14.1		8.65	1 1.00 31.97
ATOM	2873	_		ľYR	557	76.158	14.3	32	8.184	1 1.00 31.18
ATOM	2874		-	'YR	558	77.857	13.0		8.882	
ATOM	2875	-		YR	558	77.145	11.7		8.664	
ATOM	2876			YR	558	77.905	10.8		7.694	
ATOM	2877			'YR	558	78.017	11.3		6.281	1.00 32.33
ATOM	2878			YR	558	79.034	10.9		5.443	
ATOM	2879			YR	558	79.161	11.4	47	4.151	
ATOM	2880			YR	558	77.123	12.3		5.787	
ATOM	2881				558	77.248	12.83		4.493	1.00 36.43
ATOM	2882			YR YR	558	78.276	12.38	32	3.680	
ATOM	2883		_	YR	558	78.423	12.86		2.394	1.00 39.97
ATOM	2884	0		YR	558	77.000	11.07		10.004	1.00 26.63
ATOM	2885	N		AL	558	77.985	10.88		10.725	1.00 24.67
ATOM	2886	CA		AL AL	559 550	75.756	10.77		LO.365	1.00 28.15
ATOM	2887	CB			559 550	75.429	10.07		L1.610	1.00 27.70
ATOM	2888		1 V <i>I</i>		559	74.262	10.77		2.372	1.00 26.63
ATOM	2889		2 V.		559	73.876	9.95		3.603	1.00 24.70
ATOM	2890	C.	V.A		559	74.673	12.18	6 1	2.792	1.00 26.71
ATOM	2891	0	VA		559	75.061	8.63	5 1	1.205	1.00 27.08
ATOM	2892	N	IL		559	73.965	8.35	7 1	0.710	1.00 25.39
ATOM	2893	CA	IL		560	76.002	7.72		1.399	1.00 28.25
ATOM	2894	CB	IL		560	75.820	6.33	5 1	1.000	1.00 29.62
ATOM	2895		IL:		560	77.225	5.68	2 1	0.678	1.00 30.06
ATOM	2896		IL.		560	77.045	4.27		0.101	1.00 31.58
ATOM	2897		IL:		560	78.004	6.55		9.686	1.00 27.50
ATOM	2898	C			560/	79.492	6.239		9.629	1.00 23.31
ATOM	2899	0	IL		560	75.075	5.488		2.032	1.00 29.88
ATOM	2900		IL		560	75.586	5.234		3.130	1.00 27.32
ATOM		N	VA		561	73.857	5.078		L.687	1.00 29.09
ATOM	2901	CA	VAI		561	73.053	4.228		2.568	1.00 28.70
ATOM	2902 2903	CB	VAI		561	71.743	4.932		3.037	1.00 25.29
ATOM	2903		VAI		561	72.072	6.139		.872	1.00 23.29
ATOM	2904	CG2			561	70.887	5.312		.870	1.00 22.38
ATOM	2905	C	VAL		561	72.731	2.848		.945	1.00 27.99
01.1	2900	0	VAL		561	73.052	2.590			1.00 27.88

MOTA	2907	N	GLU	562	72.143	1.969	12.754	1.00	27.38
ATOM	2908	CA	GLU	562	71.759	0.616	12.347	1.00	28.01
ATOM	2909	CB	GLU	562	71.246	-0.161	13.555	1.00	25.37
ATOM	2910	CG	GLU	562	72.322	-0.487	14.570	1.00	29.22
ATOM	2911	CD	GLU	562	71.785.	-1.190	15.796	1.00	30.94
ATOM	2912	OE1	GLU	562	72.440	-2.135	16.271	1.00	34.82
ATOM	2913	OE2	GLU	562	70.716	-0.795	16.297	1.00	32.77
MOTA	2914	С	GLU	562	70.695	0.610	11.266	1.00	29.83
MOTA	2915	0	GLU	562	69.822	1.452	11.274	1.00	34.69
ATOM	2916	N	TYR	563	70.755	-0.364	10.362	1.00	31.35
ATOM	2917	CA	TYR	563	69.806	-0.527	9.255	1.00	33.79
ATOM	2918	CB	TYR	563	70.586	-0.987	8.022	1.00	32.37
ATOM	2919	CG	TYR	563	69.759	-1.232	6.778	1.00	31.70
ATOM	2920	CD1	TYR	563	68.858	-0.277	6.319		35.00
ATOM	2921	CE1	TYR	563	68.101	-0.490	5.161		35.62
ATOM	2922	CD2	TYR	563	69.888	-2.416	6.053		31.64
MOTA	2923	CE2	TYR	563	69.138	-2.644	4.894		32.96
ATOM	2924	CZ	TYR	563	68.242	-1.674	4.462		36.20
ATOM	2925	ОН	TYR	563	67.494	-1.906	3.340	1.00	
ATOM	2926	С	TYR	563	68.668	-1.527	9.593	1.00	
ATOM	2927	0	TYR	563	68.915		10.212		38.86
ATOM	2928	N	ALA	564	67.428	-1.180	9.220		39.09
ATOM	2929	CA	ALA	564	66.256	-2.027	9.467		37.64
ATOM	2930	CB	ALA	564	65.290	-1.317	10.366		41.34
ATOM	2931	C	ALA	564	65.600	-2.337	8.124		39.33
MOTA	2932	0	ALA	564	64.700	-1.628	7.661		41.28
ATOM	2933	N	SER	565	66.033	-3.432	7.515		40.21
ATOM	2934	CA	SER	565	65.567	-3.867	6.202		40.22
ATOM	2935	CB	SER	565	66.302	-5.133	5.808		38.50
ATOM	2936	OG	SER	565	66.174	-6.084	6.847		37.66
ATOM	2937	C	SER	565	64.095	-4.087	5.987		42.30
ATOM	2938	0	SER	565	63.657	-4.155	4.840		46.83
ATOM	2939	N	LYS	566	63.322	-4.248	7.054		42.84
ATOM	2940	CA	LYS	566	61.893	-4.462	6.883		41.84
ATOM	2941	CB	LYS	566	61.455	-5.681	7.684		44.88
ATOM	2942	CG	LYS	566	62.003	-6.977	7.088		48.86
ATOM	2943	CD	LYS	566	61.929	-8.148	8.040		51.41
ATOM	2944	CE	LYS	566	62.582	-9.362	7.426		53.89
ATOM	2945	NZ	LYS	566		-10.465	8.417		59.37
ATOM	2946	C	LYS	566	61.029		7.143		
ATOM	2947	0	LYS	566	59.815	-3.234			41.89
ATOM	2948	N	GLY	567		-3.337	7.341		
		CA			61.663	-2.061	7.100		39.50
ATOM	2949	CA	GLY	567 567	60.956	-0.808	7.291		36.69
MOTA	2950		GLY	567 567	60.306	-0.640	8.644		35.86
MOTA	2951	O N	GLY	567 569	60.727	-1.265	9.614		35.90
MOTA	2952	N	ASN	568	59.296	0.218	8.711		35.45
MOTA	2953	CA	ASN	568	58.615	0.447	9.966		38.10
ATOM	2954	CB	ASN	568	57.961	1.839	10.029		40.77
ATOM	2955	CG	ASN	568	56.701	1.962	9.163		43.52
ATOM	2956		ASN	568	55.718	1.241	9.338		44.01
MOTA	2957		ASN	568	56.710	2.932	8.263		45.39
ATOM	2958	С	ASN	568	57.610	-0.657	10.269	1.00	38.91

3 mo								
ATO:		_) ASI		57.21	.8 -1.42	0 9.38	4 1.00 39.95
ATO			1 LE		57.20			55.55
ATO			CA LE		56.25			7 1.00 36.49
ATO		_	B LEU		56.12			
ATO			G LE		55.15			
ATO			D1 LEU		55.55			
ATON			D2 LEU	569	55.14			
ATON			LEU	569	54.87			
ATOM			LEU	569	54.23			
ATOM			ARG	570	54.38			
ATOM		_		570	53.06			
ATOM			B ARG	570	52.73			
ATOM			-	570	51.33			
ATOM				570	51.210			10.11
ATOM				570	52.162			
ATOM				570	53.010			
ATOM			H1 ARG	570	53.032			
ATOM			12 ARG	570	53.853			1.00 65.15
ATOM	2977		ARG	570	53.046		9.193	1.00 66.56
ATOM	2978		ARG	570	52.248		9.018	1.00 35.55
ATOM	2979		GLU	571	53.978		8.320	1.00 35.33
MOTA	2980			571	54.128	_	7.030	1.00 37.20
ATOM	2981		GLU	571	55.247	-0.695	6.261	1.00 38.32
ATOM	2982			571	55.001	0.803	6.152	1.00 40.15
ATOM	2983			571	56.118	1.557	5.442	1.00 49.09
ATOM	2984			571	57.279	1.073	5.421	1.00 58.16
ATOM	2985	OE	2 GLU	571	55.824	2.660	4.914	1.00 61.41
ATOM	2986	С	GLU	571	54.406	-2.906	7.170	1.00 61.27
ATOM	2987	0	GLU	571	53.863	-3.721	6.410	1.00 36.74
ATOM	2988	N	TYR	572	55.241	-3.266	8.141	1.00 35.74
ATOM	2989	CA	TYR	572	55.591	-4.665	8.401	1.00 35.13 1.00 37.12
ATOM	2990	CB	TYR	572	56.591	-4.736	9.560	
ATOM	2991	CG	TYR	572	56.984	-6.128	10.029	1.00 34.39
ATOM	2992	CD:		572	57.980	-6.869	9.367	1.00 33.48
ATOM	2993	CE		572	58.394	-8.119	9.845	1.00 29.76
ATOM	2994	CD2		572	56.406	-6.681	11.183	1.00 27.14
ATOM	2995	CE2	TYR	572	56.814	-7.931	11.669	1.00 32.40
MOTA	2996	CZ	TYR	572	57.807	-8.641	10.995	1.00 30.83
ATOM	2997	OH	TYR	572	58.201	-9.872	11.480	1.00 33.73
ATOM	2998	C	TYR	572	54.330	-5.468	8.729	1.00 37.16
ATOM	2999	0	TYR	572	54.108	-6.553	8.183	1.00 38.92
ATOM	3000	N	LEU	573	53.507	-4.922	9.618	1.00 39.22
ATOM	3001	CA	LEU	573	52.261	-5.563		1.00 38.41
ATOM	3002	CB	LEU	573	51.573	-4.711		1.00 37.56
ATOM	3003	CG	LEU	573	52.270	-4.617		1.00 36.44
ATOM	3004		LEU	573	51.555	-3.626		1.00 33.91
ATOM	3005	CD2	LEU	573	52.313			1.00 31.60
ATOM	3006	C	LEU	573 .	51.315	-5.738		1.00 30.78
ATOM	3007	0	LEU	573	50.847	-6.836		1.00 37.51
MOTA	3008	N	GLN	574	51.045	-4.643		1.00 36.70
ATOM	3009	CA	GLN	574	50.141	-4.678		1.00 40.10
MOTA	3010	CB	GLN	574	49.938	-3.272		1.00 41.10
					~~	3.614	6.439	1.00 40.12

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ATOM	3011	CG	GLN	574	49.171	-2.381	7.374	1.00	40.77
MOTA	3012	CD	GLN	574	49.079	-0.987	6.852	1.00	43.90
MOTA	3013	OE1	GLN	574	49.679	-0.652	5.835	1.00	46.93
MOTA	3014	NE2	GLN	574	48.357	-0.143	7.558	1.00	46.85
MOTA	3015	С	GLN	574	50.546	-5.638	5.875	1.00	41.31
MOTA	3016	0	GLN	574	49.699	-6.323	5.309	1.00	44.33
MOTA	3017	N	ALA	575	51.840	-5.735	5.601	1.00	41.46
MOTA	3018	CA	ALA	575	52.317	-6.628	4.555	100	39.80
MOTA	3019	CB	ALA	575	53.745	-6.301	4.218	1.00	40.58
MOTA	3020	C	ALA	575	52.197	-8.096	4.947	1.00	40.86
ATOM	3021	0	ALA	575	52.527	-8.975	4.165	1.00	41.50
MOTA	3022	N	ARG	576	51.757	-8.359	6.168	1.00	42.47
ATOM	3023	CA	ARG	576	51.624	-9.726	6.641	1.00	42.68
ATOM	3024	CB	ARG	576	52.679	-9.988	7.716	1.00	41.04
ATOM	3025	CG	ARG	576	54.095	-9.958	7.161	1.00	42.73
ATOM	3026	CD	ARG	576	55.156	-9.943	8.257	1.00	45.59
ATOM	3027	NE	ARG	576	56.514	-9.870	7.695	1.00	43.89
ATOM	3028	CZ	ARG	576	56.981	-8.856	6.969	1.00	43.35
ATOM	3029	NH1	ARG	576	56.219	-7.803	6.703	1.00	44.85
ATOM	3030	NH2	ARG	576	58.215	-8.902	6.497	1.00	41.84
ATOM	3031	С	ARG	576	50.232	-10.014	7.180	1.00	44.86
ATOM	3032	0	ARG	576	50.043	-10.943	7.970	1.00	46.08
ATOM	3033	N	ARG	577	49.258	-9.216	6.753	1.00	46.72
ATOM	3034	CA	ARG	577	47.877	-9.401	7.196	1.00	47.61
MOTA	3035	CB	ARG	577	46.994	-8.239	6.723	1.00	46.35
MOTA	3036	CG	ARG	577	47.101	-6.995	7.581	1.00	47.71
ATOM	3037	CD	ARG	577	46.329	-5.831	6.999	1.00	49.15
ATOM	3038	NE	ARG	577	46.213	-4.735	7.957	1.00	53.23
ATOM	3039	CZ	ARG	577	45.584	-3.587	7.725	1.00	54.38
ATOM	3040	NH1	ARG	577	45.020	-3.368	6.549	1.00	56.41
MOTA	3041	NH2	ARG	577	45.481	-2.676	8.686	1.00	58.13
ATOM	3042	C	ARG	577	47.298	-10.740	6.743	1.00	47.36
ATOM	3043	0	ARG	577	47.246	-11.031	5.550	1.00	48.52
MOTA	3044	N	GLN	594	53.349	-13.948	7.960	1.00	68.05
MOTA	3045	CA	GLN	594	52.144	-14.067	8.772	1.00	66.75
ATOM	3046	CB	GLN	594	51.259	-15.220	8.277	1.00	66.87
ATOM	3047	C	GLN	594	52.535	-14.284	10.233	1.00	64.71
ATOM	3048	С	GLN	594	53.192	-15.264	10.580	1.00	64.86
MOTA	3049	N	LEU	595	52.159	-13.335	11.074	1.00	61.14
ATOM	3050	CA	LEU	595	52.489	-13.422	12.480	1.00	58.19
ATOM	3051	CB	LEU	595	52.599	-12.008	13.056	1.00	56.33
MOTA	3052	CG	LEU	595	53.532	-11.147	12.203	1.00	57.36
ATOM	3053	CD1	LEU	595	53.375	-9.692	12.533	1.00	59.51
MOTA	3054	CD2	LEU	595	54.967	-11.598	12.382	1.00	56.98
ATOM	3055	C	LEU	595	51.469	-14.237	13.251	1.00	56.25
MOTA	3056	0	LEU	595	50.314	-14.359	12.834	1.00	56.60
MOTA	3057	N	SER	596	51.927	-14.845	14.341	1.00	53.07
ATOM	3058	CA	SER	596	51.100	-15.642	15.229	1.00	48.64
MOTA	3059	CB	SER	596	51.883	-16.841	15.736	1.00	46.41
MOTA	3060	QG	SER	596	52.806	-16.435	16.737	1.00	46.50
MOTA	3061	C	SER	596	50.796	-14.756	16.423	1.00	48.95
ATOM	3062	0	SER	596	51.492	-13.767	16.649	1.00	49.39



ATC			N SE	R 597	49.833 -15.163 17.242 1.00 50 27
ATO			CA SE	R 597	19 160 31 55
ATO			CB SE	R 597	10 201 75 222
ATO			OG SE	R 597	47 540 15 05
ATO			C SEI	R 597	50 605 74 745
ATO) SEI	₹ 597	EO 702 12 222
ATO			1 LYS	5 598	51 613 75 500
ATO			CA LYS	598	52 924 14 95-
ATO			B LYS	598	E2 ECC 3.5 5.54
ATON	_		G LYS	598	E4 276 26 17
ATON		_	D LYS	598	EE 057 15 05.30
ATOM			E LYS	598	55 700 10 000 I
ATOM			Z LYS	598	54 840 30 75
ATOM	,		LYS	598	E2 720 12 000
ATOM		_	LYS	598	E4 272 72 72
ATOM			ASP	599	E2 042 12 12 12 12 12 12 12 12 12 12 12 12 12
ATOM		9 C.	A ASP	599	E4 CER 10
ATOM		_	B ASP	599	E4 EC0 10 10 10 10 10 10 10 10 10 10 10 10 10
MOTA				599	EE 000 70.71
ATOM			Ol ASP	599	EE 900 15 015
ATOM			D2 ASP	599	EE 100 31.76
ATOM	3084	4 C	ASP	599	E/ 172 22
ATOM	3085		ASP	599	E4 076 10
ATOM	3086	5 N	LEU	600	52 052 22 405
ATOM	3087		LEU	600	E2 272 30 000
ATOM	3088		LEU	600	50 774 10 11
ATOM	3089			600	50 354 30 55.23
ATOM	3090		1 LEU	600	49 950 30 30.30
ATOM	3091		2 LEU	600	E1 000 34.99
ATOM	3092	_	LEU	600	52 542 0 455
ATOM	3093		LEU	600	52 900 0 155
ATOM	3094		VAL	601	52 417 70 525
ATOM	3095	CA	VAL	601	52 695 10 155
ATOM	3096	CB	VAL	601	E2 22C 77 42-
ATOM	3097		L VAL	601	E2 254 70 555
ATOM	3098		VAL	601	EO 040 44
ATOM	3099	C	VAL	601	E4 102 0 000
ATOM	3100	0	VAL	601	54 611
ATOM	3101	N	SER	602	54 996 10 600
ATOM	3102	CA	SER	602	E6 442 10 TIO 41.33
ATOM	3103	CB	SER	602	E7 014 66
ATOM	3104	OG	SER	602	EO 424 77 7-1
ATOM	3105	C	SER	602	EC 050
ATOM	3106	0	SER	602	E7 C20 40.58
ATOM	3107	N	CYS	603	E 6 310 0 ===
ATOM	3108	CA	CYS	603	1.00 38.34
ATOM	3109	CB	CYS	603	EE 715
ATOM	3110	SG	CYS	603	EF 735
ATOM	3111	C	CYS	603	F6 202 5 7 7 7 0.30 42.18
ATOM	3112	0	CYS	603	E7 030
ATOM	3113	N	ALA	604	EE 100 37.87
ATOM	3114	CA	ALA	604	54 004 =
					54.804 -5.572 21.911 1.00 34.97

ATOM	3115	CB	ALA	604	53.393	-5.917	22.409	1.00	34.13
MOTA	3116	С	ALA	604	55.791	-5.610	23.081	1.00	36.68
MOTA	3117	0	ALA	604	56.085	-4.585	23.704	1.00	36.78
MOTA	3118	N	TYR	605	56.281	-6.807	23.385	1.00	37.68
MOTA	3119	CA	TYR	605	57.254	-7.005	24.461	1.00	38.38
MOTA	3120	CB	TYR	605	57.533	-8.498	24.643	1.00	37.62
MOTA	3121	CG	TYR	605	58.635	-8.806	25.622	1.00	36.56
MOTA	3122	CD1	TYR	605	58.498	-8.509	26.974	1.00	39.05
MOTA	3123	CE1	TYR	605	59.520	-8.809	27.893	1.00	41.37
MOTA	3124	CD2	TYR	605	59.812	-9.407	25.198	1.00	38.09
ATOM	3125	CE2	TYR	605	60.848	-9.711	26.105	1.00	38.55
MOTA	3126	CZ	TYR	605	60.692	-9.409	27.454	1.00	40.73
ATOM	3127	OH	TYR	605	61.707	-9.704	28.348	1.00	41.44
ATOM	3128	C	TYR	605	58.549	-6.267	24.123	1.00	38.44
MOTA	3129	0	TYR	605	59.053	-5.485	24.937	1.00	40.78
MOTA	3130	N	GLN	606	59.053	-6.501	22.908	1.00	36.07
MOTA	3131	CA	GLN	606	60.276	-5.872	22.398	1.00	35.28
ATOM	3132	CB	GLN	606	60.594	-6.415	21.002	1.00	34.24
MOTA	3133	CG	GLN	606	61.105	-7.851	21.005	1.00	32.26
ATOM	3134	CD	GLN	606	61.339	-8.388	19.608	1.00	30.17
ATOM	3135	OE1	GLN	606	62.274	-7.988	18.907	1.00	31.89
MOTA	3136	NE2	GLN	606	60.471	-9.285	19.182	1.00	30.68
MOTA	3137	С	GLN	606	60.210	-4.335	22.355	1.00	36.39
MOTA	3138	0	GLN	606	61.206	-3.660	22.632	1.00	39.59
ATOM	3139	N	VAL	607	59.040	-3.798	22.006	1.00	32.78
MOTA	3140	CA	LAV	607	58.839	-2.350	21.944	1.00	30.29
MOTA	3141	CB	VAL	607	57.489	-1.982	21.221	1.00	28.48
ATOM	3142	CG1		607	57.219	-0.488	21.298	1.00	28.68
ATOM	3143	CG2		607	57.535	-2.416	19.742	1.00	22.96
ATOM	3144	C	VAL	607	58.868	-1.766	23.364	1.00	30.21
ATOM	3145	0	VAL	607	59.469	-0.705	23.591		31.24
ATOM	3146	N	ALA	608	58.224	-2.451	24.311	1.00	27.88
ATOM	3147	CA	ALA	608	58.187	-2.001	25.694	1.00	27.66
ATOM	3148	CB	ALA	608	57.242	-2.874	26.494		26.42
ATOM	3149	C	ALA	608	59.585	-2.019	26.309		29.04
ATOM	3150	0	ALA	608	59.950	-1.144	27.094		27.53
ATOM	3151	N	ARG	609	60.377	-3.013	25.932		28.91
ATOM	3152	CA	ARG	609	61.733	-3.120	26.440		31.64
ATOM	3153	CB	ARG	609	62.394	-4.405	25.953		33.78
ATOM	3154	CG	ARG	609	61.672	-5.647	26.373		38.53
ATOM	3155	CD	ARG	609	62.636	-6.791	26.448		41.78
ATOM	3156	NE	ARG	609	63.319	-6.838	27.733		47.58
ATOM	3157	CZ	ARG	609	64.441	-7.510	27.955		51.52
ATOM	3158	NH1		609	65.012	-8.179	26.964		50.61
ATOM	3159	NH2		609	64.954	-7.569	29.186		54.36
ATOM	3160	C	ARG	609	62.581	-1.918	26.024		33.26
ATOM	3161	0	ARG	609	63.144	-1.221	26.885		34.50
ATOM	3162	N	GLY	610	62.624	-1.650	24.717		30.25
ATOM	3163	CA	GLY	610	63.395	-0.534	24.199		25.40
ATOM	3164	C	GLY	610	63.010	0.730	24.930		24.12
ATOM	3165	0	GLY	610	63.857	1.507	25.345		24.74
MOTA	3166	N	MET	611	61.712	0.907	25.131	1.00	25.81



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MOTA					61.192	2.062	25.843	1.00 26.95
MOTA	3168				59.672	2.121	25.702	1.00 24.60
MOTA	3169				59.215	2.462	24.303	1.00 24.10
MOTA	3170			611	59.972	4.035	23.821	1.00 26.77
ATOM	3171			611	59.546	5.090	25.184	1.00 19.21
ATOM	3172		MET	611	61.600	2.071	27.314	
ATOM	3173		MET	611	61.891	3.128	27.865	1.00 28.22
ATOM	3174		GLU	612	61.562	0.908	27.967	
ATOM	3175			612	61.955	0.791	29.382	
ATOM	3176			612	61.809	-0.659		
ATOM	3177	_		612	62.383	-0.937		
ATOM	3178			612	62.392	-2.422		
ATOM	3179		1 GLU	612	62.599	-3.275		1.00 30.09
ATOM	3180		2 GLU	612	62.226	-2.737		1.00 33.90
ATOM	3181		GLU	612	63.409	1.252	29.468	1.00 37.14
ATOM	3182		GLU	612	63.791	1.995	30.390	1.00 35.60
ATOM	3183		TYR	613	64.196	0.868	28.457	1.00 37.89
ATOM	3184		TYR	613	65.601	1.247	28.392	1.00 36.68
ATOM	3185		TYR	613	66.328	0.531	27.246	1.00 34.23
ATOM	3186	CG	TYR	613	67.801	0.888	27.175	1.00 36.59
ATOM	3187	CD:	1 TYR	613	68.734	0.263	28.005	1.00 36.83
ATOM	3188	CE:	l TYR	613	70.090	0.649	28.013	1.00 34.51
MOTA	3189	CD:	2 TYR	613	68.252	1.909	26.339	1.00 35.28
MOTA	3190	CE:	2 TYR	613	69.596	2.306	26.340	1.00 33.28
MOTA	3191	CZ	TYR	613	70.512	1.674	27.181	1.00 35.91
ATOM	3192	OH	TYR	613	71.826	2.089	27.212	1.00 29.78
MOTA	3193	C	TYR	613	65.724	2.760	28.233	1.00 23.78
ATOM	3194	. 0	TYR	613	66.362	3.414	29.056	1.00 37.38
ATOM	3195	N	LEU	614	65.081	3.326	27.214	1.00 35.53
ATOM	3196	CA	LEU	614	65.156	4.766	26.988	1.00 33.53
ATOM	3197	CB	LEU	614	64.314	5.157	25.781	1.00 31.88
ATOM	3198	CG	LEU	614	64.760	4.601	24.429	1.00 31.88
ATOM	3199	CD1	LEU	614	63.783	5.016	23.346	1.00 29.19
MOTA	3200	CD2	LEU	614	66.134	5.133	24.111	1.00 23.13
ATOM	3201	С	LEU	614	64.698	5.538	28.218	1.00 32.49
ATOM	3202	0	LEU	614	65.325	6.525	28.618	1.00 38.38
ATOM	3203	N	ALA	615	63.608	5.076	28.821	1.00 38.08
ATOM	3204	CA	ALA	615	63.066	5.711	30.018	1.00 38.08
ATOM	3205	CB	ALA	615	61.767	5.018	30.444	1.00 42.33
ATOM	3206	С	ALA	615	64.099	5.683	31.147	1.00 42.33
MOTA	3207	0	ALA	615	64.291	6.690	31.831	1.00 40.47
ATOM	3208	N	SER	616	64.788	4.553	31.307	1.00 41.28
ATOM	3209	CA	SER	616	65.806	4.441	32.347	1.00 38.78
ATOM	3210	CB	SER	616	66.354	3.009	32.454	
MOTA	3211	OG	SER	616	67.172	2.651	31.359	1.00 37.82
ATOM	3212	C	SER	616	66.941	5.416		1.00 34.73
ATOM	3213	0	SER	616	67.714	5.769	32.061 32.957	1.00 42.68
ATOM	3214	N	LYS	617	67.015	5.869		1.00 45.78
ATOM	3215	CA	LYS	617	68.025	6.816	30.815	1.00 40.92
ATOM	3216	CB	LYS	617	68.541		30.380	1.00 38.04
ATOM	3217	CG	LYS	617	69.293	6.411 5.111	29.003	1.00 38.25
ATOM	3218	CD	LYS	617	70.421		29.021	1.00 36.40
			_	•	, U. 42I	5.221	29.992	1.00 38.14

ATOM	3219	CE	LYS	617	71.215	3.941	30.086	1.00	38.43
ATOM	3220	NZ	LYS	617	72.530	4.210	30.751	1.00	43.07
MOTA	3221	С	LYS	617	67.475	8.242	30.350	1.00	38.42
MOTA	3222	0	LYS	617	68.072	9.133	29.744	1.00	41.37
ATOM	3223	N	LYS	618	66.323	8.444	30.985	1.00	37.25
ATOM	3224	CA	LYS	618	65.674	9.743	31.067	1.00	36.75
ATOM	3225	СВ	LYS	618	66.653	10.780	31.632	1.00	43.27
MOTA	3226	CG	LYS	618	67.340	10.392	32.938	1.00	51.59
ATOM	3227	CD	LYS	618	66.377	10.361	34.092	1.00	61.24
MOTA	3228	CE	LYS	618	67.070	9.945	35.373	1.00	67.83
MOTA	3229	NZ	LYS	618	66.105	10.039	36.510	1.00	75.22
ATOM	3230	С	LYS	618	65.167	10.222	29.706	1.00	36.61
ATOM	3231	0	LYS	618	64.856	11.396	29.535	1.00	35.94
MOTA	3232	N	CYS	619	65.058	9.308	28.751	1.00	36.26
ATOM	3233	CA	CYS	619	64.603	9.666	27.412	1.00	33.41
ATOM	3234	CB	CYS	619	65.351	8.843	26.365	1.00	32.17
MOTA	3235	SG	CYS	619	65.006	9.223	24.650	1.00	26.92
ATOM	3236	С	CYS	619	63.108	9.546	27.194	1.00	32.29
ATOM	3237	0	CYS	619	62.510	8.472	27.373	1.00	29.13
ATOM	3238	N	ILE	620	62.515	10.679	26.827	1.00	31.60
MOTA	3239	CA	ILE	620	61.091	10.763	26.528	1.00	31.21
ATOM	3240	CB	ILE	620	60.435	11.966	27.212	1.00	29.57
ATOM	3241	CG2	ILE	620	58.955	12.031	26.860	1.00	31.49
ATOM	3242	CG1	ILE	620	60.578	11.848	28.727	1.00	27.85
ATOM	3243	CD1	ILE	620	60.065	13.046	29.463	1.00	26.50
MOTA	3244	C	ILE	620	61.034	10.972	25.018	1.00	32.18
MOTA	3245	0	ILE	620	61.481	11.993	24.512	1.00	33.18
ATOM	3246	N	HIS	621	60.472	9.990	24.318	1.00	31.93
ATOM	3247	CA	HIS	621	60.354	9.970	22.864	1.00	32.59
ATOM	3248	CB	HIS	621	59.933	8.552	22.420	1.00	29.51
ATOM	3249	CG	HIS	621	60.076	8.288	20.951	1.00	27.45
MOTA	3250	CD2	HIS	621	60.663	7.262	20.286	1.00	25.84
MOTA	3251	ND1	HIS	621	59.528	9.106	19.979	1.00	25.20
ATOM	3252	CE1	HIS	621	59.774	8.596	18.783	1.00	25.07
MOTA	3253	NE2	HIS	621	60.456	7.473	18.942	1.00	23.24
MOTA	3254	C	HIS	621	59.365	10.992	22.320	1.00	35.31
ATOM	3255	0	HIS	621	59.555	11.481	21.220	1.00	39.24
MOTA	3256	N	ARG	622	58.256	11.216	23.028	1.00	36.50
ATOM	3257	CA	ARG	622	57.225	12.169	22.580	1.00	35.78
MOTA	3258	CB	ARG	622	57.783	13.582	22.462	1.00	32.55
ATOM	3259	CG	ARG	622	58.211	14.156	23.778	1.00	30.54
MOTA	3260	CD	ARG	622	58.799	15.551	23.635	0.50	27.28
ATOM	3261	NE	ARG	622	59.249	16.043	24.930	0.50	24.53
ATOM	3262	CZ	ARG	622	60.409	15.707	25.499		27.85
MOTA	3263		ARG	622	61.249	14.883	24.877	0.50	27.61
MOTA	3264	NH2	ARG	622	60.711	16.158	26.714	0.50	25.34
MOTA	3265	С	ARG	622	56.447	11.806	21.297	1.00	35.76
MOTA	3266	0	ARG	622	55.438	12.430	20.999	1.00	36.61
MOTA	3267	N	ASP	623	56.923	10.818	20.537		34.69
ATOM	3268	CA	ASP	623	56.197	10.400	19.335	1.00	34.09
ATOM	3269	CB	ASP	623	56.628	11.171	18.081		34.77
MOTA	3270	CG	ASP	623	55.727	10.869	16.863	1.00	43.51

7.00								
ATO			DD1 ASI		56.21	3 10.99	2 15.714	1.00 47.45
ATON			D2 ASI		54.53	8 10.50		
ATON					56.32			
ATON					56.63	5 8.435		
ATOM			LEU	624	56.08			
ATOM			A LEU	624	56.15			
ATOM		7 C	B LEU	624	56.133			1.00 31.07
ATOM	327	8 C	G LEU		55.983			1.00 28.11
ATOM	327	9 C	D1 LEU	624	57.108			1.00 27.88
ATOM		0 C	D2 LEU	624	56.00			1.00 23.96
ATOM	328		LEU		54.954			1.00 29.50
ATOM	3282	2 0	LEU		53.805			1.00 32.04
ATOM	3283	3 N		625	55.224			1.00 36.02
ATOM	3284	4 C		625	54.170			1.00 28.91
ATOM	3285		_	625				1.00 25.66
ATOM	3286		ALA	625	53.707			1.00 23.37
ATOM	3287		ALA	625	54.800		16.389	1.00 27.71
ATOM	3288		ALA	626	56.022		16.355	1.00 29.77
ATOM	3289			626	53.982		15.758	1.00 29.46
ATOM	3290				54.499		14.956	1.00 28.16
ATOM	3291		ALA	626	53.350	1.155	14.401	1.00 28.02
ATOM	3292			626	55.366	2.504	13.831	1.00 26.78
ATOM	3293	_	ALA	626	56.329	1.859	13.454	1.00 26.69
ATOM	3294		ARG	627	55.022	3.680	13.314	1.00 26.09
ATOM				627	55.777	4.301	12.246	1.00 26.78
ATOM	3295			627	55.134	5.637	11.837	1.00 27.01
	3296			627	55.046	6.672	12.961	1.00 29.34
ATOM ATOM	3297			627	54.552	8.037	12.477	1.00 34.26
	3298	NE		627	54.108	8.878	13.590	1.00 36.96
ATOM ATOM	3299	CZ	ARG	627	52.867	8.889	14.059	1.00 40.84
	3300		1 ARG	627	51.942	8.114	13.515	1.00 42.56
MOTA	3301		2 ARG	627	52.552	9.634	15.108	1.00 45.20
ATOM	3302	C	ARG	627	57.209	4.549	12.711	1.00 29.11
MOTA	3303	0	ARG	627	58.137	4.468	11.911	1.00 30.39
ATOM	3304	N	ASN	628	57.385	4.804	14.010	1.00 30.37
ATOM	3305	CA	ASN	628	58.689	5.092	14.596	1.00 30.37
ATOM	3306	CB	ASN	628	58.578	6.226	15.611	1.00 24.35
ATOM	3307	CG	ASN	628	58.383	7.571	14.941	1.00 24.35
ATOM	3308		. ASN	628	58.992	7.865		
MOTA	3309	ND2	ASN	628	57.522	8.391		
ATOM	3310	C	ASN	628	59.437	3.903		1.00 24.34
ATOM	3311	0	ASN	628	60.378	4.062		1.00 26.74
ATOM	3312	N	VAL	629	58.998	2.712		1.00 28.49
ATOM	3313	CA	VAL	629	59.621	1.450		1.00 27.34
ATOM	3314	CB	VAL	629	58.589			1.00 24.94
ATOM	3315	CG1	VAL	629	59.169	0.522		1.00 22.20
ATOM	3316		VAL	629	58.158	-0.883		1.00 18.03
ATOM	3317	С	VAL	629				1.00 18.34
MOTA	3318	0	VAL	629	60.077	0.805		1.00 26.84
ATOM	3319	N	LEU	630	59.284			L.00 26.50
ATOM	3320	CA	LEU		61.352	_		1.00 27.66
ATOM	3321	CB	LEU	630	61.862	_		00 30.14
ATOM	3322	CG	LEU	630	63.105			00 28.00
		CG	TEO	630	62.856	2.086		00 26.06

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MOTA	3323	· CD1	LEU	630	64.150	2.831	11.832	1.00	23.44
MOTA	3324	CD2	LEU	630	61.880	2.381	10.901	1.00	27.72
MOTA	3325	С	LEU	630	62.145	-1.627	12.889	1.00	32.90
ATOM	3326	0	LEU	630	62.437	-1.982	14.029	1.00	33.06
MOTA	3327	N	VAL	631	61.991	-2.478	11.873	1.00	34.83
MOTA	3328	CA	VAL	631	62.195	-3.928	12.006	1.00	33.02
MOTA	3329	CB	VAL	631	60.915	-4.700	11.584	1.00	30.92
ATOM	3330	CG1	VAL	631	61.071	-6.208	11.842		27.66
ATOM	3331		VAL	631	59.724	-4.161	12.332		24.46
ATOM	3332	С	VAL	631	63.371	-4.415	11.161		35.77
ATOM	3333	0	VAL	631	63.428	-4.171	9.954		37.57
ATOM	3334	N	THR	632	64.319	-5.098	11.797		37.96
MOTA	3335	CA	THR	632	65.511	-5.599	11.096		39.06
ATOM	3336	CB	THR	632	66.675	-5.820	12.066		35.55
ATOM	3337	OG1	THR	632	66.368	-6.903	12.955		35.76
ATOM	3338	CG2	THR	632	66.928				
ATOM	3339	C	THR	632	65.283	-4.561	12.867		35.06
						-6.893	10.331		40.66
ATOM	3340	0	THR	632	64.238	-7.515	10.466		41.79
ATOM	3341	N	GLU	633	66.282	-7.307	9.556		43.40
ATOM	3342	CA	GLU	633	66.219	-8.540	8.768		45.33
ATOM	3343	CB	GLU	633	67.501	-8.689	7.942		48.67
ATOM	3344	CG	GLU	633	67.496	-9.791	6.864	1.00	54.70
ATOM	3345	CD	GLU	633	66.599	-9.506	5.647		58.16
ATOM	3346	OE1	GLU	633	65.933	-8.452	5.567		60.68
ATOM	3347	OE2	GLU	633	66.566	-10.369	4.747		60.14
ATOM	3348	C	GLU	633	66.011	-9.774	9.648	1.00	46.02
MOTA	3349	0	GLU	633	65.637	-10.834	9.156	1.00	46.75
MOTA	3350	N	ASP	634	66.278	-9.648	10.944	1.00	46.45
MOTA	3351	CA	ASP	634	66.085	-10.774	11.843	1.00	46.14
MOTA	3352	CB	ASP	634	67.316	-10.995	12.724	1.00	52.89
MOTA	3353	CG	ASP	634	68.570	-11.399	11.929	1.00	59.65
MOTA	3354	OD1	ASP	634	68.593	-12.499	11.328	1.00	59.91
MOTA	3355	OD2	ASP	634	69.546	-10.608	11.918	1.00	62.29
MOTA	3356	С	ASP	634	64.850	-10.549	12.708	1.00	45.75
MOTA	3357	0	ASP	634	64.729	-11.138	13.776	1.00	46.38
MOTA	3358	N	ASN	635	63.940	-9.697	12.235	1.00	45.92
MOTA	3359	CA	ASN	635	62.690	-9.367	12.915	1.00	44.36
ATOM	3360	CB	ASN	635	61.750	-10.583	12.972	1.00	46.62
ATOM	3361	CG	ASN	635	61.409	-11.116	11.597	1.00	47.56
MOTA	3362	OD1	ASN	635	60.750	-10.453	10.800	1.00	50.54
ATOM	3363	ND2	ASN	635	61.876	-12.314	11.305		47.75
ATOM	3364	С	ASN	635	62.833	-8.763	14.308		42.78
ATOM	3365	0	ASN	635	62.028	-9.045	15.189		44.56
ATOM	3366	N	VAL	636	63.849	-7.927	14.503		41.03
ATOM	3367	CA	VAL	636	64.071	-7.291	15.797		36.87
ATOM	3368	CB	VAL	636	65.584	-7.162	16.083		35.99
ATOM	3369		VAL	636	65.839	-6.347	17.354		34.01
ATOM	3370		VAL	636	66.184	-8.535	16.226		33.65
ATOM	3370	C	VAL	636	63.434	-5.908			
		0					15.782		34.79
ATOM	3372		VAL	636	63.657	-5.131	14.854		36.58
ATOM	3373	N	MET	637	62.600	-5.625	16.773		32.04
MOTA	3374	CA	MET	637	61.940	-4.331	16.887	1.00	31.14

ATC	OM 3	375	СВ	MIN	T				
ATC	-	376	CG			60.7		427 17.8	17 1.00 35.49
ATO		377				59.7			
ATO			SD	ME		58.8	35 -5.3		
ATO		378	CE	MET		59.1	22 -6.8	864 15.0	
ATO		79	C	MET	• • •	62.9	35 -3.3		
		80	0	MET		63.5	25 -3.6		
ATO	_	81	N	LYS		63.04			
ATO		82	CA	LYS	638	63.97			
ATO			CB	LYS	638	65.21			
ATO			CG	LYS	638	66.14			
ATON			CD	LYS	638	67.30			
ATON		86	CE	LYS	638	68.36			
ATOM			NZ	LYS	638	68.93			
ATOM		88	С	LYS	638	63.36			
ATOM	1 338	39 (O	LYS	638		_		
ATOM	339	90 1	V	ILE	639	62.98			= - : 5 5
ATOM	339	91 (CA	ILE	639	63.27			
ATOM	339		СВ	ILE	639	62.73	_	_	6 1.00 24.75
ATOM	339			ILE	639	62.69			3 1.00 23.98
ATOM				ILE		61.91	_		5 1.00 21.11
ATOM				ILE	639	62.12		10 20.963	3 1.00 26.06
ATOM				ILE	639	60.680		92 20.758	3 1.00 28.45
ATOM					639	63.656		98 17.774	1.00 26.36
ATOM	339			ILE	639	64.884			
ATOM	339	_		ALA	640	63.073			
ATOM	340			ALA	640	63.857	5.03		
ATOM				ALA	640	63.683	4.77		
ATOM	340	-		ALA	640	63.380	6.44	9 16.548	
ATOM	340			ALA	640	62.307	6.60		
	3403			ASP	641·	64.174			
ATOM	3404		-	ASP	641	63.863			
ATOM	3405			ASP	641	62.662			
ATOM	3406			ASP	641	63.024	9.55		1.00 35.25
ATOM	3407)1 /		641	64.149	9.170		1.00 38.54
ATOM	3408	OI	2 7		641	62.192	10.144		1.00 39.85
ATOM	3409		7	ASP	641	63.661	9.311		1.00 41.38
ATOM	3410	0	A	ASP	641	63.012	10.323	_	1.00 30.61
ATOM	3411	N	P	HE	642	64.265	8.567		1.00 29.45
MOTA	3412	CA	P	HE	642	64.155			1.00 30.96
ATOM	3413	CB	P	HE	642	64.447	8.860		1.00 31.21
ATOM	3414	CG	P	HE	642	65.806	7.597		1.00 27.06
ATOM	3415	CD	1 P	HE	642	66.930	7.008		1.00 24.27
ATOM	3416		2 P		642	66.930	7.476		1.00 22.36
ATOM	3417		l Pi		642	65.962	5.978		1.00 24.87
ATOM	3418		2 PI		642	68.179	6.928	_	1:00 23.19
ATOM	3419	CZ		HE	642	67.205	5.420		1.00 23.65
ATOM	3420	C		HE		68.323	5.898	20.282	1.00 22.95
ATOM	3421	Õ		HE	642	65.069	10.007	20.623	1.00 34.88
ATOM	3422	N			642	64.920	10.549	21.729	1.00 34.84
ATOM	3423	CA	GI		643	66.000	10.377	19.737	1.00 36.20
ATOM	3424		GI		643	66.934	11.450	20.032	1.00 35.47
ATOM		C	GI		643	66.728	12.720	19.232	1.00 37.62
ATOM	3425	0	GI		643	67.581	13.593	19.269	1.00 37.62
*** 014	3426	N	LE	Ű	644	65.609	12.837	18.517	1.00 39.16
									±.00 33.68

MOTA	3427	CA	LEU	644	65.328	14.029	17.712	1.00 43.09
ATOM	3428	CB	LEU .	644	64.074	13.843	16.860	1.00 40.78
ATOM	3429	CG	LEU	644	64.076	12.876	15.681	1.00 36.94
ATOM	3430	CD1	LEU	644	62.790	13.076	14.901	1.00 37.34
ATOM	3431	CD2	LEU	644	65.240	13.157	14.783	1.00 37.72
ATOM	3432	С	LEU	644	65.154	15.261	18.591	1.00 47.32
ATOM	3433	0	LEU	644	64.639	15.170	19.702	1.00 50.33
MOTA	3434	N	ALA	645	65.598	16.406	18.088	1.00 51.23
ATOM	3435	CA	ALA	645	65.507	17.662	18.820	1.00 52.97
ATOM	3436	СВ	ALA	645	66.367	18.703	18.151	1.00 54.12
ATOM	3437	С	ALA	645	64.060	18.137	18.910	1.00 53.00
ATOM	3438	0	ALA	645	63.591	18.528	19.977	1.00 53.59
ATOM	3439	N	ASP	652	52.356	21.675	14.855	1.00 79.51
ATOM	3440	CA	ASP	652	51.194	21.821	13.993	1.00 78.74
ATOM	3441	CB	ASP	652	51.625	22.021	12.531	1.00 78.30
MOTA	3442	CG	ASP	652	50.459	22.358	11.608	1.00 77.64
ATOM	3443	OD1		652	49.473	22.968	12.079	1.00 77.67
ATOM	3444	OD2		652	50.526	22.029	10.410	1.00 78.25
ATOM	3445	С	ASP	652	50.339	20.569	14.125	1.00 78.92
ATOM	3446	0	ASP	652	50.645	19.529	13.539	1.00 79.36
ATOM	3447	N	TYR	653	49.262	20.682	14.892	1.00 79.17
ATOM	3448	CA	TYR	653	48.357	19.560	15.111	1.00 80.23
ATOM	3449	СВ		653	47.283	19.932	16.136	1.00 81.36
ATOM	3450	CG	TYR	653	47.790	20.060	17.557	1.00 84.51
ATOM	3451	CD1	TYR	653	46.998	20.649	18.544	1.00 86.09
ATOM	3452	CE1	TYR	653	47.443	20.751	19.865	1.00 88.05
ATOM	3453	CD2	TYR	653	49.049	19.576	17.925	1.00 86.22
ATOM	3454	CE2	TYR	653	49.504	19.673	19.242	1.00 87.14
ATOM	3455	CZ	TYR	653	48.698	20.260	20.207	1.00 88.37
ATOM	3456	ОН	TYR	653	49.146	20.351	21.510	1.00 88.82
ATOM	3457	C	TYR	653	47.687	19.098	13.827	1.00 80.07
ATOM	3458	0	TYR	653	47.170	17.983	13.752	1.00 81.23
ATOM	3459	N	TYR	654	47.716	19.953	12.813	1.00 79.01
ATOM	3460	CA	TYR	654	47.082	19.640	11.544	1.00 78.81
ATOM	3461	СВ	TYR	654	46.378	20.884	11.008	1.00 78.48
ATOM	3462	CG	TYR	654	45.358	21.422	11.982	1.00 78.53
ATOM	3463	CD1	TYR	654	45.752	21.948	13.213	1.00 77.46
ATOM	3464	CE1	TYR	654	44.822	22.382	14.146	1.00 78.94
ATOM	3465	CD2	TYR	654	43.997	21.350	11.704	1.00 80.18
ATOM	3466		TYR	654	43.054	21.785	12.632	1.00 82.55
ATOM	3467	CZ	TYR	654	43.473	22.295	13.851	1.00 80.98
ATOM	3468	OH	TYR	654	42.548	22.703	14.785	1.00 82.29
ATOM	3469	C	TYR	654	48.010	19.042	10.499	1.00 79.04
ATOM	3470	0	TYR	654	47.575	18.720	9.393	1.00 80.09
MOTA	3471	N	LYS	655	49.277	18.859	10.848	1.00 30.03
ATOM	3472	CA	LYS	655	50.217	18.282	9.906	1.00 78.74
ATOM	3473	CB	LYS	655 655	51.651	18.687	10.247	1.00 83.97
MOTA	3474	CG	LYS	655	52.674	18.124	9.281	1.00 89.76
MOTA	3475	CD	LYS	655	54.084	18.565	9.611	1.00 93.90
MOTA	3476	CE	LYS	655	55.075	17.844	8.708	1.00 97.62
ATOM	3477	NZ	LYS	655	56.489	18.177	9.038	1.00101.35
MOTA	3478	С	LYS	655	50.070	16.763	9.922	1.00 80.98

ATOM	3479	0	LYS	655	50	0.187	16.130	10.975	. 1 0	0 80.95
ATOM	3480	N	LYS	656		766		8.759		0 80.33
ATOM	3481	. CA	LYS	656		.599		8.630		0 81.06
ATOM	3482	CB	LYS	656		3.723	14.426	7.423		0 81.40
ATOM	3483	CG	LYS	656		.258	14.779	7.596		0 81.60
ATOM	3484	CD	LYS	656	46	.518	14.565	6.295		0 84.93
ATOM	3485	CE	LYS	656		.019	14.620	6.493		0 87.78
ATOM	3486	NZ	LYS	656		.291	14.565	5.183		91.78
ATOM	3487	С	LYS	656	50	.940	14.026	8.513		80.44
ATOM	3488	0	LYS	656	51	.923	14.596	8.032		
ATOM	3489	N	\mathtt{GLY}	660		.197	9.779	5.831	1.00	
ATOM	3490	CA	GLY	660		.231	10.860	5.961		55.59
ATOM	3491	C	GLY	660		.492	10.866	7.285		53.27
ATOM	3492	0	GLY	660		.403	11.432	7.388	1.00	
ATOM	3493	N	ARG	661		.080	10.222	8.288	1.00	
ATOM	3494	CA	ARG	661		.477	10.155	9.617	1.00	
MOTA	3495	CB	ARG	661		.900	8.861	10.338	1.00	
ATOM	3496	CG	ARG	661		.612	7.566	9.563	1.00	
ATOM	3497	CD	ARG	661		.801	6.331	10.456	1.00	-
MOTA	3498	NE	ARG	661		.691	5.061	9.734	1.00	
MOTA	3499	CZ	ARG	661		. 955	3.866	10.264	1.00	
ATOM	3500	NH1	ARG	661		. 343	3.760	11.529		48.54
ATOM	3501	NH2	ARG	661		. 836	2.772	9.523		52.75
ATOM	3502	C	ARG	661		. 894	11.379	10.439		43.81
ATOM	3503	0	ARG	661		. 833	12.096	10.063		43.51
MOTA	3504	N	LEU	662		.194	11.618	11.537		40.56
ATOM	3505	CA	LEU	662		4'96	12.735	12.428		37.52
ATOM	3506	CB	LEU	662		220	13.496	12.789		37.52
ATOM	3507	CG	LEU	662		485	14.281	11.696	1.00	
ATOM	3508	CD1	LEU	662		084	14.621	12.158		31.29 24.03
MOTA	3509	CD2	LEU	662		261	15.535	11.358		28.65
ATOM	3510	C	LEU	662		154	12.237	13.712	1.00	36.78
MOTA	3511	0	LEU	662		515	11.570	14.536		37.27
MOTA	3512	N	PRO	663		448	12.549	13.895		36.46
ATOM	3513	CD	PRO	663		320	13.216	12.914		38.35
ATOM	3514	CA	PRO	663		224	12.148	15.070		35.98
ATOM	3515	CB	PRO	663		537	12.887	14.872		34.95
ATOM	3516	CG	PRO	663		702	12.836	13.403		39.18
ATOM	3517	С	PRO	663		569	12.499	16.398		35.53
ATOM	3518	0	PRO	663	49.		11.814	17.399		38.34
ATOM	3519	N	VAL	664	48.		13.558	16.414		32.71
ATOM	3520	CA	VAL	664	48.		13.964	17.632		30.18
MOTA	3521	CB	VAL	664	47.		15.242	17.427		
ATOM	3522	CG1	VAL	664	48.		16.409	17.427		31.31
ATOM	3523		VAL	664	46.		15.038	16.345		28.93
ATOM	3524	С	VAL	664	47.		12.787			34.42
MOTA	3525	0	VAL	664	47.		12.654	18.172		29.48
MOTA	3526	N	LYS	665	46.			19.388		30.41
MOTA	3527	CA	LYS	665	46.		11.883 10.704	17.282		29.29
MOTA	3528	CB	LYS	665	45.		10.704	17.668		28.55
MOTA	3529	CG	LYS	665	44.4			16.423	1.00	
MOTA	3530	CD	LYS	665	43.9			15.786	1.00	
•					43.1	113	10.366	14.418	1.00	29.41

MOTA	3531	CE	LYS	665	42.785	11.162	13.899	1.00 26.35
ATOM	3532	NZ	LYS	665	42.363	10.809	12.508	1.00 26.16
ATOM	3533	C	LYS	665	46.890	9.730	18.556	1.00 28.81
ATOM	3534	0	LYS	665	46.315	8.802	19.113	1.00 29.38
ATOM	3535	N	TRP	666	48.181	9.976	18.736	1.00 28.98
MOTA	3536	CA	TRP	666	49.005	9.128	19.599	1.00 31.67
ATOM	3537	CB	TRP	666	50.323	8.755	18.913	1.00 29.46
ATOM	3538	CG	TRP	666	50.205	7.582	17.977	1.00 28.92
ATOM	3539	CD2	TRP	666	49.676	7.603	16.642	1.00 27.62
ATOM	3540	CE2	TRP	666	49.740	6.276	16.162	1.00 27.15
ATOM	3541	CE3	TRP	666	49.151	8.607	15.818	1.00 25.27
ATOM	3542	CD1	TRP	666	50.565	6.289	18.238	1.00 24.30
ATOM	3543	NE1	TRP	666	50.287	5.506	17.147	1.00 27.82
ATOM	3544	CZ2	TRP	666	49.295	5.930	14.872	1.00 26.95
ATOM	3545	CZ3	TRP	666	48.707	8.256	14.536	1.00 25.95
ATOM	3546	CH2	TRP	666	48.778	6.929	14.081	1.00 28.35
ATOM	3547	С	TRP	666	49.316	9.836	20.907	1.00 33.46
ATOM	3548	0	TRP	666	49.790	9.219	21.867	1.00 34.77
ATOM	3549	N	MET	667	49.021	11.128	20.947	1.00 35.61
ATOM	3550	CA	MET	667	49.306	11.948	22.110	1.00 37.94
ATOM	3551	CB	MET	667	49.308	13.419	21.723	1.00 40.22
ATOM	3552	CG	MET	667	50.606	13.939	21.150	1.00 40.77
ATOM	3553	SD	MET	667	50.479	15.723	20.906	1.00 44.04
ATOM	3554	CE	MET	667	50.932	15.858	19.204	1.00 39.07
ATOM	3555	C	MET	667	48.432	11.775	23.346	1.00 39.61
ATOM	3556	0	MET	667	47.211	11.672	23.255	1.00 42.46
ATOM	3557	N	ALA	668	49.072	11.820	24.505	1.00 38.46
ATOM	3558	CA	ALA	668	48.383	11.704	25.773	1.00 37.78
ATOM	3559	CB	ALA	668	49.388	11.473	26.894	1.00 38.21
ATOM	3560	C	ALA	668	47.666	13.033	25.966	1.00 37.46
ATOM	3561	Ō	ALA	668	48.156	14.072	25.521	1.00 35.74
ATOM	3562	N	PRO	669	46.521	13.027	26.665	1.00 37.55
ATOM	3563	CD	PRO	669	45.868	11.840	27.243	1.00 38.19
ATOM	3564	CA	PRO	669	45.723	14.229	26.923	1.00 39.30
ATOM	3565	CB	PRO	669	44.638	13.708	27.864	1.00 39.82
ATOM	3566	CG	PRO	669	44.444	12.301	27.379	1.00 39.13
ATOM	3567	C	PRO	669	46.517	15.391	27.535	1.00 40.55
ATOM	3568	Ō	PRO	669	46.442	16.523	27.056	1.00 39.87
ATOM	3569	N	GLU	670	47.303	15.113	28.569	1.00 41.15
ATOM	3570	CA	GLU	670	48.096	16.169	29.200	1.00 42.80
ATOM	3571	CB	GLU	670	48.776	15.657	30.464	1.00 42.97
ATOM	3572	CG	GLU	670	49.928	14.705	30.205	1.00 42.82
ATOM	3573	CD	GLU	670	49.506	13.252	30.150	1.00 44.16
ATOM	3574		GLU	670	50.395	12.384	30.257	1.00 40.43
ATOM	3575	OE2	GLU	670	48.297	12.974	30.013	1.00 46.36
ATOM	3576	C	GLU	670	49.145	16.795	28.276	1.00 43.00
ATOM	3577	0	GLU	670	49.435	17.979	28.380	1.00 40.37
ATOM	3578	N	ALA	671	49.697	15.999	27.367	1.00 44.03
ATOM	3579	CA	ALA	671	50.708	16.495	26.440	1.00 44.00
ATOM	3580	CB	ALA	671	51.460	15.333	25.814	1.00 42.47
ATOM	3580	СВ	ALA	671	50.063	17.364	25.361	1.00 47.79
ATOM	3582	0	ALA	671	50.602	18.398	24.977	1.00 47.73
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ATOM	3583		LEU	672	48.877	7 16.952	24.922	2 1.00 51.20
MOTA	3584			672	48.131	17.650	23.881	
ATOM	3585			672	47.092	16.685		
MOTA	3586			672	46.307	17.010		;
ATOM	3587		_	672	47.230	17.328		
ATOM	3588		2 LEU	672	45.443			
ATOM	3589	C	LEU	672	47.456		24.445	
ATOM	3590	0	LEU	672	47.502		23.841	
ATOM	3591	N	PHE	673	46.866		25.627	
MOTA	3592	CA	PHE	673	46.179		26.281	
ATOM	3593	CB	PHE	673	44.974		27.060	
ATOM	3594			673	43.967		26.200	1.00 52.79
MOTA	3595		1 PHE	673	43.477		26.580	
ATOM	3596	CD:	2 PHE	673	43.491	19.173	25.022	1.00 53.89
ATOM	3597	CE:	1 PHE	673	42.530	16.702	25.808	1.00 55.44
ATOM	3598	CE:	2 PHE	673	42.540	18.507	24.239	1.00 54.80
ATOM	3599	CZ	PHE	673	42.062	17.269	24.637	1.00 54.86
ATOM	3600	C	PHE	673	47.071	20.733	27.200	1.00 58.97
MOTA	3601	0	PHE	673	47.084	21.959	27.095	1.00 58.37
ATOM	3602	N	ASP	674	47.832	20.086	28.077	1.00 60.63
MOTA	3603	CA	ASP	674	48.698	20.798	29.026	1.00 61.52
ATOM	3604	CB	ASP	674	48.638	20.137	30.410	1.00 61.32
ATOM	3605	CG	ASP	674	47.247	20.143	31.010	1.00 62.87
MOTA	3606	OD1	ASP	674	46.706	19.039	31.246	1.00 62.87
MOTA	3607	OD2	ASP	674	46.698	21.239	31.253	1.00 63.55
MOTA	3608	C	ASP	674	50.176	20.898	28.618	1.00 61.58
MOTA	3609	0	ASP	674	51.014	21.284	29.446	1.00 60.41
ATOM	3610	N	ARG	675	50.499	20.519	27.380	1.00 60.41
MOTA	3611	CA	ARG	675	51.885	20.526	26.883	1.00 59.23
ATOM	3612	CB	ARG	675	52.336	21.944	26.515	1.00 59.25
ATOM	3613	CG	ARG	675	51.548	22.564	25.367	1.00 59.03
MOTA	3614	CD	ARG	675	52.036	23.967	25.014	1.00 68.61
ATOM	3615	NE	ARG	675	53.348	23.969	24.359	1.00 69.16
ATOM	3616	CZ	ARG	675	54.076	25.061	24.145	1.00 68.19
ATOM	3617	NH1	ARG	675	53.622	26.250	24.531	1.00 66.97
ATOM	3618	NH2	ARG	675	55.265	24.965	23.564	1.00 67.00
ATOM	3619	C	ARG	675	52.849	19.885	27.892	1.00 57.00
ATOM	3620	0	ARG	675	54.002	20.300	28.033	1.00 57.05
ATOM	3621	N	ILE	676	52.356	18.867	28.591	1.00 55.44
ATOM	3622	CA	ILE	676	53.136	18.140	29.589	1.00 53.44
ATOM	3623	CB	ILE	676	52.314	17.899	30.874	1.00 50.96
ATOM	3624	CG2	ILE	676	52.934	16.787	31.718	1.00 47.57
ATOM	3625	CG1	ILE	676	52.213	19.196	31.669	
MOTA	3626	CD1	ILE	676	51.443	19.073	32.964	1.00 50.88
MOTA	3627	С	ILE	676	53.608	16.801	29.029	1.00 53.09
ATOM	3628	0	ILE	676	52.810	15.891		1.00 54.75
ATOM	3629	N	TYR	677	54.902	16.681	28.824 28.777	1.00 57.06
ATOM	3630	CA	TYR	677	55.459	15.447		1.00 53.61
ATOM	3631	CB	TYR	677	56.332	15.747	28.243	1.00 52.80
ATOM	3632	CG	TYR	677	55.554	16.184	27.023	1.00 53.40
ATOM	3633	CD1	TYR	677	55.256		25.794	1.00 57.32
ATOM	3634	CE1	TYR	677	54.574		25.575	1.00 55.94
	_			,	J4.5/4	17.946	24.436	1.00 54.18

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3635 CD2 TYR 677 MOTA 55.140 15.251 24.829 1.00 56.63 677 MOTA 3636 CE2 TYR 54.459 15.654 23.680 1.00 54.84 **ATOM** 3637 CZTYR 677 54.183 17.004 23.490 1.00 56.38 MOTA 3638 OH TYR 677 53.555 17.426 22.340 1.00 57.46 ATOM 3639 С TYR 677 56.268 14.713 29.304 1.00 51.49 MOTA 3640 0 TYR 677 57.186 15.283 29.904 1.00 52.65 MOTA 3641 N THR 678 55.881 13.471 29.579 1.00 48.54 3642 CA THR 678 ATOM 56.571 12.648 30.568 1.00 46.14 3643 CB THR 678 ATOM 55.776 12.597 31.910 1:00 47.34 3644 OG1 THR 678 ATOM 54.615 11.764 31.764 1.00 50.96 **ATOM** 3645 CG2 THR 678 55.346 13.996 32.345 1.00 47.47 **ATOM** 3646 С THR 678 56.742 11.218 30.041 1.00 43.21 **ATOM** 3647 0 THR 678 10.917 56.371 28.912 1.00 41.64 **ATOM** 3648 HIS 679 N 57.334 10.351 30.854 1.00 42.21 ATOM. 3649 CA HIS 679 8.969 30.456 57.507 1.00 39.96 MOTA 3650 CB HIS 679 8.216 31.428 58.410 1.00 39.23 **ATOM** HIS 3651 CG 679 59.833 8.677 31.418 1.00 43.24 MOTA 3652 CD2 HIS 679 60.501 9.505 32.253 1.00 43.12 ND1 HIS 30.498 **ATOM** 3653 679 60.759 8.236 1.00 42.63 CE1 HIS **ATOM** 3654 679 8.762 61.938 30.774 1.00 42.66 NE2 HIS ATOM 3655 679 61.807 9.539 31.832 1.00 43.80 MOTA 3656 C HIS 679 56.145 8.301 30.429 1.00 40.78 0 HIS ATOM 3657 679 55.930 7.358 29.678 1.00 42.66 3658 GLN 680 MOTA N 55.227 8.803 31.254 1.00 40.26 MOTA 3659 CA GLN 680 8.261 53.881 31.324 1.00 39.10 MOTA 3660 CB GLN 680 53..187 8.664 32.625 1.00 39.23 MOTA 3661 CG GLN 680 53.762 7.980 33.874 1.00 41.07 MOTA 3662 CD GLN 680 53.813 6.450 33.770 1.00 39.96 MOTA 3663 OE1 GLN 680 52.818 5.762 33.993 1.00 39.53 ATOM 3664 NE2 GLN 680 54.990 5.919 33.464 1.00 32.85 MOTA 3665 GLN 680 C 53.070 8.676 30.103 1.00 39.20 MOTA 3666 GLN 680 7.933 0 52.194 29.656 1.00 39.29 MOTA 3667 N SER 681 53.368 9.843 29.531 1.00 38.01 ATOM 3668 CA SER 681 52.656 10.264 28.325 1.00 39.27 MOTA 3669 CB SER 681 52.979 11.712 27.968 1.00 40.93 MOTA 3670 OG SER 681 54.366 11.936 27.943 1.00 39.70 **ATOM** 3671 С SER 681 53.090 9.309 27.208 1.00 39.93 MOTA 3672 0 SER 681 52.285 8.953 26.335 1.00 40.46 MOTA 3673 N ASP 682 54.356 8.881 27.269 1.00 37.28 MOTA 3674 ASP CA 682 54.920 7.921 26.315 1.00 35.38 MOTA 3675 CB ASP 682 56.411 7.673 26.586 1.00 33.58 ATOM 3676 CG ASP 682 57.332 8.520 25.717 1.00 33.16 ATOM 3677 OD1 ASP 8.283 682 58.545 25.828 1.00 31.76 **ATOM** 3678 OD2 ASP 682 56.886 9.391 24.936 1.00 30.06 MOTA 3679 C · ASP 682 54.178 6.599 26.463 1.00 34.70 MOTA 3680 0 ASP 682 5.868 25.488 54.012 1.00 35.67 MOTA 3681 N VAL 683 53.758 6.296 27.691 1.00 34.44 MOTA 3682 CA VAL 683 5.072 1.00 35.14 53.011 27.987 MOTA 3683 CBVAL 4.852 683 52.895 29.544 1.00 35.48 MOTA 3684 CG1 VAL 683 3.900 51.752 29.890 1.00 34.95 ATOM CG2 VAL 683 3685 54.202 4.282 30.080 1.00 28.77 MOTA 3686 C VAL 683 51.638 5.091 27.279 1.00 32.81

ATO	M 36	87	0 v	AL 683	F-1			
ATO	M 36	88		RP 684	51.17		0 26.801	1.00 31.24
ATO		89		RP 684	51.01	-	1 27.187	1.00 30.88
ATO					49.73		26.502	1.00 31.79
ATO			CG TE		49.18	-		1.00 34.88
ATO			CD2 TF	_	47.97	_		1.00 37.61
ATO		93	CE2 TR		46.63		26.305	
ATO					45.85		25.184	1.00 38.42
ATON			CE3 TR CD1 TR	_	46.02			
ATON				-	47.93		24.476	1.00 36.48
ATON			NE1 TR		46.66		24.085	1.00 38.70
ATOM			CZ2 TR		44.48		25.290	1.00 37.82
ATOM			CZ3 TR		44.668	8.644		1.00 38.19
ATOM			CH2 TR	_	43.918	8.980		1.00 37.68
ATOM	_	-			49.947		25.020	1.00 37.68
ATOM		_			49.214		24.430	1.00 31.09
ATOM		_			50.977		24.444	1 00 32.25
ATOM			A SEI		51.345	6.536	23.052	1.00 28.90
	•	_	B SEI		52.620		22.748	1.00 27.10
MOTA			G SEF		52.459		22.974	1.00 23.88
ATOM				685	51.567		22.786	1.00 25.82
MOTA	•	_		685	51.172		21.746	1.00 27.85
ATOM	370		PHE	686	52.178		23.741	1.00 28.89
ATOM	370		A PHE	686	52.410	2.893	23.622	1.00 28.84
ATOM	371			686	53.255	2.403	24.800	1.00 27.86
ATOM	371:				53.498	0.914	24.800	1.00 28.14
ATOM	3712		O1 PHE		54.256	0.313		1.00 28.41
ATOM	3713		D2 PHE		52.949	0.109	23.802	1.00 27.54
ATOM	3714	CE	El PHE	686	54.465	-1.057	25.796	1.00 29.15
ATOM	3715		2 PHE	686	53.151	-1.268	23.792	1.00 24.25
ATOM	3716		PHE	686	53.912	-1.850	25.790	1.00 27.86
MOTA	3717	С	PHE	686	51.072	2.122	24.782	1.00 26.09
ATOM	3718	_	PHE	686	50.960	1.109	23.566	1.00 30.99
ATOM	3719	N	GLY	687	50.051	2.603	22.873	1.00 29.21
ATOM	3720	CA	GLY	687	48.758	1.939		1.00 30.57
ATOM	3721	C	${ t GLY}$	687	48.202			1.00 31.78
ATOM	3722	0	\mathtt{GLY}	687	47.687	_		1.00 32.51
ATOM	3723	N	VAL	688	48.292		22.373	1.00 31.25
ATOM	3724	CA	VAL	688	47.825			1.00 32.58
ATOM	3725	CB	VAL	688	47.804			1.00 30.66
ATOM	3726	CG:	L VAL	688	47.231			1.00 28.55
MOTA	3727	CG2	Z VAL	688	46.944			1.00 27.25
ATOM	3728	C	VAL	688	48.684		21.320	1.00 27.12
ATOM	3729	0	VAL	688	48.160			00 29.96
MOTA	3730	N	LEU	689	49.973		18.974 j	00 30.83
ATOM	3731	CA	LEU	689	50.893			00 30.02
ATOM	3732	CB	LEU	689				.00 30.48
ATOM	3733	CG	LEU	689	52.359			.00 28.13
ATOM	3734		LEU	689	53.466		L8.995 <u>1</u>	.00 26.34
ATOM	3735		LEU	689	54.790		19.174 1	.00 25.54
ATOM	3736	C	LEU	689		-0.505 1		.00 24.99
MOTA	3737	0	LEU				.9.567 1	.00 30.54
ATOM	3738	N	LEU	689	.		8.602 1	.00 27.86
				690	50.013	-0.468 2		.00 33.73
								. =



MOTA	3739	CA	LEU	690	49.553	-1.830	21.029	1.00 32.47
MOTA	3740	CB	LEU	690	49.141	-1.982	22.496	1.00 31.82
ATOM	3741	CG	LEU	690	50.136	-2.220	23.634	1.00 29.71
ATOM	3742	CD1	LEU	690	49.396	-2.129	24.956	1.00 31.53
ATOM	3743	CD2	LEU	690	50.771	-3.605	23.483	1.00 31.69
MOTA	3744	C	LEU	690	48.335	-2.101	20.136	1.00 33.01
MOTA	3745	0	LEU	690	48.223	-3.168	19.521	1.00 32.68
ATOM	3746	N	TRP	691	47.423	-1.131	20.089	1.00 32.37
MOTA	3747	CA	TRP	691	46.230	-1.215	19.256	1.00 32.11
MOTA	3748	СВ	TRP	691	45.424	0.083	19.373	1.00 33.19
MOTA	3749	CG	TRP	691	44.086	0.055	18.678	1.00 33.95
MOTA	3750	CD2	TRP	691	43.812	0.469	17.337	1.00 30.48
ATOM	3751	CE2	TRP	691	42.434	0.294	17.118	1.00 32.75
MOTA	3752	CE3	TRP	691	44.599	0.989	16.301	1.00 29.47
ATOM	3753	CD1	TRP	691	42.889	-0.352	19.199	1.00 34.34
ATOM	3754	NE1	TRP	691	41.894	-0.211	18.272	1.00 36.53
MOTA	3755	CZ2	TRP	691	41.831	0.601	15.900	1.00 30.85
MOTA	3756	CZ3	TRP	691	44.003	1.289	15.100	1.00 30.51
MOTA	3757	CH2	TRP	691	42.630	1.104	1.4.907	1.00 30.29
ATOM	3758	С	TRP	691	46.661	-1.421	17.805	1.00 31.49
ATOM	3759	0	TRP	691	46.062	-2.221	17.092	1.00 31.20
ATOM	3760	N	GLU	692	47.669	-0.656	17.374	1.00 32.90
ATOM	3761	CA	GLU	692	48.207	-0.734	16.019	1.00 29.78
ATOM	3762	CB	GLU	692	49.383	0.233	15.809	1.00 25.56
ATOM	3763	CG	GLU	692	49.009	1.696	15.713	1.00 25.85
ATOM	3764	CD	GLU	692	50.195	2.570	15.363	1.00 27.76
ATOM	3765	OE1	GLU	692	51.001	2.850	16.265	1.00 29.52
ATOM	3766	OE2	GLU	692	50.333	2.981	14.191	1.00 26.84
MOTA	3767	C	GLU	692	48.682	-2.136	15.696	1.00 31.08
MOTA	3768	0	GLU	692	48.545	-2.593	14.553	1.00 32.57
MOTA	3769	N	ILE	693	49.262	-2.804	16.689	1.00 31.81
ATOM	3770	CA	ILE	693	49.774	-4.163	16.506	1.00 31.87
MOTA	3771	CB	ILE	693	50.666	-4.614	17.699	1.00 33.50
ATOM	3772	CG2	ILE	693	51.140	-6.075	17.513	1.00 33.06
ATOM	3773	CG1	ILE	693	51.879	-3.703	17.827	1.00 34.04
MOTA	3774	CD1	ILE	693	52.744	-4.008	19.025	1.00 31.52
MOTA	3775	C	ILE	693	48.643	-5.177	16.335	1.00 31.43
MOTA	3776	0	ILE	693	48.633	-5.982	15.403	1.00 29.55
MOTA	3777	N	PHE	694	47.654	-5.087	17.207	1.00 33.58
ATOM	3778	CA	PHE	694	46.550	-6.027	17.178	1.00 36.72
MOTA	3779	CB	PHE	694	45.980	-6.179	18.589	1.00 36.27
MOTA	3780	CG	PHE	694	46.988	-6.724	19.547	1.00 34.29
ATOM	3781	CD1	PHE	694	47.500	-5.949	20.581	1.00 34.95
MOTA	3782	CD2	PHE	694	47.560	-7.972	19.297	1.00 31.60
MOTA	3783		PHE	694	48.576	-6.413	21.344	1.00 35.73
MOTA	3784	CE2	PHE	694	48.633	-8.443	20.049	1.00 31.12
MOTA	3785	CZ	PHE	694	49.149	-7.661	21.066	1.00 33.97
ATOM	3786	С	PHE	694	45.516	-5.870	16.065	1.00 37.70
MOTA	3787	0	PHE	694	44.684	-6.756	15.839	1.00 37.99
MOTA	3788	N	THR	695	45.604	-4.745	15.355	1.00 36.11
MOTA	3789	CA	THR	695	44.747	-4.485	14.205	1.00 31.23
MOTA	3790	CB	THR	695	44.107	-3.081	14.236	1.00 30.49



ATOM		1 0	Gl THR	695	45.133	-2.079	9 14.134	1 1.00 30.14
ATOM			G2 THR	695	43.329	-2.888		
ATOM		3 C	THR	695	45.612	-4.619		
ATOM	379	4 0	THR	695	45.163	-4.325		
ATOM	379	5 N	LEU	696	46.859	-5.051		
MOTA	3796	5 CZ	A LEU	696	47.826	-5.259		
MOTA	3797	7 CE	3 LEU	696	47.456	-6.495		
ATOM	3798		LEU	696	47.281	-7.848		
ATOM	3799	CI	01 LEU	696	47.142	-8.941		
ATOM	3800	CI	2 LEU	696	48.468	-8.138		
ATOM	3801	. C	LEU	696	48.101	-4.076	11.160	
ATOM	3802	0	LEU	696	48.210	-4.235	9.946	20.70
ATOM	3803	N	\mathtt{GLY}	697	48.314	-2.900	11.745	
ATOM	3804	CA	GLY	697	48.609	-1.705	10.960	
ATOM	3805	C	GLY	697	47.432	-0.763	10.817	1.00 31.69
ATOM	3806	0	\mathtt{GLY}	697	47.398	0.099	9.941	1.00 32.24
ATOM	3807	N	\mathtt{GLY}	698	46.455	-0.922	11.700	1.00 31.81 1.00 32.63
ATOM	3808	CA	GLY	698	45.277	-0.081	11.643	1.00 32.63
ATOM	3809		GLY	698	45.504	1.411	11.820	1.00 31.93
ATOM	3810	0	GLY	698	46.454	1.858	12.449	1.00 28.95
ATOM	3811	N	SER	699	44.569	2.174	11.282	1.00 26.03
ATOM	3812	CA	SER	699	44.608	3.618	11.352	1.00 30.03
ATOM	3813	CB	SER	699	44.095	4.219	10.046	1.00 30.32
ATOM	3814	OG	SER	699	44.047	5.639	10.095	1.00 31.24
ATOM	3815	C	SER	699	43.695	4.024	12.492	1.00 33.61
MOTA	3816	0	SER	699	42.490	3.755	12.450	1.00 30.45
MOTA	3817	N	PRO	700	44.259	4.591	13.573	1.00 29.11
ATOM	3818	CD	PRO	700	45.693	4.761	13.881	1.00 32.27
ATOM	3819	CA	PRO	700	43.408	5.007	14.695	1.00 29.81
ATOM	3820	CB	PRO	700	44.428	5.358	15.777	1.00 31.34
ATOM	3821	CG	PRO	700	45.662	5.745	14.989	1.00 29.66
ATOM	3822	C	PRO	700	42.574	6.208	14.279	1.00 29.65
ATOM	3823	0	PRO	700	43.032	7.062	13.527	1.00 30.44
ATOM	3824	N	TYR	701	41.306	6.190	14.660	1.00 30.37
ATOM	3825	CA	TYR	701	40.359	7.272	14.367	1.00 30.01
ATOM	3826	CB	TYR	701	40.655	8.474	15.269	1.00 35.19
ATOM	3827	CG	TYR	701	40.452	8.215	16.749	1.00 39.32
ATOM	3828	CD1		701	41.452	8.518	17.675	1.00 43.08
ATOM	3829		TYR	701	41.258	8.305	19.041	1.00 46.20
ATOM	3830		TYR	701	39.256	7.688	17.229	1.00 40.66
ATOM	3831	CE2	TYR	701	39.060	7.469	18.584	1.00 43.51
MOTA	3832	cz	TYR	701	40.056	7.782	19.485	1.00 45.75
ATOM	3833	OH	TYR	701	39.847	7.592	20.837	1.00 43.75
ATOM	3834	C	TYR	701	40.273	7.722	12.909	1.00 30.92
MOTA	3835	0	TYR	701	40.393	8.904	12.611	
ATOM	3836	N .	PRO	702	40.015	6.777	11.986	1.00 28.53 1.00 28.69
ATOM	3837	CD	PRO	702	39.761	5.346	12.186	
ATOM	3838	CA	PRO	702	39.920	7.145	10.569	1.00 26.94
ATOM	3839	CB	PRO	702	39.709	5.800	9.882	1.00 27.55
ATOM	3840	CG	PRO	702	39.054			1.00 27.91
ATOM	3841	С	PRO	702	38.790	_		1.00 29.04
ATOM	3842	0	PRO	702	37.631			1.00 29.20
						,	10.617	1.00 32.39

MOTA	3843 .	N	GLY	703	39.148	9.213	9.591	1.00	28.34
MOTA	3844	CA	GLY	703	38.191	10.236	9.226	1.00	25.97
ATOM	3845	C	GLY	703	37.960	11.289	10.297	1.00	28.00
ATOM	3846	0	GLY	703	37.175	12.213	10.079	1.00	26.40
MOTA	3847	N	VAL	704	38.621	11.139	11.448	1.00	29.54
MOTA	3848	CA	VAL	704	38.480	12.061	12.576	1.00	30.61
MOTA	3849	CB	VAL	704	38.606	11.324	13.944	1.00	32.54
MOTA	3850	CG1	VAL	704	38.577	12.324	15.111	1.00	31.95
MOTA	3851	CG2	VAL	704	37.482	10.311	14.103	1.00	34.62
ATOM	3852	C	VAL	704	39.490	13.210	12.557	1.00	31.37
MOTA	3853	0	VAL	704	40.683	13.001	12.757	1.00	31.73
MOTA	3854	N	PRO	705	39.030	14.430	12.281	1.00	32.70
MOTA	3855	CD	PRO-	705	37.669	14.770	11.819	1.00	33.75
MOTA	3856	CA	PRO	705	39.910	15.599	12.243	1.00	31.90
ATOM	3857	CB	PRO	705	39.065	16.641	11.518	1.00	32.66
MOTA	3858	CG	PRO	705	37.674	16.273	11.906	1.00	35.32
ATOM	3859	C	PRO	705	40.331	16.053	13.635	1.00	31.85
ATOM	3860	0	PRO	705	39.709	15.686	14.634	1.00	31.50
MOTA	3861	N	VAL	706	41.372	16.879	13.676	1.00	32.32
ATOM	3862	CA	VAL	706	41.945	17.389	14.925	1.00	36.88
ATOM	3863	CB	VAL	706	42.991	18.505	14.664	1.00	39.77
ATOM	3864	CG1	VAL	706	43.657	18.907	15.974	1.00	39.17
ATOM	3865	CG2	VAL	706	44.035	18.057	13.618	1.00	38.70
MOTA	3866	C	VAL	706	40.938	17.923	15.953	1.00	37.80
ATOM	3867	0	VAL	706	40.994	17.581	17.140	1.00	37.45
MOTA	3868	N	GLU	707	39.991	18.724	15.483	1.00	38.19
MOTA	3869	CA	GLU	707	39.009	19.308	16.370	1.00	37.31
MOTA	3870	CB	GLU	707	38.208	20.361	15.619	1.00	37.46
ATOM	3871	C	GLU	707	38.084	18.264	16.994	1.00	39.56
MOTA	3872	0	GLU	707	37.739	18.344	18.177	1.00	41.39
ATOM	3873	N	GLU	708	37.724	17.260	16.206	1.00	39.99
ATOM	3874	CA	GLU	708	36.840	16.212	16.684	1.00	40.08
MOTA	3875	CB	GLU	708	36.334	15.377	15.515	1.00	43.96
MOTA	3876	CG	GLU	708	35.505	16.163	14.496	1.00	46.61
MOTA	3877	CD	GLU	708	34.288	16.851	15.099	1.00	52.77
MOTA	3878	OE1	GLU	708	33.659	16.305	16.040	1.00	52.52
MOTA	3879	OE2	GLU	708	33.954	17.955	14.604	1.00	57.04
MOTA	3880	C	GLU	708	37.551	15.337	17.704	1.00	39.89
MOTA	3881	0	GLU	708	36.944	14.900	18.684	1.00	39.47
MOTA	3882	N	LEU	709	38.838	15.086	17.471	1.00	38.99
MOTA	3883	CA	LEU	709	39.638	14.277	18.393	1.00	37.51
ATOM	3884	CB	LEU	709	41.079	14.120	17.892	1.00	34.15
ATOM	3885	CG	LEU	709	42.061	13.338	18.787	1.00	30.94
ATOM	3886	CD1	LEU	709	41.861	11.834	18.689	1.00	28.48
MOTA	3887	CD2	LEU	709	43.459	13.712	18.395	1.00	29.02
MOTA	3888	C	LEU	709	39.644	14.961	19.751	1.00	38.18
ATOM	3889	0	LEU	709	39.460	14.313	20.787	1.00	38.08
ATOM	3890	N	PHE	710	39.833	16.276	19.749	1.00	39.68
MOTA	3891	CA	PHE	710	39.845	17.021	21.001	1.00	43.27
ATOM	3892	CB	PHE	710	40.024	18.524	20.747		43.66
MOTA	3893	CG	PHE	710	41.376	18.888	20.225	1.00	46.36
MOTA	3894	CD1	PHE	710	42.459	18.024	20.403	1.00	48.33

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ATOM	3895	5 CI	D2 PHE	710	41.579	20.084	19.544	1.00 47.76
ATOM	3896	CE CE	El PHE	710	43.723	18.343		
ATOM	3897	7 CE		710	42.839			
ATOM	3898	CZ	PHE	710	43.916			
ATOM	3899) C	PHE	710	38.558			
MOTA	3900	0	PHE	710	38.587			
ATOM	3901	. N	LYS	711	37.445			
ATOM	3902	CA	LYS	711	36.146			
ATOM	3903	CB	LYS	711	35.031	16.870		
ATOM	3904	CG	LYS	711	33.645	16.758		
ATOM	3905		LYS	711	32.556	17.224		
ATOM	3906	CE	LYS	711	31.197	16.809		
ATOM	3907	NZ	LYS	711	30.101	17.220		1.00 63.51
ATOM	3908	C	LYS	711	36.052	15.078	22.120	1.00 42.15
ATOM	3909	0	LYS	711	35.635	14.827	23.250	1.00 40.85
ATOM	3910	N	LEU	712	36.467	14.125	21.294	
MOTA	3911	CA	LEU	712	36.432	12.719	21.691	1.00 40.98 1.00 42.26
ATOM	3912	CB	LEU	712	37.012	11.814	20.597	
MOTA	3913	CG	LEU	712	36.159	11.449	19.381	
MOTA	3914	CD:	1 LEU	712	36.899	10.440	18.504	
ATOM	3915	CD:	2LEU	7.12		10.868		
ATOM	3916	C	LEU	712	37.232	12.513	22.974	1.00 36.48
MOTA	3917	0	LEU	712	36.796	11.785	23.875	1.00 44.10
ATOM	3918	N	LEU	713	38.407	13.141	23.038	1.00 43.57
MOTA	3919	CA	LEU	713	39.271	13.034	24.207	1.00 43.57
MOTA	3920	CB	LEU	713	40.619	13.726	23.958	1.00 43.87
ATOM	3921	CG	LEU	713	41.569	13.004	22.989	1.00 42.24
ATOM	3922	CD1	LEU	713	42.856	13.796	22.817	1.00 30.86
ATOM	3923	CD2	LEU	713	41.873	11.591	23.519	1.00 34.27
MOTA	3924	C	LEU	713	38.589	13.594	25.450	1.00 34.27
ATOM	3925	0	LEU	713	38.548	12.919	26.472	1.00 46.04
ATOM	3926	N	LYS	714	38.002	14.785	25.344	1.00 44.72
MOTA	3927	CA	LYS	714	37.304	15.394	26.471	1.00 44.34
ATOM	3928	CB	LYS	714	36.818	16.799	26.114	1.00 43.76
ATOM	3929	CG	LYS	714	37.955	17.761	25.926	1.00 46.37
ATOM	3930	CD	LYS	714	37.497	19.174	25.628	1.00 52.22
ATOM	3931	CE	LYS	714	38.701	20.044	25.235	1.00 57.37
MOTA	3932	NZ	LYS	714	39.792	20.059	26.279	1.00 58.02
ATOM	3933	C	LYS	714	36.142	14.534	26.972	1.00 44.17
ATOM	3934	0	LYS	714	35.861	14.499	28.167	1.00 45.14
ATOM	3935	N	GLU	715	35.498	13.809	26.068	1.00 43.86
ATOM	3936	CA	GLU	715	34.392	12.935	26.430	1.00 42.94
ATOM	3937	CB	GLU	715	33.518	12.652	25.195	1.00 46.57
ATOM	3938	CG	GLU	715	32.930	13.897	24.532	1.00 51.37
ATOM	3939	CD	GLU	715	32.032	13.571	23.338	1.00 54.24
MOTA	3940	OE1	GLU	715	32.215	12.503	22.704	1.00 54.19
ATOM	3941	OE2	GLU	715	31.139	14.392	23.033	1.00 55.01
ATOM	3942	С	GLU	715	34.878	11.607	27.036	1.00 41.36
MOTA	3943	0	GLU	715		10.730	27.348	1.00 41.36
ATOM	3944	N	GLY	716	36.184	11.452	27.182	1.00 38.24
MOTA	3945	CA	GLY	716		10.225	27.102	1.00 41.41
MOTA	3946	C	GLY	716	36.602	9.034	26.799	
							-0.733	1.00 42.65

MOTA	3947	0	GLY	716	36.661	7.874	27.225	1.00	41.41
MOTA	3948	N	HIS	717	36.439	9.321	25.513	1.00	44.56
MOTA	3949	CA	HIS	717	36.286	8.291	24.502	1.00	45.91
ATOM	3950	CB	HIS	717	35.935	8.926	23.153	1.00	46.65
MOTA	3951	CG	HIS	717	35.860	7.946	22.024	1.00	50.03
MOTA	3952	CD2	HIS	717	34.842	7.171	21.581	1.00	49.92
ATOM	3953	ND1	HIS	717	36.946	7.634	21.235	1.00	51.38
ATOM	3954	CE1	HIS	717	36.604	6.708	20.360	1.00	50.10
MOTA	3955	NE2	HIS	717	35.335	6.408	20.550	1.00	49.34
ATOM	3956	C	HIS	717	37.535	7.434	24.354	1.00	47.68
MOTA	3957	0	HIS	717	38.649	7.949	24.287	1.00	49.77
MOTA	3958	N	ARG	718	37.328	6.118	24.283	1.00	48.18
ATOM	3959	CA	ARG	718	38.403	5.148	24.116	1.00	46.95
MOTA	3960	СВ	ARG	718	38.571	4.307	25.385	1.00	45.75
MOTA	3961	CG	ARG	718	38.945	5.125	26.618	1.00	47.15
ATOM	3962	CD	ARG	718	40.273	5.852	26.420	1.00	46.61
ATOM	3963	NE	ARG	718	40.722	6.579	27.608	1.00	45.57
MOTA	3964	CZ	ARG	718	40.601	7.896	27.779	1.00	45.48
MOTA	3965	NH1	ARG	718	40.033	8.644	26.845	1.00	44.14
ATOM	3966	NH2	ARG	718	41.122	8.480	28.854	1.00	43.32
ATOM	3967	C	ARG	718	38.109	4.250	22.912	1.00	47.56
ATOM	3968	0	ARG	718	36.946	3.991	22.589	1.00	48.37
ATOM	3969	N	MET	719	39.149	3.873	22.181	1.00	47.33
MOTA	3970	CA	MET	719	38.984	3.021	21.013	1.00	47.90
ATOM	3971	CB	MET	719	40.282	2.939	20.198	1.00	47.21
ATOM	3972	CG	MET	719	40.652	4.245	19.509	1.00	45.79
ATOM	3973	SD	MET	719	42.095	4.104	18.440	1.00	42.81
ATOM	3974	CE	MET	719	43.377	3.970	19.604	1.00	43.02
ATOM	3975	C	MET	719	38.519	1.629	21.392	1.00	49.99
ATOM	3976	0	MET	719	38.889	1.102	22.450	1.00	47.98
ATOM	3977	N	ASP	720	37.690	1.050	20.523	1.00	53.40
ATOM	3978	CA	ASP	720	37.135	-0.288	20.722	1.00	53.19
ATOM	3979	CB	ASP	720	36.089	-0.638	19.647	1.00	56.95
ATOM	3980	CG	ASP	720	34.916	0.333	19.605	1.00	61.65
MOTA	3981	OD1	ASP	720	34.908	1.331	20.356	1.00	68.60
MOTA	3982	OD2	ASP	720	33.996	0.095	18.792	1.00	61.19
MOTA	3983	С	ASP	720	38.208	-1.372	20.713	1.00	51.12
MOTA	3984	0	ASP	720	39.263	-1.229	20.081	1.00	50.71
MOTA	3985	N	LYS	721	37.926	-2.453	21.432	1.00	48.85
ATOM	3986	CA	LYS	721	38.833	-3.576	21.509	1.00	47.92
ATOM	3987	CB	LYS	721	38.335	-4.560	22.562	1.00	47.79
ATOM	3988	CG	LYS	721	39.024	-5.901	22.521	1.00	51.08
ATOM	3989	CD	LYS	721	38.493	-6.810	23.597	1.00	53.21
MOTA	3990	CE	LYS	721	38.484	-8.255	23.141	1.00	54.60
ATOM	3991	NZ	LYS	721	38.158	-9.176	24.268	1.00	61.37
ATOM	3992	С	LYS	721	38.861	-4.261	20.155		49.01
MOTA	3993	0	LYS	721	37.822	-4.688	19.653		52.79
ATOM	3994	N	PRO	722	40.053	-4.366	19.541		48.92
ATOM	3995	CD	PRO	722	41.356	-3.839	19.972	1.00	51.11
MOTA	3996	CA	PRO	722	40.167	-5.011	18.233		46.01
ATOM	3997	CB	PRO	722	41.663	-4.904	17.918	1.00	45.64
ATOM	3998	CG	PRO	722	42.090	-3.690	18.646		47.86

ATO			PRO	722	39.745 -6.466 18.303 1.00 43.57
ATO			PRO	722	30 710
ATO			SEF	723	30 360 7 35
ATON)2 C	A SER	723	20 001 0 001
ATOM	400	3 C	B SER	723	20 250
ATOM	400	4 0	G SER		20 110
ATOM	1 400	5 C	SER		40 220
ATOM	1 400	6 0			41 200
ATOM	400	7 N			10 105
ATOM	400	8 C.			40.405 -10.275 17.683 1.00 45.99
ATOM	400				41.651 -11.034 17.800 1.00 49.22
ATOM	401				42.342 -11.215 16.453 1.00 52.35
ATOM	4013		O1 ASN	724	41.768 -12.357 15.668 1.00 58.07
ATOM			D2 ASN	724	41.821 -13.506 16.103 1.00 62.42
ATOM			ASN	724	41.186 -12.054 14.513 1.00 62.13
ATOM			ASN		42.558 -10.323 18.787 1.00 49.77
ATOM		-	CYS	724 725	43.698 -9.982 18.494 1.00 51.48
ATOM	4016			725	41.995 -10.054 19.954 1.00 50.34
ATOM	4017		-	725	42.698 -9.398 21.028 1.00 49.83
ATOM	4018			725	42.623 -7.878 20.868 1.00 47.11
ATOM			CYS CYS	725	43.485 -6.992 22.169 1.00 38 55
ATOM	4020				42.001 - 9.861 - 22.299 - 1.00.50.11
ATOM	4021		CYS	725	40.772 -9.852 22.383 1.00 50 63
ATOM	4021		THR	726	42.788 -10.350 23.244 1.00 50 37
ATOM	4023			726	42.261 ~10.843 24.497 1.00 51 05
ATOM	4023			726	43.341 -11.663 25.234 1.00 53.50
ATOM	4024			726	44.292 -10.780 25.829 1.00 57 56
ATOM	4025		2 THR	726	44.074 -12.554 24.241 1.00 52.55
ATOM		C	THR	726	41.843 -9.665 25.354 1.00 52.18
ATOM	4027 4028	0	THR	726	42.403 -8.574 25.219 1.00 55 14
ATOM		N	ASN	727	40.868 -9.860 26.237 1.00 52.55
ATOM	4029	CA	ASN	727	40.401 -8.781 27.114 1.00 53 17
ATOM	4030	CB	ASN	727	39.246 -9.265 27.992 1.00 60.65
ATOM	4031	CG	ASN	727	39.584 -10.545 28.751 1.00 68.99
ATOM	4032		ASN	727	40.704 -10.718 29.243 1.00 73.66
ATOM	4033		ASN	727	38.629 -11.454 28.825 1.00 74.66
	4034	C	ASN	727	41.537 -8.254 27.976 1.00 50.79
ATOM ATOM	4035	0	ASN	727	41.513 -7.107 28.414 1.00 48.17
ATOM	4036	N	GLU	728	42.527 -9.111 28.215 1.00 50.18
	4037	CA	GLU	728	43.693 -8.764 29.020 1.00 49.68
ATOM	4038	CB	GLU	728	44.544 -10.011 29.289 1.00 50.61
ATOM	4039	CG	GLU	728	45.801 -9.758 30.120 1.00 55.44
ATOM	4040	CD	GLU	728	46.509 -11.045 30.542 1.00 56.45
MOTA	4041		GLU	728	46.737 -11.930 29.685 1.00 53.73
ATOM	4042	OE2	GLU -	728	46 065 11 77
ATOM	4043	C	GLU	728	44 500
ATOM	4044	0	GLU	728	14 750
ATOM	4045	N	LEU	729	14 060
ATOM	4046	CA	LEU	729	45 642
ATOM	4047	CB	LEU	729	45 050
ATOM	4048	CG	LEU	729	17 004 5 555
ATOM	4049	CD1	LEU	729	16 060
ATOM	4050	CD2	LEU	729	10 11 11 11 11 11 11 11 11 11 11 11 11 1
					48.404 -8.320 25.139 1.00 33.63

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MOTA 4051 C LEU 729 44.909 -5.817 25.985 1.00 40.58 45.524 -4.760 MOTA 4052 0 LEU 729 25.929 1.00 40.10 4053 TYR 730 1.00 39.32 MOTA N 43.591 -5.886 25.917 -4.694 4054 CA TYR 730 42.807 25.720 1.00 41.49 MOTA 41.384 -5.052 25.302 1.00 39.70 4055 CB TYR 730 ATOM 4056 CG TYR 730 40.507 -3.846 25.099 1.00 39.53 ATOM 4057 CD1 TYR 730 40.828 -2.879 ATOM 24.142 1.00 35.10 4058 CE1 TYR 730 MOTA 40.019 -1.758 23.958 1.00 36.33 CD2 TYR **MOTA** 4059 730 39.352 -3.661 25.874 1.00 38.44 -2.541 MOTA 4060 CE2 TYR 730 38.537 25.696 1.00 37.68 MOTA 4061 CZTYR 730 38.876 -1.601 24.730 1.00 36.85 4062 OH TYR 730 38.041 -0.541 24.489 ATOM 1.00 40.58 4063 C TYR 730 42.814 -3.849 26.993 1.00 43.50 ATOM ATOM 4064 0 TYR 730 42.880 -2.621 26.931 1.00 44.45 ATOM 4065 N MET 731 42.753 -4.492 28.151 1.00 46.53 ATOM 4066 CA MET 731 42.782 -3.744 29.406 1.00 48.67 ATOM 4067 CB MET 731 42.488 -4.668 30.590 1.00 54.90 ATOM 4068 MET 41.072 -5.229 30.577 CG 731 1.00 63.75 MET ATOM 4069 SD 731 39.766 -3.998 30.763 1.00 69.82 4070 CE MET 32.581 ATOM 731 39.849 -3.788 1.00 68.20 4071 C **ATOM** MET 731 44.148 -3.087 29.551 1.00 45.73 4072 0 MET 30.160 **ATOM** 731 44.273 -2.024 1.00 42.09 -3.728 ATOM 4073 N MET 732 28.986 1.00 43.47 45.168 ATOM 4074 CA MET 732 46.519 -3.189 29.024 1.00 43.85 ATOM 4075 CB MET 732 47.515 -4.154 28.365 1.00 40.67 ATOM 4076 CG MET 732 48.966 -3.646 28.369 1.00 39.96 ATOM 4077 SD MET 732 50.252 -4.870 27.887 1.00 35.34 4078 ATOM CE MET 732 50.523 -5.667 29.390 1.00 35.15 46.460 -1.860 28.275 1.00 43.91 4079 .ATOM С MET 732 46.924 -0.835 28.782 MOTA 4080 0 MET 732 1.00 47.29 MOTA 4081 N MET 733 45.798 -1.860 27.120 1.00 42.51 ATOM 4082 CA MET 733 45.639 -0.652 26.319 1.00 39.85 ATOM 4083 CB MET 733 44.888 -0.932 25.013 1.00 38.08 ATOM 4084 CG MET 733 45.614 -1.805 23.991 1.00 37.14 ATOM 4085 SD MET 733 -2.170 22.578 1.00 37.32 44.509 4086 CE -3.684 MOTA MET 733 45.198 21.929 1.00 28.98 **ATOM** 4087 MET C 733 44.838 0.363 27.123 1.00 41.12 ATOM 4088 MET 45.228 1.532 27.213 1.00 44.38 0 733 MOTA 4089 ARG 43.737 -0.084 27.731 1.00 40.28 N 734 ATOM 4090 CA ARG 734 42.893 0.813 28.516 1.00 40.23 0.095 29.007 1.00 39.95 ATOM 4091 734 CB ARG 41.632 40.723 -0.384 27.894 1.00 36.41 MOTA 4092 CG ARG 734 0.741 26.995 1.00 39.31 MOTA 4093 CD ARG 734 40.323 MOTA 4094 NE ARG 734 39.510 1.733 27.682 1.00 48.97 MOTA 4095 CZ ARG 734 38.182 1.681 27.774 1.00 53.99 MOTA 4096 NH1 ARG 734 37.503 0.681 27.222 1.00 56.64 **ATOM** 4097 NH2 ARG 734 37.526 2.633 28.416 1.00 56.79 4098 29.675 MOTA C ARG 734 43.694 1.387 1.00 39.38 4099 MOTA 0 ARG 734 43.538 2.564 30.010 1.00 41.82 MOTA 4100 N ASP 0.572 30.244 1.00 37.67 735 44.583 MOTA 4101 CA ASP 735 45.465 1.000 31.339 1.00 39.58 46.392 -0.137 31.773 1.00 42.90 MOTA 4102 CB ASP 735

ATO			CG AS			45.69	90 -1.1	75 32.60	04 7 00 47 70
ATO			OD1 AS			46.11			
ATO			OD2 AS	P 735		44.73	33 -0.8		
ATO			C AS:	P 735		46.33			
ATO		07 () AS	P 735		46.44			
ATO			V CYS	736		46.99			
ATON		9 (CA CYS	736		47.85			
ATOM		0 0	B CYS	736		48.49			
MOTA		.1 \$	G CYS			49.63			
ATOM		.2 C	CYS	736		47.05			
ATOM	411	.3 C	CYS			47.59			
ATOM		4 N	TRP			45.74			
ATOM	411	5 C	A TRP			44.88			
ATOM	411	6 C	B TRP			43.89			
ATOM	411	7 C	G TRP				_		
ATOM	411	8 C	D2 TRP			44.53	_		
ATOM	411		E2 TRP			43.976			
MOTA	412		E3 TRP	737		44.932			
ATOM	412		Ol TRP	737		42.763			
ATOM	4122		E1 TRP	737		45.766			1.00 39.14
MOTA	412		22 TRP			46.011			1.00 37.93
MOTA	4124			737		44.708		_	
ATOM	4125			737		42.549			
ATOM	4126		TRP	737		43.518			
ATOM	4127		TRP	737		44.159			
ATOM	4128	_	HIS			43.163			
ATOM	4129			738		44.685			1.00 43.61
ATOM	4130			738		44.059		31.941	1.00 44.35
ATOM	4131			738		44.698			1.00 45.31
ATOM	4132		2 HIS	738		43.970	5.922	34.446	1.00 50.87
ATOM	4133		1 HIS	.738		43.685	7.111	35.026	1.00 49.13
ATOM	4134		1 HIS	738		43.401	4.961	35.252	1.00 52,48
ATOM	4135		2 HIS	738		42.798	5.541	36.275	1.00 55.70
ATOM	4136	C	HIS	738		42.955	6.848	36.159	1.00 51.42
ATOM	4137	0		738		44.202	7.714	31.969	1.00 44.15
ATOM	4138	Ŋ	HIS	738		45.294	8.223	31.787	1.00 43.14
ATOM	4139		ALA	739		43.115	8.428	32.272	1.00 45.42
ATOM	4140	CA	ALA	739		43.141	9.895	32.318	1.00 47.29
ATOM	4141	CB C	ALA	739		11.792	10.426	32.752	1.00 49.75
ATOM			ALA	739		4.240	10.454	33.223	
ATOM	4142 4143	0	ALA	739		4.921	11.415	32.868	1.00 49.32
ATOM	4144	N	VAL	740		4.331	9.893	34.425	1.00 50.51
ATOM		CA	VAL	740	4	5.332	10.262	35.424	1.00 51.32
ATOM	4145	CB	VAL	740	4	4.861	9.880	36.842	1.00 52.29
	4146		VAL	740	4	5.905	10.254	37.869	1.00 53.73
ATOM	4147		VAL	740	4	3.551	10.575	37.152	1.00 53.73
ATOM	4148	С	VAL	740	4	6.656	9.535	35.121	1.00 51.06
ATOM	4149	0	VAL	740	4	6.780	8.320	35.348	1.00 50.81
ATOM	4150	N	PRO	741		7.670	10.280	34.657	
ATOM	4151	CD	PRO	741		7.595	11.738	34.454	1.00 50.12
ATOM	4152	CA	PRO	741		9.003	9.775	34.434	1.00 50.19
ATOM	4153	CB	PRO	741		9.790	11.060	34.024	1.00 51.10
MOTA	4154	CG	PRO	741		B.731	11.978	33.492	1.00 50.35
								-J.432	1.00 50.13

ATOM	4155	. C	PRO	741	49.687	8.902	35.340	1.00	52.02
ATOM	4156	0	PRO	741	50.374	7.941	34.998	1.00	50.79
ATOM	4157	N	SER	742	49.482	9.228	36.613	1.00	53.75
MOTA	4158	CA	SER	742	50.079	8.474	37.708	1.00	54.58
MOTA	4159	CB	SER	742	49.921	9.245	39.020	1.00	57.25
ATOM	4160	OG	SER	742	48.572	9.629	39.237	1.00	61.69
ATOM	4161	С	SER	742	49.479	7.077	37.851	1.00	53.33
ATOM	4162	0	SER	742	50.074	6.189	38.464	1.00	52.98
ATOM	4163	N	GLN	743	48.286	6.897	37.305	1.00	52.97
ATOM	4164	CA	GLN	743	47.616	5.613	37.390	1.00	52.15
MOTA	4165	CB	GLN	743	46.108	5.827	37.505	1.00	56.12
MOTA	4166	CG	GLN	743	45.506	5.374	38.838	1.00	60.50
ATOM	4167	CD	GLN	743	46.269	5.887	40.046	1.00	64.45
MOTA	4168	OE1	GLN	743	46.910	5.114	40.752	1.00	65.64
MOTA	4169	NE2	GLN	743	46.199	7.194	40.290	1.00	67.99
ATOM	4170	C	GLN	743	47.963	4.690	36.229	1.00	49.54
ATOM	4171	0	GLN	743	47.629	3.499	36.246	1.00	50.07
ATOM	4172	N	ARG	744	48.605	5.241	35.202	1.00	46.93
MOTA	4173	CA	ARG	744	49.010	4.437	34.044	1.00	44.51
MOTA	4174	СВ	ARG	744	49.478	5.330	32.894	1.00	39.30
ATOM	4175	CG	ARG	744	48.433	6.300	32.360	1.00	32.53
ATOM	4176	CD	ARG	744	48.991	7.178	31.254	1.00	25.50
MOTA	4177	NE	ARG	744	48.034	8.218	30.932	1.00	32.16
ATOM	4178	CZ	ARG	744	48.352	9.454	30.542	1.00	34.35
MOTA	4179	NH1	ARG	744	49.622	9.814	30.400	1.00	30.49
MOTA	4180	NH2	ARG	744	47.382	10.349	30.350	1.00	32.23
MOTA	4181	С	ARG	744	50.153	3.498	34.472	1.00	44.61
MOTA	4182	0	ARG	744	50.833	3.741	35.474	1.00	47.68
MOTA	4183	N	PRO	745	50.319	2.365	33.765	1.00	43.21
ATOM	4184	CD	PRO	745	49.444	1.737	32.763	1.00	42.00
MOTA	4185	CA	PRO	745	51.414	1.470	34.157	1.00	40.11
MOTA	4186	CB	PRO	745	51.004	0.132	33.532	1.00	37.54
ATOM	4187	CG	PRO	745	50.251	0.515	32.335	1.00	36.49
ATOM	4188	C	PRO	745	52.744	1.956	33.612	1.00	39.15
MOTA	4189	0	PRO	745	52.807	2.654	32.602	1.00	40.56
MOTA	4190	N	THR	746	53.812	1.626	34.316	1.00	37.77
MOTA	4191	CA	THR	746	55.135	2.020	33.886	1.00	37.61
MOTA	4192	CB	THR	746	56.113	2.132	35.091	1.00	39.14
MOTA	4193	OG1	THR	746	56.439	0.824	35.600	1.00	35.16
MOTA	4194	CG2	THR	746	55.489	2.990	36.195	1.00	36.82
MOTA	4195	C	THR	746	55.687	1.036	32.852	1.00	36.75
MOTA	4196	0	THR	746	55.228	-0.103	32.772	1.00	32.89
MOTA	4197	N	PHE	747	56.649	1.482	32.043	1.00	36.56
ATOM	4198	CA	PHE	747	57.267	0.599	31.055	1.00	33.79
ATOM	4199	CB	PHE	747	58.305	1.350	30.226	1.00	28.85
MOTA	4200	CG	PHE	747	57.702	2.123	29.103	1.00	30.71
MOTA	4201	CD1	PHE	747	57.060	1.455	28.059	1.00	26.42
MOTA	4202	CD2	PHE	747	57.749	3.510	29.080	1.00	28.73
MOTA	4203	CE1	PHE	747	56.469	2.154	27.025	1.00	26.56
MOTA	4204	CE2	PHE	747	57.150	4.216	28.047	1.00	28.97
ATOM	4205	CZ	PHE	747	56.518	3.535	27.018	1.00	28 95
ATOM	4206	С	PHE	747	57.901	-0.593	31.732	1.00	34.64

ATO	M 420	77 (
ATON			O PHI		58.00		7 31.156	1.00 31.47
ATOM			1 LYS		58.32		9 32.972	1.00 38.86
ATOM			CA LYS	-	58.92	0 -1.480		
ATOM			B LYS		59.52	9 -0.952	35.026	
			G LYS		60.20	0 -2.047		
ATOM			D LYS		60.91	7 -1.515		
ATOM			E LYS	748	61.35			
ATOM			Z LYS	748	62.13			
ATOM			LYS	748	57.81			
ATOM		6 0	LYS	748	58.02			
ATOM		7 N	GLN	749	56.62			
ATOM		8 C.	A GLN	749	55.454			1.00 41.20
ATOM	4219	9 C:	B GLN	749	54.254			1.00 40.49
ATOM	4220	0 C	G GLN	749	54.378			1.00 45.70
ATOM	4221	l Ci	O GLN	749	53.203			1.00 50.61
ATOM	4222	2 01	E1 GLN	749	53.392			1.00 55.26
ATOM	4223		E2 GLN	749	51.988		37.123	1.00 58.00
ATOM	4224		GLN	749			36.665	1.00 59.25
ATOM	4225	5 0	GLN	749	55.049		33.397	1.00 37.42
ATOM	4226		LEU	750	54.964		33.369	1.00 36.00
ATOM	4227			750	54.810		32.340	1.00 36.76
ATOM	4228				54.409		31.033	1.00 35.39
ATOM	4229			750	54.358		29.984	1.00 30.97
ATOM	4230		1 LEU	750	53.369		30.177	1.00 27.36
ATOM	4231			750	53.745	0.037	29.217	1.00 29.15
ATOM	4232		_	750	51.941	-1.578	29.934	1.00 29.22
ATOM	4232		LEU	750	55.369	-4.437	30.557	1.00 35.16
ATOM	4233		LEU	750	54.934	~5.449	30.014	1.00 34.45
ATOM		N	VAL	751	56.673	-4.212	30.721	1.00 38.76
ATOM	4235	CA		751	57.656	-5.217	30.312	1.00 38.69
ATOM	4236	CB	VAL	751	59.129	-4.724	30.485	1.00 33.81
ATOM	4237		1 VAL	751	60.092	-5.836	30.120	1.00 32.04
ATOM	4238		2 VAL	751	59.415	-3.535	29.598	1.00 30.67
	4239	C	VAL	751	57.428	-6.493	31.131	1.00 41.68
ATOM	4240	0	VAL	751	57.492	-7.599	30.594	1.00 39.92
ATOM	4241	N	GLU	752	57.109	-6.338	32.414	1.00 44.22
ATOM	4242	CA	GLU	752	56.854	-7.501	33.266	1.00 47.43
ATOM	4243	CB	GLU	752	56.779	-7.078	34.743	1.00 47.43
ATOM	4244	CG	GLU	752	58.093	-6.448	35.212	1.00 49.29
ATOM	4245	CD	GLU	752	58.215	-6.249	36.707	
ATOM	4246	OE1	GLU	752	58.554	-5.123		1.00 53.05
ATOM	4247	OE2	GLU	752	58.021	-7.228		1.00 53.63
MOTA	4248	C	GLU	752	55.594	-8.256		1.00 56.18
MOTA	4249	0	GLU	752	55.646	-9.464		1.00 46.90
ATOM	4250	N	ASP	753	54.490			1.00 43.85
ATOM	4251	CA	ASP	753	53.232	_		1.00 48.05
MOTA	4252	СВ	ASP	753	52.119			1.00 48.46
ATOM	4253	CG	ASP	753				1.00 51.25
MOTA	4254		ASP	753 753	51.579			1.00 54.20
ATOM	4255		ASP	753 753	51.440		34.330	1.00 57.31
ATOM	4256	C	ASP		51.281			1.00 55.58
ATOM	4257	0	ASP	753	53.371		30.837	1.00 48.59
ATOM	4258	И		753	53.001	-9.930		L.00 49.69
	12,70	TA	LEU	754	53.903	-8.009		1.00 47.21

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MOTA	4259	CA	LEU	754	54.102	-8.489	28.523	1.00	46.37
ATOM	4260	CB	LEU	754	54.664	-7.385	27.625	1.00	44.16
ATOM	4261	CG	LEU	754	53.621	-6.366	27.152	1.00	46.35
ATOM	4262	CD1	LEU	754	54.296	-5.272	26.343	1.00	45.11
ATOM	4263	CD2	LEU	754	52.514	-7.070	26.349	1.00	42.89
ATOM	4264	C	LEU	754	55.004	-9.703	28.481	1.00	47.08
ATOM	4265	0	LEU	754	54.818	-10.590	27.659	1.00	45.02
MOTA	4266	N	ASP	755	55.969	-9.755	29.385	1.00	49.68
MOTA	4267	CA	ASP	755	56.890	-10.876	29.487	1.00	51.62
MOTA	4268	CB	ASP	755	57.883	-10.586	30.615	1.00	54.90
ATOM	4269	CG	ASP	755	59.009	-11.589	30.702	1.00	59.00
ATOM	4270	OD1	ASP	755	59.694	-11.608	31.746	1.00	63.70
MOTA	4271	OD2	ASP	755	59.223	-12.346	29.728	1.00	60.31
MOTA	4272	С	ASP	755	56.059	-12.117	29.817	1.00	51.50
ATOM	4273	0	ASP	755	56.119	-13.150	29.138	1.00	47.11
MOTA	4274	N	ARG	756	55.237	-11.958	30.844	1.00	51.81
ATOM	4275	CA	ARG	756	54.362	-13.009	31.328	1.00	51.44
MOTA	4276	CB	ARG	756	53.635	-12.519	32.582	1.00	54.52
MOTA	4277	CG	ARG	756	52.459	-13.358	33.027	1.00	55.00
ATOM	4278	CD	ARG	756	51.815	-12.727	34.255	1.00	59.54
MOTA	4279	NE	ARG	756	51.417	-11.335	34.026	1.00	64.01
ATOM	4280	CZ	ARG	756	50.366	-10.960	33.301	1.00	65.76
ATOM	4281	NH1	ARG	756	49.598	-11.866	32.721	1.00	63.56
ATOM	4282	NH2	ARG	756	50.061	-9.676	33.183	1.00	66.59
MOTA	4283	С	ARG	756	53.361	-13.440	30.260	1.00	50.03
ATOM	4284	0	ARG	756	53.267	-14.622	29.960	1.00	49.98
MOTA	4285	N	ILE	757	52.645	-12.483	29.673	1.00	46.87
MOTA	4286	CA	ILE	757	51.656	-12.789	28.644	1.00	44.28
MOTA	4287	CB	ILE	757	50.919	-11.532	28.125	1.00	40.46
MOTA	4288	CG2	ILE	757	49.923	-11.923	27.062	1.00	38.44
ATOM	4289	CG1	ILE	757	50.202	-10.830	29.277	1.00	39.74
ATOM	4290	CD1	ILE	757	49.481	-9.551	28.920	1.00	40.68
MOTA	4291	C	ILE	757	52.251	-13.528	27.454	1.00	44.20
ATOM	4292	0	ILE	757	51.643	-14.469	26.959	1.00	40.28
ATOM	4293	N	VAL	758	53.440	-13.111	27.014	1.00	47.56
ATOM	4294	CA	VAL	758	54.102	-13.745	25.874	1.00	48.90
ATOM	4295	CB	VAL	758	55.543	-13.177	25.609	1.00	47.01
ATOM	4296	CG1	VAL	758	56.198	-13.920	24.456	1.00	44.38
MOTA	4297	CG2	VAL	758	55.493	-11.714	25.262	1.00	47.85
ATOM	4298	С	VAL	758	54.249	-15.232	26.149	1.00	51.79
MOTA	4299	0	VAL	758	54.043	-16.055	25.258	1.00	49.80
MOTA	4300	N	ALA	759	54.622	-15.550	27.386	1.00	54.80
MOTA	4301	CA	ALA	759	54.825	-16.925	27.814	1.00	57.15
MOTA	4302	CB	ALA	759	55.406	-16.948	29.212	1.00	56.77
ATOM	4303	C	ALA	759	53.524	-17.717	27.777	1.00	60.83
MOTA	4304	0	ALA	759	53.487	-18.849	27.296		63.59
MOTA	4305	N	LEU	760		-17.112	28.271	1.00	61.74
ATOM	4306	CA	LEU	760	51.151	-17.760	28.295		61.29
MOTA	4307	CB	LEU	760		-17.149	29.388		60.41
MOTA	4308	CG	LEU	760	50.808	-17.323	30.812		58.68
ATOM	4309	CD1	LEU	760		-16.603	31.815		59.64
MOTA	4310	CD2		760 [°]		-18.799	31.138		57.84

ATO	vr 421	1 0						
ATO		_				9 -17.70		1.00 63.42
ATOM					49.28	2 -18.12	1 26.842	
				761	51.11	3 -17.20	0 25.924	
ATON			A THR	761	50.51	2 -17.10	9 24.586	-
ATOM				761		1 -15.73		
ATOM			G1 THR	761		3 -14.699		
ATOM		7 C	G2 THR	761		-15.684		· - ·
ATOM		8 C	THR	761		-18.225		
ATOM	431	9 0	THR	761		-18.492		
ATOM	432	0 S	G CYS	1603	18.668			
ATOM	432	1 C	S MET	534	69.414			
MOTA	4322	2 SI) MET	534	69.162			
ATOM	4323	3 CI	MET	534	70.204			
ATOM	4324	ı so		603				
ATOM	4325			1	56.218		_	0.50 37.35
ATOM				2	71.863			1.00 24.40
ATOM				3	39.671			1.00 36.87
ATOM	4328				83.765	19.802		1.00 26.81
ATOM	4329			4	83.844	20.193		1.00 30.07
ATOM	4330		2 TIP	5	75.192	16.430	6.693	1.00 26.76
ATOM	4331		2 TIP	6	86.579	19.662	9.323	1.00 36.11
MOTA	4332			7	52.204	10.911	24.392	1.00 36.83
ATOM				8	55.174	9.435	22.514	1.00 21.93
ATOM	4333		2 TIP	9	57.077	4.556	32.580	1.00 25.17
ATOM	4334	-		10	52.281	4.737	13.300	1.00 20.79
	4335			11	41.402	5.304	22.893	1.00 39.17
ATOM	4336	OH		12	45.088	8.857	21.604	1.00 35.14
ATOM	4337	OH		13	64.519	-2.772	28.799	1.00 47.52
ATOM	4338	OH:		14	77.327	12.960	23.832	1.00 34.47
ATOM	4339	OH:		15	79.366	17.021	18.247	1.00 47.49
ATOM	4340	OH:		16	83.087	11.573	15.986	1.00 22.80
ATOM	4341	OH2		17	13.977	-9.804	0.222	1.00 24.88
ATOM	4342	OH	TIP	18	38.451	0.155	5.081	1.00 24.88
ATOM	4343	OH	TIP	20	27.109	6.286	4.902	
MOTA	4344	OH	TIP	21	34.379	-1.750	16.771	1.00 27.69
MOTA	4345	OH2	TIP	22	20.394	2.449	27.821	1.00 47.69
ATOM	4346	OH2		23	50.587		38.062	1.00 54.32
ATOM	4347	OH2	TIP	24	17.137	-5.949		1.00 45.31
ATOM	4348	OH2	TIP	25	27.604	7.961	-1.716	1.00 27.63
ATOM	4349	OH2	TIP	26	31.446		15.119	1.00 47.19
ATOM	4350	OH2	TIP	27	27.030	0.136	6.605	1.00 29.98
ATOM	4351		TIP	28			27.803	1.00 28.86
ATOM	4352		TIP	29	28.477		13.067	1.00 37.44
ATOM	4353		TIP	30	88.748	14.279	8.091	1.00 32.72
ATOM	4354		TIP		-2.392	-3.684	11.343	1.00 41.86
ATOM	4355		TIP	31	34.968	-4.221	18.549	1.00 40.51
ATOM	4356		TIP	32	80.581	17.982	9.655	1.00 27.85
ATOM	4357			33	5.522	3.773		1.00 24.60
ATOM	4358		TIP	34	-10.747	5.416		1.00 29.27
ATOM	4358		TIP	35	29.049	-8.816		1.00 35.24
ATOM		OH2		36	5.871	3.463		1.00 26.62
	4360	OH2		37	31.834	2.899		1.00 49.70
ATOM	4361	OH2		38	19.799	_		1.00 29.67
ATOM	4362	OH2	TIP	39	62.060			1.00 54.86
								50 24.00

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MOTA	4363	. OH2	TIP	40	21.100	-6.883	-4.054	1.00	22.33
MOTA	4364	OH2	TIP	41	-15.675	8.744	22.559	1.00	44.54
ATOM	4365	OH2	TIP	42	40.066	2.225	8.567	1.00	57.00
ATOM	4366	OH2	TIP	43	19.477	11.293	-0.049	1.00	
ATOM	4367	OH2	TIP	44	67.060	9.047	17.334	1.00	25.14
ATOM	4368	OH2	TIP	45	87.829	18.937	18.529		45.92
MOTA	4369	OH2	TIP	46	74.741	16.956	3.987		40.33
ATOM	4370	OH2	TIP	47	29.411	16.888	10.525		38.41
ATOM	4371	OH2		48	66.592	7.020	15.108		36.15
MOTA	4372	OH2	TIP	49	85.071	21.432	5.755		19.89
ATOM	4373	OH2	TIP	50	-4.842	3.281	3.118		28.22
ATOM	4374	OH2	TIP	51	19.454	5.250	4.876		34.86
ATOM	4375	ОН2	TIP	53	34.785	5.433	24.743		30.40
ATOM	4376	OH2	TIP	54	34.792	-17.150	13.665		35.81
MOTA	4377	ОН2	TIP	55	59.956	7.380	27.941	1.00	36.76
MOTA	4378	OH2	TIP	56	-7.327	-1.518	6.428	1.00	39.13
ATOM	4379	OH2	TIP	57	55.164	12.120	25.338		38.87
ATOM	4380	OH2	TIP	58	68.637	6.832	16.698		54.96
ATOM	4381	OH2	TIP	59 ·	73.778	20.869	19.031		35.01
ATOM	4382	OH2	TIP	60	3.582	-8.363	-8.103		16.71
ATOM	4383	OH2	TIP	61	38.051	10.933	5.487		32.85
ATOM	4384	OH2	TIP	62	29.727	-9.630	-1.370		30.92
ATOM	4385	OH2	TIP	64	49.186	1.253	12.066		42.67
ATOM	4386	OH2	TIP	65	41.375	3.989	28.951		37.95
ATOM	4387	OH2	TIP	66	10.798	-13.119	1.125		38.26
MOTA	4388	OH2	TIP	67	-1.079	-4.386	21.428	1.00	
ATOM	4389	OH2	TIP	68	30.327	16.346	13.295		53.21
MOTA	4390	OH2	TIP	69	8.319	4.437	3.449		23.63
ATOM	4391	OH2	TIP	70	73.152	18.809	22.631		36.45
ATOM	4392	OH2	TIP	71	-7.984	-3.476	25.048		33.16
ATOM	4393	OH2	TIP	72	66.529	-4.720	28.421		66.32
ATOM	4394	OH2	TIP	73	21.577	-20.723	4.868		48.14
ATOM	4395	OH2	TIP	74	59.417	-6.760	4.957		48.73
ATOM	4396	OH2	TIP	75		-13.306	-2.942		41.02
ATOM	4397	OH2	TIP	76	-15.064	7.473	4.275	1.00	26.77
MOTA	4398	OH2	TIP	77	33.118	2.917	13.384		41.38
ATOM	4399	OH2	TIP	78	0.112	-2.913	10.809		27.49
MOTA	4400	OH2	TIP	79	17.448	2.562	5.507		16.32
ATOM	4401	OH2	TIP	81	27.445	3.796	6.134		29.83
MOTA	4402		TIP	82	-8.708	6.231	9.598		27.66
MOTA	4403	OH2		83	1.565	-1.998	8.758		33.46
ATOM	4404		TIP	84	-4.774	-3.153	7.049		36.59
MOTA	4405		TIP	85	17.443	3.105	1.795		20.39
MOTA	4406		TIP	86	20.120	3.387	2.918		30.35
ATOM	4407	OH2		87	0.466	-2.238	22.190		20.30
ATOM	4408	OH2		88	19.749	-6.018	-1.687		21.33
ATOM	4409	OH2		89		-15.695	6.861		38.80
MOTA	4410		TIP	90		-12.113	11.774		34.18
ATOM	4411	OH2		91	6.297	1.090	-3.192		24.40
ATOM	4412		TIP	92	-13.540	1.554	5.413		34.94
ATOM	4413		TIP	93	15.607	-7.315	0.017		26.30
MOTA	4414		TIP	94	-1.868	-5.461	3.839		37.12
				- -				~	

ATOM	1 443	r 0	770 MT					
ATOM			H2 TIF		12.718		-4.40	1.00 40.61
ATOM			H2 TIF	_	69.849			
			H2 TIP			-13.311	0.143	
ATOM	_		H2 TIP		60.424	-4.582	34.237	
ATOM			H2 TIP		10.589	5.757		· —
ATOM			H2 TIP		-9.564	-3.999		
ATOM			H2 TIP		73.085	-1.967		
ATOM			H2 TIP		-3.172	5.701		
ATOM			H2 TIP	103	36.672			
ATOM			12 TIP	104	21.408			= 1 0 0 0 0 0 0 1 7 7
ATOM		5 OF	H2 TIP	105	31.224			
ATOM	4426	OI	H2 TIP	106	5.660		22.197	
ATOM	4427	7 OF	12 TIP	107	-12.988	8.471	17.441	
ATOM	4428	OF	12 TIP	108		-10.524		· - -
ATOM	4429	OH		109	24.182	2.026	-0.894	
ATOM	4430	OH	2 TIP	110	-1.822		18.156	1.00 35.87
ATOM	4431	. OH		111	59.584	12.848	3.561	1.00 35.44
ATOM	4432			112		13.491	33.225	1.00 40.47
ATOM	4433			113	4.402	-10.813	1.929	1.00 47.07
ATOM	4434			114	8.032	2.916	0.940	1.00 40.79
ATOM	4435			115	75.905	1.522	25.912	1.00 55.51
ATOM	4436				48.960	15.737	14.249	1.00 38.97
ATOM	4437			116		-11.271	9.174	1.00 29.12
ATOM	4438			117	83.062	26.404	12.925	1.00 41.17
ATOM	4439			118	8.816	-6.440	-3.424	1.00 48.26
ATOM				119	-8.594	4.575	4.258	1.00 32.68
ATOM	4440	OH:		120	7.695	-13.769	8.481	1.00 39.22
ATOM	4441	OH:		121	51.500	6.285	10.369	1.00 25.18
ATOM	4442	OH:		122	20.720	3.849	15.625	1.00 22.46
	4443	OH:		123	73.111	3.718	20.617	1.00 28.26
ATOM	4444	OH:		124	5.312	-11.608	22.516	1.00 32.74
ATOM	4445	OH2		125	34.207	2.437	16.601	1.00 65.04
ATOM	4446	OH2		126	9.535	-11.998	7.085	1.00 25.13
ATOM	4447	OH2		127	8.227	3.912	-1.495	1.00 43.73
ATOM	4448	OH2		129	.7.312	7.072	2.922	1.00 47.65
MOTA	4449		TIP	130	35.824	-1.660	0.135	1.00 30.43
ATOM	4450		TIP	131	44.723	10.285	11.144	1.00 30.43
ATOM	4451		TIP	132	27.941		18.733	1.00 58.65
ATOM	4452		TIP	133	45.301	11.497	21.408	1.00 35.00
ATOM	4453	OH2	TIP	134	57.705 -		14.202	1.00 33.00
MOTA	4454	OH2	TIP	135	-3.108	15.385	16.685	
MOTA	4455	OH2	TIP	136	85.884	11.182	9.044	1.00 38.07
ATOM	4456	OH2	TIP	137	12.840	-2.444		1.00 32.04
ATOM	4457		TIP	138	75.645	3.496	1.983	1.00 30.08
MOTA	4458	OH2	TIP	139	13.020		20.607	1.00 33.94
ATOM	4459		TIP	140		7.518		1.00 40.68
ATOM	4460		TIP	141	11.245 -			1.00 26.02
ATOM	4461		TIP	142	59.563	10.829		1.00 71.34
ATOM	4462		TIP		13.671 -			1.00 39.47
ATOM	4463		TIP	143		-3.421		1.00 37.08
ATOM	4464		TIP	144	25.629 -		3.534	1.00 50.51
ATOM	4465			145		10.869		1.00 38.40
ATOM	4466	OH2		146		12.840		1.00 47.80
111014	4400	OH2	LIP	147	32.139	-4.674		1.00 32.43

ATOM	4467	OH2	TIP	148	44.890	7.505	11.806	1.00	32.46
MOTA	4468	OH2	TIP	149	80.781	12.432	16.562	1.00	47.77
ATOM	4469	OH2	TIP	150	3.017	-7.101	-1.917	1.00	40.92
MOTA	4470	OH2	TIP	151	31.784	-6.139	20.968	1.00	38.23
ATOM	4471	OH2	TIP	152	74.835	-2.597	12.290	1.00	48.89
ATOM	4472	OH2	TIP	153	7.509	6.768	-1.083	1.00	46.02
MOTA	4473	OH2	TIP	154	71.732	5.360	21.908	1.00	33.30
ATOM	4474	OH2	TIP	155	68.150	-5.075	8.794	1.00	39.31
ATOM	4475	OH2	TIP	156	0.148	-9.544	6.872	1.00	41.37
ATOM	4476	OH2	TIP	157	67.878	18.204	10.861	1.00	51.19
ATOM	4477	OH2	TIP	158	3.652	8.829	4.428	1.00	31.24
MOTA	4478	OH2	TIP	159	52.100	11.362	18.433	1.00	40.73
ATOM	4479	OH2	TIP	161	-10.357	6.783	4.861	1.00	35.13
ATOM	4480	OH2	TIP	162	76.471	1.562	-0.853	1.00	59.17
ATOM	4481	OH2	TIP	163	10.073	-12.056	17.071	1.00	44.69
MOTA	4482	OH2	TIP	164	34.163	14.271	18.254	1.00	39.59
MOTA	4483	OH2	TIP	165	2.320	-7.990	16.820	1.00	38.19
MOTA	4484	OH2	TIP	166	29.696	1.908	6.098	1.00	38.02
MOTA	4485	OH2	TIP	167	32.626	-17.410	11.766	1.00	48.15
ATOM	4486	OH2	TIP	168	42.244	18.049	11.043	1.00	50.95
MOTA	4487	OH2	TIP	169	87.907	10.574	5.721	1.00	60.28
ATOM	4488	OH2	TIP	170	70.313	-3.998	25.141	1.00	72.64
MOTA	4489	OH2	TIP	171	77.603	5.679	23.952	1.00	43.23
MOTA	4490	OH2	TIP	172	-0.942	-8.153	4.508	1.00	55.10
MOTA	4491	OH2	TIP	173	34.297	15.574	1.690	1.00	34.19
ATOM	4492	OH2	TIP	174	-9.643	7.829	7.414	1.00	50.48
MOTA	4493	OH2	TIP	175	11.618	5.655	7.455	1.00	43.37
MOTA	4494	OH2	TIP	176	-8.705	13.841	13.642	1.00	72.49
ATOM	4495	OH2	TIP	177	32.009	3.416	18.257	1.00	44.16
ATOM	4496	OH2	TIP	178	-8.651	10.180	24.352	1.00	44.85
MOTA	4497	OH2	TIP	179	-1.153	-6.532	15.548	1.00	32.90
MOTA	4498	OH2	TIP	180	80.235	0.749	15.508	1.00	34.75
MOTA	4499	OH2	TIP	181	67.222	20.490	-1.574	1.00	40.76
MOTA	4500	OH2	TIP	182	-0.471	4.367	1.248	1.00	36.58
MOTA	4501	OH2	TIP	183	0.149	6.517	2.578	1.00	40.12
MOTA	4502	OH2	TIP	184	-1.186	8.867	1.311	1.00	44.77
MOTA	4503	OH2	TIP	185	-5.093	9.260	2.252	1.00	52.07
MOTA	4504	OH2	TIP	186	-7.235	10.227	3.913	1.00	58.53
MOTA	4505	OH2	TIP	187	2.724	7.169	0.879	1.00	47.77
MOTA	4506		TIP	188	5.527	11.031	8.519		34.40
MOTA	4507	OH2		189	63.927	12.721	22.689		40.75
MOTA	4508	OH2		190	79.264	1.066	18.321	1.00	41.34
MOTA	4509	OH2	TIP	191	59.247	-11.825	7.256	1.00	79.86
MOTA	4510		TIP	192	13.994	-0.972	-4.310	1.00	31.15
MOTA	4511	OH2	TIP	193	59.546	3.024	33.227	1.00	40.34
MOTA	4512	OH2	TIP	194	32.179	13.637	19.964	1.00	48.25
MOTA	4513	OH2	TIP	195	72.178	16.188	22.879	1.00	42.72
MOTA	4514		TIP	196	0.898	-8.663	14.348		41.76
MOTA	4515		TIP	197	-0.490	5.455	30.574	1.00	38.30
MOTA	4516	OH2	TIP	199	-1.277	-4.244	27.691	1.00	56.27
MOTA	4517	OH2	TIP	200	81.605	15.360	17.272	1.00	42.05
MOTA	4518	OH2	TIP	201	-17.534	4.081	23.779	1.00	59.65

MOTA		OH2 TI	202	27.748 10.634 14.595 1.00 49.97
ATOM				24 005
MOTA				1.00 00.26
ATOM		OH2 TIP	205	10 705
ATOM	4523	OH2 TIP	206	F2 002
ATOM	4524	OH2 TIP	207	25 075
ATOM	4525	OH2 TIP		7 704
ATOM	4526	OH2 TIP		06 686
ATOM	4527	OH2 TIP		55 000 72.92
ATOM	4528	OH2 TIP		53 530 58.73
ATOM	4529	OH2 TIP		10.000
ATOM	4530	OH2 TIP	213	20 005
MOTA	4531	OH2 TIP	214	26 446
ATOM	4532	OH2 TIP	215	26 520
ATOM	4533	OH2 TIP	216	16 008 00 50.30
ATOM	4534	OH2 TIP	217	16.807 -20.725 14.119 1.00 56.03
MOTA	4535	OH2 TIP	218	28.203 -14.485 6.172 1.00 62.90
. ATOM	4536	OH2 TIP	219	31.519 1.503 -2.010 1.00 56.19
ATOM	4537	OH2 TIP	220	10.014 -16.571 15.451 1.00 46.37
ATOM	4538	OH2 TIP	221	7.126 -11.922 5.526 1.00 56.89
ATOM	4539	OH2 TIP	222	-12.414 14.643 10.965 1.00 67.36
ATOM	4540	OH2 TIP	223	10.978 9.734 -1.436 1.00 38.81
ATOM	4541	OH2 TIP	224	11.293 12.362 -1.306 1.00 52.56
ATOM	4542	OH2 TIP	225	34.011 13.162 -1.255 1.00 52.58
ATOM	4543	OH2 TIP	226	31.195 17.923 8.021 1.00 75.88
ATOM	4544	OH2 TIP	227	36.957 11.949 -1.947 1.00 50.99
ATOM	4545	OH2 TIP	228	35.179 3.114 10.888 1.00 58.55
ATOM	4546	OH2 TIP	229	64.027 13.281 26.577 1.00 51.98
ATOM	4547	OH2 TIP	230	36.514 6.155 15.292 1.00 45.57
ATOM	4548	OH2 TIP	231	90.627 4.339 6.386 1.00 56.65
ATOM	4549	OH2 TIP	231	49.907 -11.937 10.792 1.00 53.49
ATOM	4550	OH2 TIP	232	60.296 -10.212 16.610 1.00 79.85
ATOM	4551	OH2 TIP	233	18.154 -21.314 7.018 1.00 53.60
ATOM		OH2 TIP	235	66.186 -1.068 30.882 1.00 56.92
ATOM		OH2 TIP	236	75.153 18.983 20.700 1.00 34.22
ATOM		OH2 TIP		-2.885 10.207 3.295 1.00 68.34
ATOM		OH2 TIP	237 238	5.834 -3.507 25.370 1.00 34.75
ATOM		OH2 TIP	239	35.910 6.163 12.569 1.00 37.31
ATOM		OH2 TIP	239	-5.494 16.637 14.033 1.00 65.17
ATOM		OH2 TIP	241	46.332 -11.698 26.865 1.00 55.30
ATOM		OH2 TIP		6.179 6.434 13.895 1.00 45.92
MOTA		OH2 TIP	242	-3.869 -4.958 20.821 1.00 41.96
ATOM		OH2 TIP	243	1.690 -3.598 -0.200 1.00 41.42
ATOM		OH2 TIP	244	86.181 11.454 23.000 1.00 56.22
ATOM		OH2 TIP	245	10.501 7.621 5.627 1.00 77.40
ATOM		OH2 TIP	246	5.007 8.485 2.181 1.00 89.31
ATOM		OH2 TIP	247	64.552 -8.093 20.595 1.00 45.86
ATOM		OH2 TIP	248	11.243 -17.828 13.332 1.00 65.30
ATOM		OH2 TIP	249	42.226 -6.785 14.857 1.00 81.78
ATOM			250	2.875 -4.176 22.032 1.00 53.45
ATOM		H2 TIP	251	72.048 1.134 -2.037 1.00 38.85
ATOM		H2 TIP	252	50.357 -3.142 32.887 1.00 67.13
111011	±3/0 (H2 TIP	254	57.772 9.500 11.808 1.00 40.03

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MOTA	4571	OH2	TIP	255	43.306	20.459	30.366	1.00	47.59
MOTA	4572	OH2	TIP	256	67.064	16.514	15.765	1.00	57.51
ATOM	4573	OH2	TIP	257	87.612	21.648	5.147	1.00	70.52
MOTA	4574	OH2	TIP	258	21.095	9.853	-9.308	1.00	78.97
MOTA	4575	OH2	TIP	261	71.914	28.544	7.912	1.00	83.90
MOTA	4576	OH2	TIP	262	25.727	-8.133	27.190	1.00	54.87
ATOM	4577	OH2	TIP	263	-18.738	10.877	12.767	1.00	71.80
MOTA	4578	OH2	TIP	264	30.524	11.543	16.329	1.00	46.98
ATOM	4579	OH2	TIP	265	22.211	-16.242	-2.763	1.00	55.17
MOTA	4580	OH2	TIP	266	29.755	9.037	18.396	1.00	67.93
ATOM	4581	C1	MON	1000	67.458	4.500	11.935	1.00	0.00
ATOM	4582	C2	MON	1000	67.015	3.958	10.687	1.00	0.00
ATOM	4583	И3	MON	1000	67.367	2.732	10.160	1.00	0.00
ATOM	4584	C4	MON	1000	66.127	4.618	9.793	1.00	0.00
MOTA	4585	C5	MON	1000	65.620	5.919	10.125	1.00	0.00
MOTA	4586	C6	MON	1000	66.041	6.508	11.380	1.00	0.00
MOTA	4587	C7	MON	1000	66.948	5.809	12.276	1.00	0.00
MOTA	4588	C8	MON	1000	65.933	3.759	8.668	1.00	0.00
ATOM	4589	C10	MON	1000	66.745	2.518	8.922	1.00	0.00
ATOM	4590	C11	MON	1000	65.043	4.051	7.483	1.00	0.00
MOTA	4591	012	MON	1000	66.862	1.516	8.241	1.00	0.00
MOTA	4592	C13	MON	1000	64.479	2.990	6.570	1.00	0.00
MOTA	4593	C14	MON	1000	63.459	3.330	5.617	1.00	0.00
ATOM	4594	C15	MON	1000	62.923	2.333	4.727	1.00	0.00
ATOM	4595	C16	MON	1000	63.379	0.956	4.754	1.00	0.00
ATOM	4596	C17	MON	1000	64.960	1.637	6.605	1.00	0.00
ATOM	4597	C18	MON	1000	64.418	0.642	5.713	1.00	0.00
ATOM	4598	N19	MON	1.000	62.848	-0.025	3.880	1.00	0.00
ATOM	4599	C20	MON	1000	63.429	-1.407	3.816	1.00	0.00
ATOM	4600	C21	MON	1000	61.888	0.343	2.786	1.00	0.00
MOTA	4601	C22	MON	1000	61.085	-0.818	2.152	1.00	0.00
ATOM	4602	N23	MON	1000	61.868	-2.035	1.930	1.00	0.00
MOTA	4603	C24	MON	1000	62.562	-2.492	3.133	1.00	0.00
MOTA	4604	025	MON	1000	61.481	-2.328	-0.389	1.00	0.00
MOTA	4605	C26	MON	1000	62.001	-2.670	0.659	1.00	0.00
ATOM	4606	Cl	MON	1001	5.458	3.340	18.422	1.00	0.00
ATOM	4607	C2	MON	1001	6.049	3.475	19.718	1.00	0.00
ATOM	4608	из	MON	1001	5.935	2.580	20.763	1.00	0.00
MOTA	4609	C4	MON	1001	6.857	4.573	20.124	1.00	0.00
MOTA	4610	C5	MON	1001	7.121	5.641	19.202	1.00	0.00
MOTA	4611	- C6	MON	1001	6.543	5.548	17.877	1.00	0.00
MOTA	4612	C7	MON	1001	5.722	4.412	17.489	1.00	0.00
MOTA	4613	C8	MON	1001	7.250	4.340	21.477	1.00	0.00
MOTA	4614	C10	MON	1001	6.647	3.023	21.886	1.00	0.00
MOTA	4615	C11	MON	1001	8.138	5.242	22.302	1.00	0.00
MOTA	4616	012	MON	1001	6.735	2.426	22.943	1.00	0.00
MOTA	4617	C13	MON	1001	8.918	4.783	23.509	1.00	0.00
ATOM	4618	C14	MON	1001	9.913	5.641	24.091	1.00	0.00
ATOM	4619	C15	MON	1001	10.654	5.224	25.253	1.00	0.00
ATOM	4620	C16	MON	1001	10.435	3.935	25.881	1.00	0.00
ATOM	4621		MON	1001	8.670	3.508	24.123	1.00	0.00
ATOM	4622		MON	1001	9.416	3.095	25.285	1.00	0.00

ATOM ATOM ATOM ATOM	4623 4624 4625 4626	N19 MON C20 MON C21 MON C22 MON	1001 1001 1001	11.168 10.831 12.107	3.525 2.255 4.463	27.023 27.749 27.725	1.00 1.00 1.00	0.00 0.00 0.00
ATOM ATOM ATOM	4627 4628	N23 MON C24 MON	1001	13.125 12.570 11.902	3.821 2.742 1.711	28.698 29.518 28.725	1.00 1.00 1.00	0.00 0.00 0.00
ATOM	4629 4630	O25 MON C26 MON	1001 1001	13.118 12.610	3.569 2.731	31.669 30.944	1.00	0.00

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CLAIMS

What is claimed is:

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1. A crystalline form of a polypeptide corresponding to the catalytic domain of a protein tyrosine kinase.

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2. The crystalline form of claim 1, wherein said protein tyrosine kinase is a receptor protein tyrosine kinase.

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3. The crystalline form of claim 2, wherein said receptor protein tyrosine kinase is selected from the group consisting of PDGF-R, FLK, CCK4, MET, TRKA, AXL, TIE, EPH, RYK, DDR, ROS, RET, LTK, ROR1, and MUSK.

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4. The crystalline form of claim 1, wherein said protein tyrosine kinase is a non-receptor protein tyrosine kinase.

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5. The crystalline form of claim 4, wherein said non-receptor protein tyrosine kinase is selected from a group consisting of SRC, BRK, BTK, CSK, ABL, ZAP70, FES, FAK, JAK, and ACK.

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6. The crystalline form of claim 1, comprising one or more heavy metal atoms.

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7. The crystalline form of claim 1, wherein said

protein tyrosine kinase is FGFR.

8. The crystalline form of claim 7, wherein said FGFR is FGFR1.

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- 9. The crystalline form of claim 8, defined by atomic structural coordinates set forth in Table 1.
- 10. The crystalline form of claim 7, comprising at least one compound.
 - 11. The crystalline form of claim 10, wherein said compound is a nucleotide analog.

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12. The crystalline form of claim 11, wherein said nucleotide analog is AMP-PCP.

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- 13. The crystalline form of claim 12, defined by atomic structural coordinates set forth in Table 2.
- 14. The crystalline form of claim 10, wherein said compound is an indolinone compound.
- 15. The crystalline form of claim 14, wherein said indolinone compound has a structure set forth in formula I or II:

$$\begin{array}{c|c}
R_{3}' & R_{4}' \\
R_{5}' & R_{5}' \\
R_{5} & R_{6}' \\
R_{6} & R_{7} & R_{1}
\end{array}$$

$$(I)$$

$$R_{5}$$
 A_{2}
 A_{1}
 A_{2}
 A_{3}
 A_{4}
 A_{7}
 A_{1}
 A_{1}
 A_{2}
 A_{1}
 A_{2}
 A_{3}
 A_{4}
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 A_{3}
 A_{4}
 A_{1}
 A_{2}
 A_{3}
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 A_{7}
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 A_{7

or a pharmaceutically acceptable salt, isomer, metabolite, ester, amide, or prodrug thereof, wherein

- (a) A_1 , A_2 , A_3 , and A_4 are independently carbon or nitrogen;
 - (b) R₁ is hydrogen or alkyl;
- (c) R_2 is oxygen in the case of an oxindolinone or sulfur in the case of a thiolindolinone;
 - (d) R₃ is hydrogen;
 - (e) R_4 , R_5 , R_6 , and R_7 are optionally present and are

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either (i) independently selected from the group consisting of hydrogen, alkyl, alkoxy, aryl, aryloxy, alkaryl, alkaryloxy, halogen, trihalomethyl, S(0)R, SO_2NRR' , SO_3R , SR, NO_2 , NRR', OH, CN, C(0)R, OC(0)R, NHC(0)R, $(CH_2)_nCO_2R$, and CONRR' or (ii) any two adjacent R_4 , R_5 , R_6 , and R_7 taken together form a fused ring with the aryl portion of the oxindole-based portion of the indolinone;

- (f) R₂', R₃', R₄', R₅', and R₆' are each
 independently selected from the group consisting of
 hydrogen, alkyl, alkoxy, aryl, aryloxy, alkaryl,
 alkaryloxy, halogen, trihalomethyl, S(O)R, SO₂NRR', SO₃R,
 SR, NO₂, NRR', OH, CN, C(O)R, OC(O)R, NHC(O)R, (CH₂)_nCO₂R,
 and CONRR';
 - (g) n is 0, 1, 2, or 3;
 - (h) R is hydrogen, alkyl or aryl;
 - (i) R' is hydrogen, alkyl or aryl; and
- (j) A is a five membered heteroaryl ring selected from the group consisting of thiophene, pyrrole, pyrazole, imidazole, 1,2,3-triazole, 1,2,4-triazole, 20 oxazole, isoxazole, thiazole, isothiazole, furan, 1,2,3oxadiazole, 1,2,4-oxadiazole, 1,2,5-oxadiazole, 1,3,4oxadiazole, 1,2,3,4-oxatriazole, 1,2,3,5-oxatriazole, 1,2,3-thiadiazole, 1,2,4-thiadiazole, 1,2,5-thiadiazole, 1,3,4-thiadiazole, 1,2,3,4-thiatriazole, 1,2,3,5-25 thiatriazole, and tetrazole, optionally substituted at one or more positions with alkyl, alkoxy, aryl, aryloxy, alkaryl, alkaryloxy, halogen, trihalomethyl, S(O)R, SO_2NRR' , SO_3R , SR, NO_2 , NRR', OH, CN, C(O)R, OC(O)R, 30 NHC(O)R, $(CH_2)_nCO_2R$ or CONRR'.

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16. The crystalline form of claim 15, wherein said indolinone compound is 3-[(3-(2-carboxyethyl)-4-methylpyrrol-5-yl)methylene]-2-indolinone.

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17. The crystalline form of claim 15, wherein said indolinone compound is 3-[4-(4-formylpiperazine-1-yl)benzylidenyl]-2-indolinone.

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18. The crystalline form of claim 16, defined by the atomic structural coordinates of Table 3.

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19. The crystalline form of claim 17, defined by the atomic structural coordinates of Table 4.

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monoclinic unit cells.

21. The crystalline form of claim 20, wherein said monoclinic unit cells have dimensions of about a=208.3 Å, b=57.8 Å, c=65.5 Å and β =107.2°.

The crystalline form of claim 1, having

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22. The crystalline form of claim 20, wherein said monoclinic unit cells have dimensions of about a=211.6 Å, b=51.3 Å, c=66.1 Å and β =107.7°.

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23. The crystalline form of claim 10, comprising one or more heavy metal atoms.

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24. A polypeptide corresponding to the catalytic domain of a protein tyrosine kinase, containing at least about 20 amino acid residues upstream of the first

glycine in the conserved glycine-rich region of the catalytic domain, and at least about 17 amino acid residues downstream of the conserved arginine located at the C-terminal boundary of the catalytic domain.

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25. The polypeptide of claim 24, wherein said protein tyrosine kinase is a receptor protein tyrosine kinase.

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26. The polypeptide of claim 24, wherein said protein tyrosine kinase is a non-receptor protein tyrosine kinase.

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27. The polypeptide of claim 25, wherein said receptor tyrosine kinase is selected from the group consisting of FGF-R, PDGF-R, KDR, CCK4, MET, TRKA, AXL, TIE, EPH, RYK, DDR, ROS, RET, LTK, ROR1, and MUSK.

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28. The polypeptide of claim 26, wherein said non-receptor kinase is selected from the group consisting of SRC, BRK, BTK, CSK, ABL, ZAP70, FES, FAK, JAK, and ACK.

- 29. The polypeptide of claim 24 having the amino acid sequence shown in SEQ ID NO:4.
- 30. A method of using the polypeptide of claim 24 to form a crystal, comprising the steps of:
- (a) mixing a volume of polypeptide solution with a reservoir solution; and
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- (b) incubating the mixture obtained in step(a) over the reservoir solution in a closed container,

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under conditions suitable for crystallization.

- 31. A method of obtaining an FGF receptor tyrosine kinase domain polypeptide in crystalline form, comprising the steps of:
- (a) mixing a volume of polypeptide solution with an equal volume of reservoir solution, wherein said polypeptide solution comprises 1 mg/mL to 60 mg/mL FGF-type tyrosine kinase domain protein, 10 mM to 200 mM buffering agent, 0 mM to 20 mM dithiothreitol and has a pH of about 5.5 to about 7.5, and wherein said reservoir solution comprises 10% to 30% (w/v) polyethylene glycol, 0.1 M to 0.5 M ammonium sulfate, 0% to 20% (w/v) ethylene glycol or glycerol, 10 mM to 200 mM buffering agent and has a pH of about 5.5 to about 7.5; and
- (b) incubating the mixture obtained in step (a) over said reservoir solution in a closed container at a temperature between 0° and 25° °C until crystals form.

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32. The method of claim 31, wherein said polypeptide solution comprises about 10 mg/mL FGF receptor tyrosine kinase domain, about 10 mM sodium chloride, about 2 mM dithiothreitol, about 10 mM Tris-HCl and has a pH of about 8; the reservoir buffer comprises about 16% (w/v) polyethylene glycol (MW 10000), about 0.3 M ammonium sulfate, about 5% ethylene glycol or glycerol, about 100 mM bis-Tris and has a pH of about 6.5; and the temperature is about 4°C.

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33. The method of claim 31, wherein said

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polypeptide solution comprises a compound.

- 34. A cDNA encoding an FGF receptor tyrosine kinase domain protein, wherein a coding strand of the cDNA has the nucleotide sequence of SEQ ID NO:5.
- 35. A method of determining three dimensional structures of protein tyrosine kinases with unknown structure comprising the step of applying structural atomic coordinates set forth in Table 1, Table 2, Table 3, or Table 4.
- 36. The method of claim 35, comprising the following steps:
- (a) aligning a first computer representation of an amino acid sequence of a protein tyrosine kinase of unknown structure with a second computer representation of a protein tyrosine kinase of known structure by matching homologous regions of amino acid sequences of said first computer representation and said second computer representation;
- (b) transferring computer representations of amino acid structures in said protein tyrosine kinase of known structure to computer representations of corresponding amino acid structures in said protein tyrosine kinase with unknown structure; and
- (c) determining a low energy conformation of the protein tyrosine kinase structure resulting from step (b).
 - 37. The method of claim 35, comprising the

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following steps:

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- (a) aligning the positions of atoms in the unit cell by matching electron diffraction data from two crystals; and
- (b) determining a low energy conformation of the resulting protein tyrosine kinase structure.
- 38. The method of claim 35, comprising the following steps:
- (a) determining the secondary structure of a protein tyrosine kinase structure using NMR data; and
- (b) simplifying the assignment of throughspace interactions of amino acids.
- 39. The method of any one of claims 35, 36, 37, or 38, wherein said protein tyrosine kinase with or without known structure is a receptor protein tyrosine kinase.
- 40. The method of claim 39, wherein said receptor protein tyrosine kinase with or without known structure is selected from the group consisting of FGF-R, PDGF-R, FLK, CCK4, MET, TRKA, AXL, TIE, EPH, RYK, DDR, ROS, RET, LTK, ROR1, and MUSK.
- 25 41. The method of anyone of claims 35, 36, 37, or 38, wherein said protein tyrosine kinase with or without known structure is a non-receptor protein tyrosine kinase.
- 30 42. The method of claim 41, wherein said protein tyrosine kinase with or without known structure is

selected from the group consisting of SRC, BRK, BTK, CSK, ABL, ZAP70, FES, FAK, JAK, and ACK.

- 43. A method of identifying a potential modulator of protein tyrosine kinase function by docking a computer representation of a structure of a compound with a computer representation of a structure of a cavity formed by the active-site of a protein tyrosine kinase, wherein said structure of said protein tyrosine kinase is defined by atomic structural coordinates set forth in Table 1, Table 2, Table 3, or Table 4.
- 44. The method of claim 43, comprising the following steps:
- (a) removing a computer representation of a compound complexed with a protein tyrosine kinase and docking a computer representation of a compound from a computer data base with a computer representation of the active-site of the protein tyrosine kinase;
- (b) determining a conformation of the complex resulting from step (a) with a favorable geometric fit and favorable complementary interactions; and
- (c) identifying compounds that best fit said active-site as potential modulators of protein tyrosine kinase function.
- 45. The method of claim 43, comprising the following steps:
- (a) modifying a computer representation of compound complexed with a protein tyrosine kinase by the deletion of a chemical group or groups or by the

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addition of a chemical group or groups;

- (b) determining a conformation of the complex resulting from step (a) with a favorable geometric fit and favorable complementary interactions; and
- (c) identifying compounds that best fit the protein tyrosine kinase active-site as potential modulators of protein tyrosine kinase function.
- 46. The method of claim 43, wherein said method comprises the following steps:
- (a) removing a computer representation of a compound complexed with a protein tyrosine kinase; and
- (b) searching a data base for data base compounds similar to said compounds using a compound searching computer program or replacing portions of said compound with similar chemical structures from a data base using a compound construction computer program.
- 47. The method of any one of claims 43, 44, 45, or 46, wherein said protein tyrosine kinase is a receptor protein tyrosine kinase.
- 48. The method of claim 47, wherein said receptor protein tyrosine kinase is selected from the group consisting of FGF-R, PDGF-R, FLK, CCK4, MET, TRKA, AXL, TIE, EPH, RYK, DDR, ROS, RET, LTK, ROR1, and MUSK.
- 49. The method of anyone of claims 43, 44, 45, or 46, wherein said protein tyrosine kinase is a non-receptor protein tyrosine kinase.

- 50. The method of claim 49, wherein said protein tyrosine kinase is selected from the group consisting of SRC, BRK, BTK, CSK, ABL, ZAP70, FES, FAK, JAK, and ACK.
- 5 51. a potential modulator of protein tyrosine kinase function identified by the method of any one of claims 43, 44, 45, or 46.
 - 52. The potential modulator of claim 51, wherein said modulator is selected from a computer data base.
 - 53. The potential modulator of claim 51, wherein said modulator is constructed from chemical groups selected from a computer data base.
 - 54. The potential modulator of protein tyrosine kinase function of claim 51, wherein said modulator is an indolinone compound of formula I or II:

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$$R_{3}$$

$$R_{4}$$

$$R_{5}$$

$$R_{6}$$

$$R_{7}$$

$$R_{1}$$

$$R_{1}$$

$$R_{4}$$

$$R_{6}$$

$$R_{6}$$

$$R_{6}$$

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or a pharmaceutically acceptable salt, isomer, metabolite, ester, amide, or prodrug thereof, wherein

- (a) A_1 , A_2 , A_3 , and A_4 are independently carbon or nitrogen;
 - (b) R₁ is hydrogen or alkyl;
- (c) R₂ is oxygen in the case of an oxindolinone or sulfur in the case of a thiolindolinone;
 - (d) R₃ is hydrogen;
- (e) R_4 , R_5 , R_6 , and R_7 are optionally present and are either (i) independently selected from the group consisting of hydrogen, alkyl, alkoxy, aryl, aryloxy, alkaryl, alkaryloxy, halogen, trihalomethyl, S(O)R, SO_2NRR' , SO_3R , SR, NO_2 , NRR', OH, CN, C(O)R, OC(O)R, NHC(O)R, (CH₂)_nCO₂R, and CONRR' or (ii) any two adjacent R_4 , R_5 , R_6 , and R_7 taken together form a fused ring with the aryl portion of the oxindole-based portion of the indolinone;
- (f) R_2' , R_3' , R_4' , R_5' , and R_6' are each independently selected from the group consisting of hydrogen, alkyl, alkoxy, aryl, aryloxy, alkaryl, alkaryloxy, halogen, trihalomethyl, S(O)R, SO2NRR', SO3R,

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SR, NO₂, NRR', OH, CN, C(O)R, OC(O)R, NHC(O)R, $(CH_2)_nCO_2R$, and CONRR';

- (g) n is 0, 1, 2, or 3;
- (h) R is hydrogen, alkyl or aryl;
- (i) R' is hydrogen, alkyl or aryl; and
- (j) A is a five membered heteroaryl ring selected from the group consisting of thiophene, pyrrole, pyrazole, imidazole, 1,2,3-triazole, 1,2,4-triazole, oxazole, isoxazole, thiazole, isothiazole, furan, 1,2,3-oxadiazole, 1,2,4-oxadiazole, 1,2,5-oxadiazole, 1,3,4-oxadiazole, 1,2,3,4-oxatriazole, 1,2,3,5-oxatriazole, 1,2,3-thiadiazole, 1,2,4-thiadiazole, 1,2,5-thiadiazole, 1,3,4-thiadiazole, 1,2,3,4-thiatriazole, 1,2,3,5-thiatriazole, and tetrazole, optionally substituted at one or more positions with alkyl, alkoxy, aryl, aryloxy, alkaryl, alkaryloxy, halogen, trihalomethyl, S(O)R, SO₂NRR', SO₃R, SR, NO₂, NRR', OH, CN, C(O)R, OC(O)R, NHC(O)R, (CH₂)_nCO₂R or CONRR'.
- 55. A method of identifying a potential modulator of protein tyrosine kinase function as a modulator of protein tyrosine kinase function, comprising the following steps:
 - (a) administering said potential modulator to cells;
 - (b) comparing the level of protein tyrosine kinase phosphorylation between cells not administered the potential modulator and cells administered said potential modulator; and
- (c) identifying said potential modulator as a modulator of protein tyrosine kinase function based on

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the difference in the level of protein tyrosine kinase phosphorylation.

- 56. A method of identifying a potential modulator of protein tyrosine kinase function as a modulator of protein tyrosine kinase function, wherein said method comprises the following steps:
- (a) administering a preparation of saidpotential modulator to cells;
- (b) comparing the rate of cell growth between cells not administered the modulator and cells administered the modulator; and
- (c) identifying said potential modulator as a modulator of protein tyrosine kinase function based on the difference in the rate of cell growth.
- 57. A method of treating a disease associated with a protein tyrosine kinase with inappropriate activity in a cellular organism, wherein said method comprises the steps of:
- (a) administering a modulator of protein tyrosine kinase function to the organism, wherein said modulator is in an acceptable pharmaceutical preparation; and
- (b) activating or inhibiting the protein tyrosine kinase function to treat the disease.
- 58. The method of any one of claims 55, 56, or 57, wherein said protein tyrosine kinase is a receptor protein tyrosine kinase.

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59. The method of claim 58, wherein said receptor protein tyrosine kinase is selected from the group containing FGF-R, PDGF-R, FLK, CCK4, MET, TRKA, AXL, TIE, EPH, RYK, DDR, ROS, RET, LTK, ROR1, and MUSK.

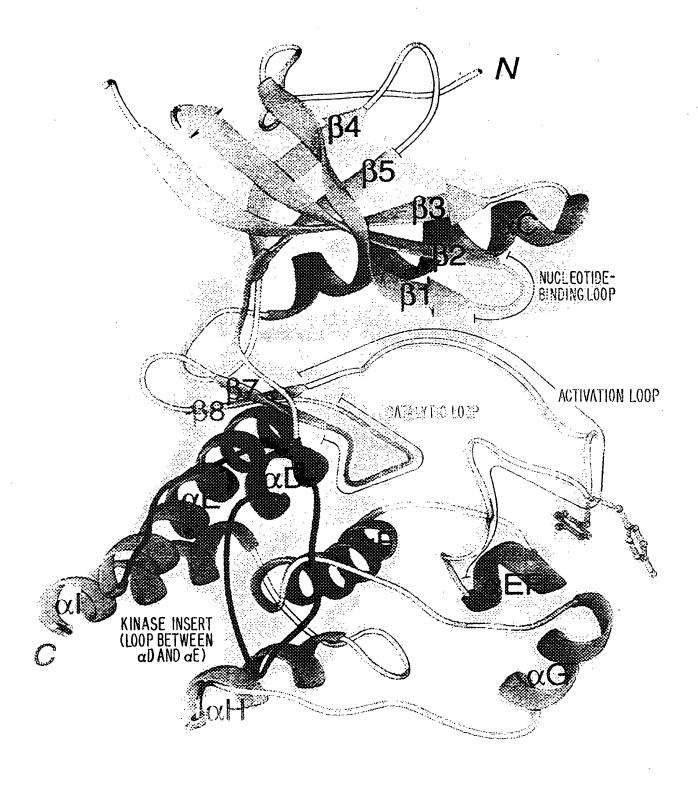
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60. The method of any one of claims 55, 56, or 57, wherein said protein tyrosine kinase is a non-receptor protein tyrosine kinase.

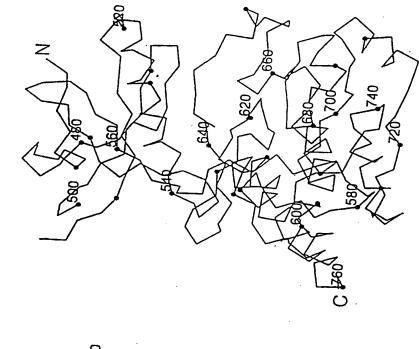
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61. The method of claim 60, wherein said non-receptor protein tyrosine kinase is selected from a group consisting of SRC, BRK, BTK, CSK, ABL, ZAP70, FES, FAK, JAK, and ACK.

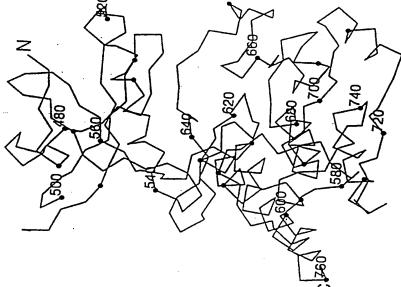
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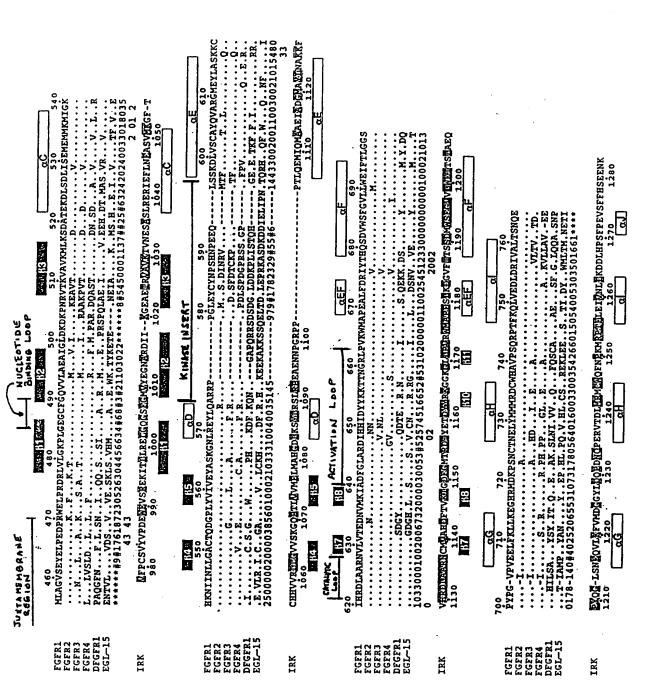
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SUBSTITUTE SHEET (RULE 26)

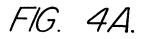












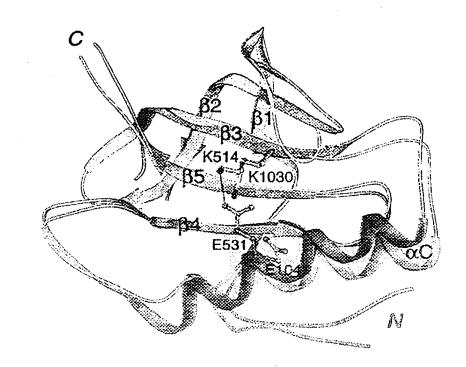
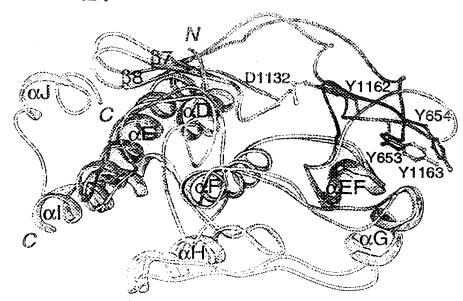


FIG. 4B.



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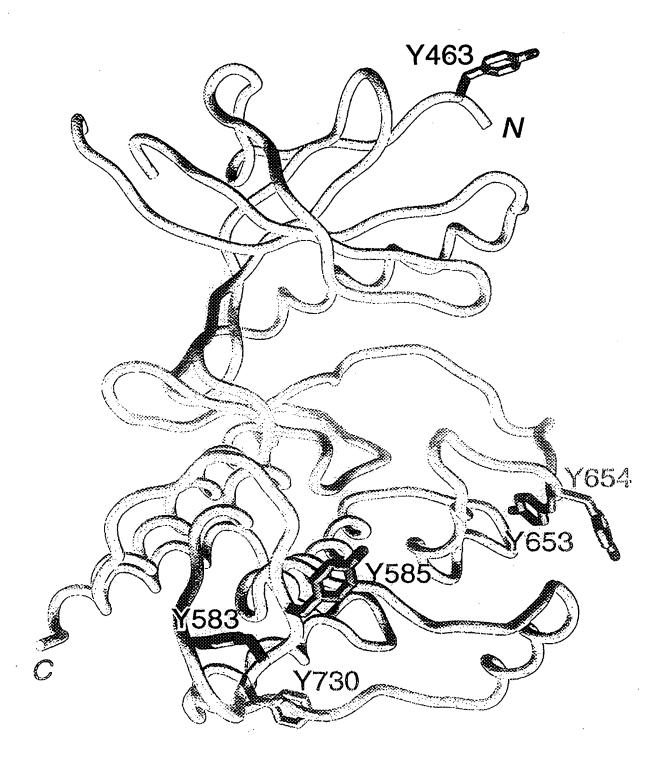


FIG. 5.

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			-DATEKDLSD LISEMEMMKM	-ATSPKANKE ILDEAYVMAS	-SASLRERIE FLNEASVMKG	-TARSSEKQA LMSELKIMTH	-GATHSEHRA LMSELKILIH	-SKDEQQQLD FRRELEMFGK	-ITDIGEVSQ FLTEGIIMKD	-EASESAROD FOREAELLTM	AICTRSELED FLSEAVCMKE	-YASENDHRD FAGELEVLCK	-TSPGGQWWN FLREATIMGO	-QASEIQVTM MLTESCKLRG	-DATKNARND FLKEVKIMSR	-GSTDQEKIE FLKERHLMSK	-NASPSELRD LLSEFNVLKO	-LCSPODELD FLMEALIISK	-YNNPQQWME FQQEASLMAE	-EASADMQAD FOREALMAE	III
٠			PNRV TKVAVKMLKS	IPVAIRELRE	A-E TRVAVKTVNE	P-V MKVAVKMLKP	T-C RTVAVKMLKE	TLVLVKSLQ-	IHCAVKSLNR	D-K MLVAVKALK-	LKVAVKTMKI 1	MNAAIKMLKE .	KTVAIKTLKD	KQAFVKTVKD		IKVAVKTLKK	G-Y TTVAVKMLKE	S-P LQVAIKTLPE	H-A QLVAIKILKD	P-F TMVAVKMLKE	II
			PNRV	V-K	A-E	V-4	D-L	A-E	XK	D-K	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	 	J	K-E	POD-LVSLDF PLNVRKGH-P LLVAVALLRP			S-P	H-A	P-F	
			LDK-DK	E-G-EK	IIK-GE	LSR-SQ	IDK-TA	LEE-GV	N-D-GK	LLP-EQ	D-D-SI	D-GLK	P-S-QD	EKD-PN	PQD-LVSLDF	ILGVGS	LKG-RA	LPG-DS	P-G-MD	LLP-YE	
VE.	_	Т	LP-ED-PRW- ELPRDRLV LGKPLGFGCF GOVVLAEAIG LDK-DK	GTVYKGLWIP	GMVYEGNARD	GKVVEGTAYG	GOELEADAFG	GEVFLAKAQG	CCVYHGTLLD	GKVFLAECHN	CAVMEGQLNQ	COVIRAMIKK	GEVYRGTLRL	GRIFHGILID	GEVHLCEVDS	GEVYEGTAVD	GKVVKATAFH	GEVYEGLVIG	GKIYKGHLYL	GRVFQARAPG	
GLYCINE	RICH		LGKPLGEGCF	IGSGAF	LLRELGOGSF	LGRVLGSGAF	LGKPLCRGAF	PITTLOKSEF	FNEVICACHE	LKWELCEGAF	LGKTLGEGEF	FEDLIGEONF	VDTVICEGEF	LKDVLQEGTF	FKEKLGEGOF	LRLLLGSGAF	LGKTLGEGEF	LLRALGHGAF		YVRDIGEGAF	н
			ELPRDRLV	PNQALLRILK ETEFKKIKV-	VYVPDEW- EVSREKIT LLRELGOGSF	LP-YD-SRW- EFPRDGLV LGRVL	EFPRDRLN	HSTSDKM- HFPRSSLQ	AVQHVVIGPS SLIVH FNEVICHF	FSDACVHHIKRRDIV LKWEL	KEKLR- DVMVDRHKVA	-P-EPLS- YPVLEWEDIT	WSNFPSR- ELDPAWLM VDTVI	KGKVK- DIAISRERIT	GDG-P-PRV- DFPRSRLR FKEKL	EEIEN- LPAFPREKLT LRLLL	EFPRKNLV	-P-LP-PGVT EVSPANVT	KPKSKAK- ELPLSAVR	NPKLLSL- EYPRNNIE	
		466	LP-ED-PRW-	PNQALLRILK	VYVPDEW-	LP-YD-SRW-	-P-YDASKW-	HSTSDKM-	AVQHVVIGPS	FSDACVHHIK	KEKLR-	-P-EPLS-	WSNFPSR-	KGKVK-	GDG-P-PRV-	EEIEN-	IL-ED-PKW-	-P-LP-PGVT	KPKSKAK-	NPKLLSL-	
			FGFR1_h	EGFR_h	INSR_h	PDGFRa_h	KDR_h	CCK4_h	MET_h	TRKA_h	AXL_h	TIE_h	EPH_h	RYK_h	DDR_h	ROS_h	RET_h	LTK_h	ROR1_h	MUSK_m	

Fig. 6A-



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T		- I GSQI - I - DDDTI,OFM	SEGL-TLLDL	KDFL-TLEHL	-QPL-STKQK	P-TVKDL	-GPL-GLGQL	-VYL-PTQML		L-VPGQL	-QAI-SQQDL	-PTI-SYPML	-PLL-TLVDL	L-TMGDL	-SPL-VMRDL	-SSL-DHGDF	-PPL-SCAEQ	VIa
	NPE-	1		KTK(55)	KS-	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		QP-	GTA-	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	-d	PGDGQAAQG-	TFYG-		LGQP-		FLR-SMSP-H TVCSLSHS DLSTRARVSS PGPPPL-SCAEQ	
		RNN		YLR-SKR-NE FVPY	t t t 1 1	HN	DVA		\$ 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NNNN	FLS-AHQLED KAA EGA	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	FLR-ESRKVG PGYLGSGGSR NSSSLDHPDE		FLI-MRSP-H SDVGCSSDED GTVK	DLSTRARVSS	
NSERT	YLQ-ARRPPG LEYCYNPSH-		YLH-KNR-DS FLSH-	FVPY-	KL	L	FLR-SHGPDA KLLAGGE	1 1 1 1 1 1 1 1	TDPAFAREH-		CKLVEA	KAA		PGYLGSGGSR	1 1 1 1 1 1 1	SDVGCSSDED	TVCSLSHS	
- KINASE INSERT	YLQ-ARRPPG	YI.R-ST.RD	YLH-KNR-DS			FIR-NE	FLR-SHGPDA	FLLYSRLGD-	FLR-KSRVLE				YLR-KARM-A	FLR-ESRKVG	FLR-HSRP-H		FLR-SMSP-H	
		QLMPFGCLLD FIMAHCDIKS		EFCKFGNLST	EYVDLGDLKQ	PYMKHGDLRN	EYMRHGDLNR	PFMKHGDLHS	EYAPYGNLLD	EFMENGALDA	PYMNWGNLKL	DYMENGDLNQ	ELMEGGDLLT	EYAKYGSLRG	ELMSGGDMKS	EYINQGDLHE	EYMAYGDLNE	Λ
	LYVIV	TL1-T	ДI	LMVIV	HYMVL	SPLVVL	LLMVF	ESFPAPVVIL	LYIAI	II	KPMVIL	LCMIT	\sim	LLLIV	RLILL	VCMLF	MCLLF	
1	IGKHKNIINL LGACTQD-GP LY	LGICLTS-TV	LGACTKS-GP	LGACTKPGGP	LGLCREA-EP	LGICLRS-EG	FGVCTEG-RP	IGVCFQGSER	LGACKNR-GY	EGVVTKR-KP	THVCIEE-GE	LGVCVQD-DP	LGVCLLN-EP	YGACSQD-GP	VGLSLRA-TP	LGAVTQE-QP	LGVCAVG-KP	IΛ
538	IGKHKNIINL	VDN-PHVCKL	LGPHLNIVNL	IGHHUNVVNL	LNH-ANVVRL	FSH-PNVLSL	LOH-QHIVRF	FDH-PNVMRL	LGHHPNIINL	FSH-PHILHL	LHH-RNLLPI	LKD-PNIIRL	FNH-PNILKO	VNH-PHVIKL	FRH-QNIVRC	LHH-PNIVCL	FDN-PNIVKL	
	FGFR1_h	EGFR_n	PDGFRa h	KDR_h	CCK4_h	MET_h	TRKA_h	AXL_h	TIE_h	EPH	RYK	DDR h	ROS_h	RET_h	LTK_h	ROR1_h	MUSK_m	

Fig. 6A-:

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	DRIYTHQS	HRIYTHOS	DGVFTTSSD	DNLYTTLS	DRVYTIQS	EGDFSTKSD	TOKFTTKSD	YRKFTTESD	DRVYTSKSD	YSVYTTKSD	HRIFTTASD	NNEFSSASD	MGKFTTASD	DGIFTTOSD	DHIYTTQS	EGIFTSKT	YGKFSSDSD	YNRYTTESDV	•
	VKWMAPEALF	IKWMALESIL	VRWMAPESLK	VKWMAPESIF	LKWMAPETIF	LRWMSPEAIL	VKWMALESLO	IRWMPPESIL	VKWIAIESLA	VRWMAIESLN	IRWTAFEAIA	VRWMALESLV	IRWMAWECIL	VRWMAPESLM	VKWMAIESLF	VKWMPPEAFL	IRWMPPEAIM	IRWMPPESIF	VIII
LOOP	KTTNGRLP	HAEGGKVP	KGGKGLLP	SKGSTFLP	RKGDARLP	FRQAWVP	VHNKTGAKLP	VGGRTMLP	QGRIAKMP	KKTMGRLP	ETQGGKIP	LGDNENRP	VQGRAVLP	KRGEGLLP	KRSQGRIP	RGDRALLP	VQSKSLLP	ADGNDAIP	
ACTIVATION LOOP	RDIHHIDYYK	KLLGAEEKEY	RDIYETDYYR	RDIMHDSNYV	RDIYKDPDYV	KDVYNSEYYH	RDMYDKEYYS	RDIYSTDYYR	KKIYNGDYYR	RG-EEVYV	RLLDDFDGTY	RDLFPMDYHC	RNLYAGDYYR	RDIYKNDYYR	RDVYEEDSYV	RDIYRASYYR	REIYSADYYR	RNIYSADYYK	
	VMKI ADFGLA	HVKITDFGLA	TVKIGDEGMT	IVKICDFGLA	VVKICDEGLA	OVKVSALGLS	TVKVADFGLA	VVKICEDECMS	SVCVADFGLS	ASKIADFGLS	CCKVSDFGLT	OVKITDNALS	TIKIADFGMS	IVKIGDEGLA	KMKISDFGLS	VAKIGDEGMA	HVKISDLGLS	VVKIADFGLS	VII
	VTEDN	VKTPQ	VAHDF	LAQGK	LSEKN	VSAQR	LDEKF	VGQGL	LNENM	VGENL	VNQNL	IDDTL	VGENF	VSVKDYTSPR	VAEGR	LSCAGPSR	IGEQL	VGETM	
CATALYTIC LOOP	HRELAARMVL	HRDLAARNVL	HRDLAARWCM	HRDLAARWVL	HRDLAARNIL	HKDLAARNCL	HRDLAARNCM	HRDLATRNCL	HRDLAARNCM	HRDLAARNVL	HRDLAARNIL	HKDLAARNCV	HRDLATRNCL	HRDLAARNCL	HELAARNIL	HRDIAARNCL	HKULAARNIL	HRDLATRINCL]
	VSCAYQVARG MEYLASKKCI		MAYLNAKKFV	MEFLASKNCV	MEFLASRKCI	MEHLSNNRFV	MKYLASKKFV	MVYLAGLHFV	MEYLSTKRFI	MOYLSEKQFI	MNYLSNHNYV	MSYLARREVI	MRYLATLNFV	CVYLERMHFI	MOYLAEMKLV HADLAARN	CHYLEENHFI	MEYLSSHFFV	MAYLSERKFV HHDLATHNCL	VIb
601	VSCAYQVARG	LNWCVQIAKG	IQMAAEIADG	LSFTYQVARG	ICYSFQVAKG	VALCTQVALG	IGFGLQVAKG	LAVASQVAAG	VKFMADIASG	LRFASDAANG	VAMLQGIASG	VHMAIQIACG	LHVAAQIASG	VDLCVDISKG	ISFAWQISQG	LQLAQDIAQG	LHIAIQIAAG	LCIARQVAAG	
,	FGFR1_h	EGFR_h	INSR_h	PDGFRa_h	KDR_h	CCK4_h	MET_h	TRKA_h	AXL_h	TIE_h	EPH_h	RYK_h	DDR_h	ROS_h	RET_h	LTK_h	ROR1_h	MUSK_m	

Fig. 6A-

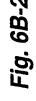


FSKMARDPQR LKDDLHPSFP LGNLLOANAO LGDSTVDSKP LENTLKALPP VENLLPGOYK ISAIFSTFIG LQALAQAPPV LGRMLEARKA LOLFRNFFLN LDRIVALTSN LEOLLANPHS LTEFHAALGA LAEDALNTV-LEKMMVKRRD LOYCTODPDV LRSWEGLSSH LORMCERAE RPKFRELIIE RPTFSELVEH RPSFTELRED RPTFKOLVED RPTFLEIUNL RPSFYHLSEI RPSFSEIASA RPSFSELVSR RHSIKDVHAR RPPFAQIALQ RPHFQKLQAH RPRFQQLVQC RPPFSQLHRF RPTFHRIQNO RPVFADISKD RPRFKDIHVR RPSFCSIHRI ACCWALDPEE LRCWSRESEQ RDCWHAVPSQ SRCWELNPOD RMCWDFNPKM LDCWHGEPSQ ORCMALSPKD RGCWDREPQQ ROCWRDRPYE KNOWAYDRAR TOCHROEPDO RLCWSKLPAD VKCWMIDADS VKCWNSEPEK LKCWHPKAEM COEPDK **POCMOHEPEL** TECHNEIPSR LOCAN NCTNELYMM ICTIDUYMIM NCPERVTDLM HATSEVYEIM KEGTRMRAPD YTTPEMYOTM YCPDPLYEVM NCPLELYNLM GCPSKLYRLM ACPPEVYAIM TCPDELFAVM ACPOGLYELM NCSEEMYRLM DCPPRMYSLM DCLDGLYALM NCDDEVYELM DCPAPLYELM NCPDDLWNLM GCPGPVYRIM TOGRELERPR EKGERLPOPP MDGGYLDOPD KSGYRMAKPD RQGNRLKQPA EDGYRLPPPV GRQVYLSRPP OTGGRLEPPR KTGHRMERPD KEGHRMDKPS AGKARLPOPE LOGRRLLOPE POGYRMEOPR VGGGRMDPPR RKRQLLPCSE RDGNILACPE KDGYRIAQPI ----IS-SIL ----IY-DYL ----LF-NLL ----EFCRRL ----VLADLQ ----IT-VYL ----LY-EKL ----VM-KSI ----VL-KFV ----TFYNKI ----AI-DCI ----MAA-YL ENAGEFFRDQ ----VL-DFV ----VI-EMV VYY-IV-------VL-NYV D-GIPASE--Q-GLSNEQ--P-GVKIDE--G-GQADDE--P-DVNTFD--Y-QLSNTE--P-GVENSE--C-GMTCAE--G-EMSNQE--G-QLTDEQVI P-AHSNLD--P-GMMVDS--P-GVPVEE--TLDIDPFE-P-GIPPER-Y-GFSNQE Y-GMAHEE IFTYGK-QPW IFSYGL-QPY IFTLGG-SPY LMTFGS-KPY ITSLAE-QPY IFSLGG-TPY IFSLGA-SPY VFTHGE-MPH LMTRGA-PPY IATRGQ-TPY IVSLGG-TPY VLSFGD-KPY LMTLGQ-TPY VLMLCRAOPF ILTLGH-OPY IVTLGG-NPY IFSFGL-OPY IFSLGY-MPY WSFGV-LLWE WSFGV-VLWE WSFGV-LLWE WAFGV-LMWE WSFGV-TMWE WSYGV-TVWE WSYGI-LLWE WSFGV-VLWE WSFGI-VMWE WAFGVNSLWE WSFGI-LIWE WSFGV-LLWE WSFGV-VLWE MAYGV-VLWE WSFGV-VLWE WSFGV-LLWE WAFGV-TVWE WSFGV-LLWE MET_h RET_h INSR_h KDR_h AXL_h EPH_h ROS_h LTK_h CCK4_h FGFR1_h EGFR_h PDGFRa_h rrka_h TIE h RYK_h DDR_h ROR1_h

Fig. 6A-4

, • .	•
LAEAIGLDKD KPNRVTKVAV KMLKSDATEK DLSDLISEME MMKMI-GKHK MGTW NGTTRVAI KTLKPGTMSP -EAFLQ-E AQVMKKLRHE EGLW KDRVQVAI KVISRDNLLH -QQMLQSE IQAMKKLRHK YGKW RGQYDVAI KMIKEGSMSE -DEFIE-E AKVMMNLSHE LGDY RGNKVAV KCIKNDA-TA -QAFL-AE ASVMTQLRHS EGVW RGNKVSLTVAV KTLKEDTMEV -EEFLK-E AAVMKEIKHP QGVYRM RKKQ-IDVAI KVLKQGTE KADTEEMMRE AQIMHQLDNP SGR LRADNTLVAV KSCRETLPPD LKAK-FLQ-E ALTMRQFDHP LCRYDP EDNTGEQVAV KSLKPESG GNHIADLKKE IEILRNLYHE RGEWDA PSGKTVSVAV KCLKPDVLSQ PEAMDDFIRE VNAMHSLDHR III	PEEQLSSKDL VSCAYQVARG MEYLASKKCI -GKYLRLPQL VDMAAQIASG MAYVERMNYV -EKVLPVSEL LDIAWQVAEG MCYLESQNYI -RHRFQTQQL LEMCKDVCEA MEYLESKQFL -RSVLGGDCL LKFSLDVCEA MEYLEGNNFV -REEIPVSNV LYMATQISSA MEYLEKKNFI -REEIPVSNV AELLHQVSMG MKYLEEKNFV -GARLRVKTL LQMVGDAAAG MEYLESKCCI -KYSLDLASL ILYAYQLSTA LAYLESKRFV -KNKINLKQQ LKYAVQICKG MDYLGSRQYV -QGHFLLGTL SRYAVQVAEG MGYLESKRFI VIA
MLK TLK VIS WLK VLK VLK SCR SCR	GKY GKY GKY RHR RRSV RQE GAR KYS
KPNRVTKVAV K NGT TRVAI K KDR VQVAI K RGQYD VAI K K- KYSLTVAV K K-KXQ-IDVAI K LRADNTLVAV K PENPALAVAI K PENPALAVAI K II	LEYCYNPSHN P
•	EYLQARRPPG DFLKGET ELLRDSD NYLRE-M DYLRSRG DYLRECN TFLVGK TFLRTE SFLQVR SFLQVR BYLPKN
RDRLVLGK-P IGEGCFGQVV RESIRLEV-K IGSGYFGEVF PKDLTFLK-E IGTGQFGVVK MKELKLLQ-T IGKGEFGDVM RTDITMKH-K IGGGYGEVY RDNLLIADIE IGGGNFGEVF HEDLVLGE-Q IGRGNFGEVF RERIELGRC- IGEGFGDVH KRFLKRIR-D LGEGHFGKVE EKDLRLLE-K LGDGSFGVR	VEYASKGNLR TEYMSKGSLL TELMAKGSLL TEYMANGCLL TEYMAKGSLV TEFMTYGNLL MEMAGGGPLH MELVQGGDFL MELCTLGELR MELCTLGELR TELAPLGSLL
	-QDGP-LYVI -E-EP-IYIV VG-DP-VYII KQR-P-IFII EEKGG-LYIV REP-P-FYII AEALMLV -QKQP-IYIV ENPVWII EDGGNGIKLI
465 LPEDPRWELP GLAKDAWEIP LPHWDDWERP GLGYGSWEID EFYRSGWALN SPNYDKWEME LKDKKLF-LK AVPKDKWVLN MPSTRDYEIQ PTEVDPTHFE	543 NIINLLGACT KLVQLYAVVS HILALYAVVS KLVQLLGVCT NLVQLLGVCT YIVRLIGVCT HIVKLIGVCT HIVKLIGVCT NIVKLGVCT
FGFR1_h SRC_h BRK_h BTK_h CSK_h ABL_h ZAP70_h FES_h FAK_h JAK1_h ACK_h	FGFR1_h SRC_h BRK_h BTK_h CSK_h ABL_h ZAP70_h FES_h FAK_h JAK1_h

Fig. 6B-1



LLWEIFTLGG EHIKTHELHL ETMFQESSIS RACYYSLASK OSIR--KRHR STILEEEKAQ LLTELTTKGR LLHEMFSRGO LMWEIYSLGK LLWEIYSFGR TLHELLTYCD TLWEMFTYGO EDYFISTEPO LEAQPTDMRA LLWEIATYGM TMWEALSYGO LLWETFSLGA CMWEILMHGV PTFKOLVEDL DRIVALTSNO SSFTSYENPT LDVMDEES-HASDIWMFGV PDFLTVEORM HOSDVWSFGV SRSDVWSYGC SASDVWMFGV IASDVWSFGV PTFEYLQAFL PCFKALRERL PSFLQLREQL PSFAEIHQAF PSFSTIYQEL PRFTELKAQL TSFONLIEGF PTFVALRDFL SKSDIWAFGV IKSDVWAFGV SESDAWSFGI PTFKILLSNI IKSDVWSFGI TKSDVWSFGI TKSDVWSFGI CINELYMMMR DOWHAVPSOR **OCMRKEPEER** TCWCRDPEOR SCHEKADER DOMIYKWEDR **QCWAYEPGOR** KCWAYDPSRR **OCHAHKPEDR** GKLPIKWMAP ESINFRR-FT CPPAVYEVMK NCWHLDAAMR ACMOMNPSDR KCMEFOPSNR EAL-FDRIYT EAALYGR-FT EALSRGH-YS EVLMYSK-FS EALREKK-FS ESLAYNK-FS ECINFRK-FS EALNYGR-YS ECLMOSK-FY ESLKTRT-FS CPPELYALMS GRLPVKWMAP RQVPVKWTAP RDSPVFWYAP RKVPFAWCAP CPESLHDLMC ASEKVYTIMY CPEKVYELMR CPDAVFRLME -KFPIKWTAP -NIPYKWTAP -KFPVRWSPP GKWPLKWYAP CPPSVHKLML CPPTLYSLMT CPDEVYOLMR CPQDIYNVMV - KLPVKWTAP -KFPIKWTAP DKEYYTVKDD EGERLPRPED NDDHYVMQEH -GYRMPCPPE -GLRLYRPHL -EASSTODIG DDSYYTARSA DGVYAASGGS DSTYYKA-SK -GHRMDKPSN -GYRMPCPLE -GYKMDAPDG -DYRMERPEG QGKRMECPPE -GGRLPCPEL NGERLPMPPN EGKRLPCPPN HIDYYKKTTN DNEYTAROGA GDTYTAHAGA EDVYLSHD-H DDEYTSSVGS -- PYPGVP VEELFKLLKE NSETAEHIAQ LSQVYELLEK ---PYPNLS NQQTREFVEK ---PFQGVK NNDVIGRIE-KMIGPTHGOM TVTRLVNTLK GSQILHKIDK DFGLTKAIET DEGLMRALPQ NREVLDQVER NHEAFLRVDA ---PYPRIP LKDVVPRVEK DFGMSREEA-GPEVMAFIE-DFGLARDIH-DFGLSKALGA DFGLSRYME-DFGLARLIE-DFGLARLIK-DFGLSRYVL-DFGLTK----DFGLSRLMT---- PYPGMS PYPGMV PYERFT --PYPGID --- PYKKMK VSSNDCVKLG VESEHQVKIG LATRDLVKIG VTEKNVLKIS --PWIGLN VGENTLCKVG VNDQGVVKVS VSEDNVAKVS LVNRHYAKIS VTEDNVMKIA VGENLVCKVA VGENHLVKVA HRDLAARMUL HEDLAARNCL HRDLAARWL SDSSPMALFL HRDLAARNVL HRDLRAANIL HRDLAARMIL HRDLAARMVL HRDLAARNCL HRDLAARMVL HEDLAARNCL HEDITARRIVE 669 ABL_h ZAP70_h FES_h FAK_h JAK1_h ACK_h SRC_h BRK_h ABL_h ZAP70_h BTK_h CSK_h FES_h FAK_h JAK1_h BTK_h CSK_h

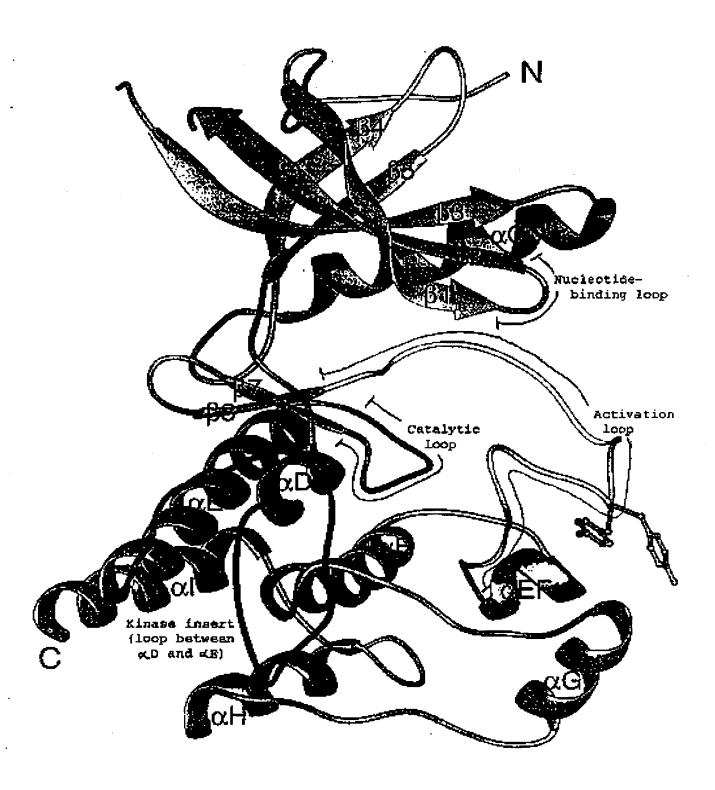
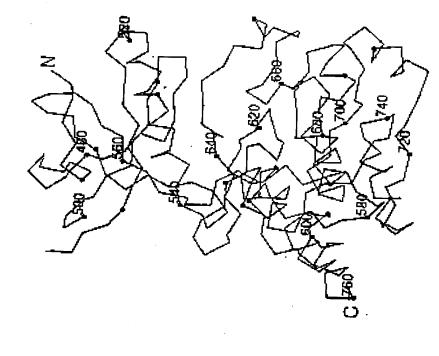
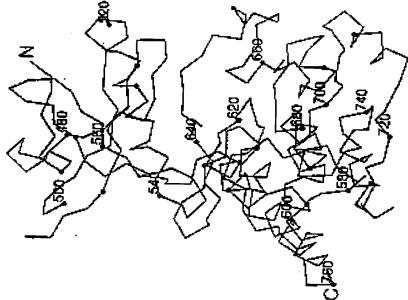


FIGURE 1









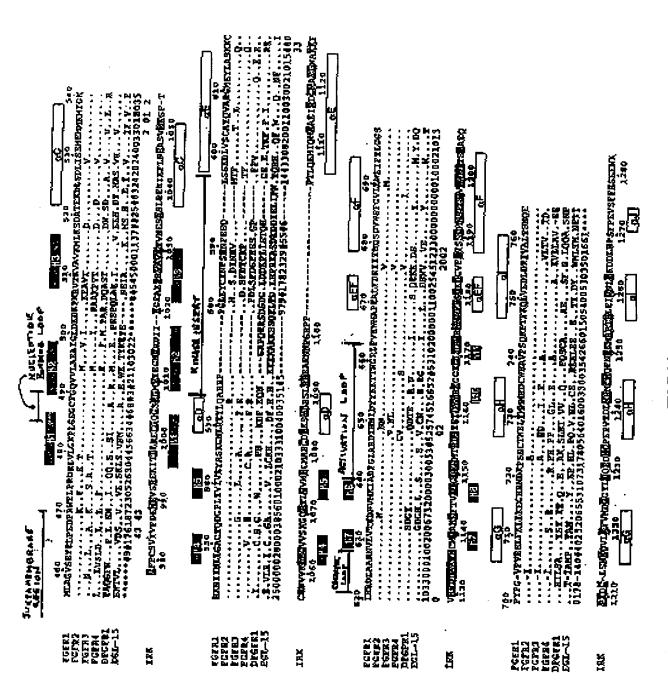
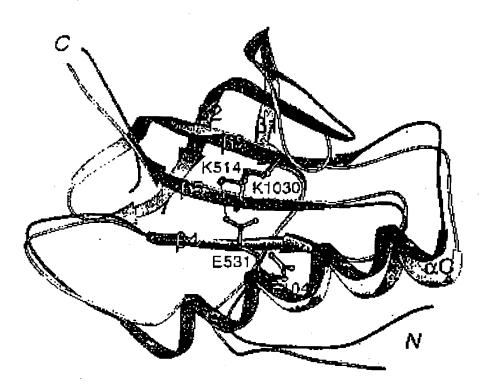


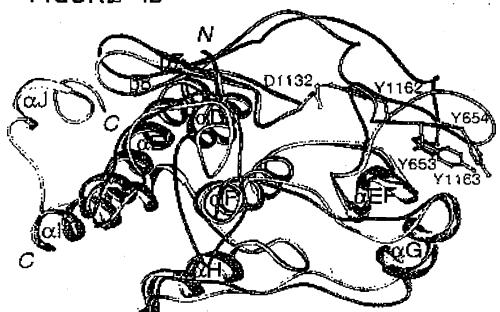
FIGURE 3

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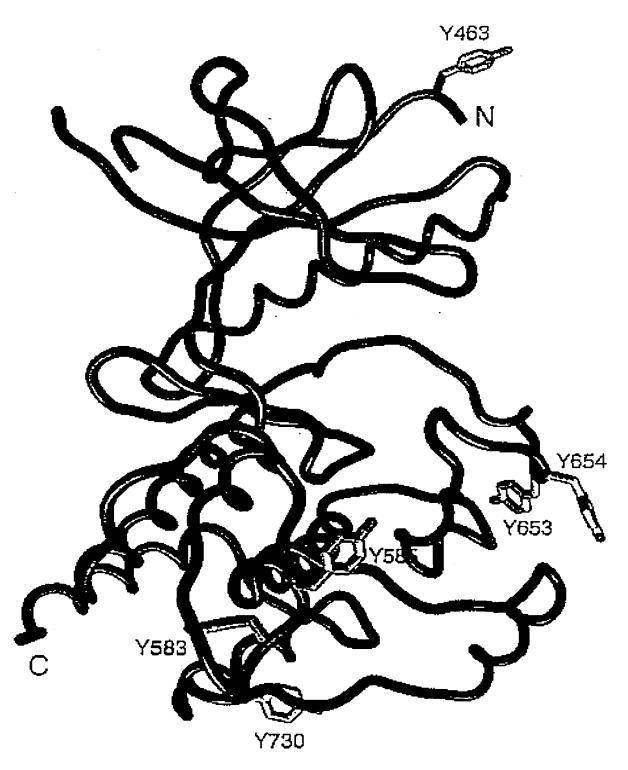


FIGURE 5

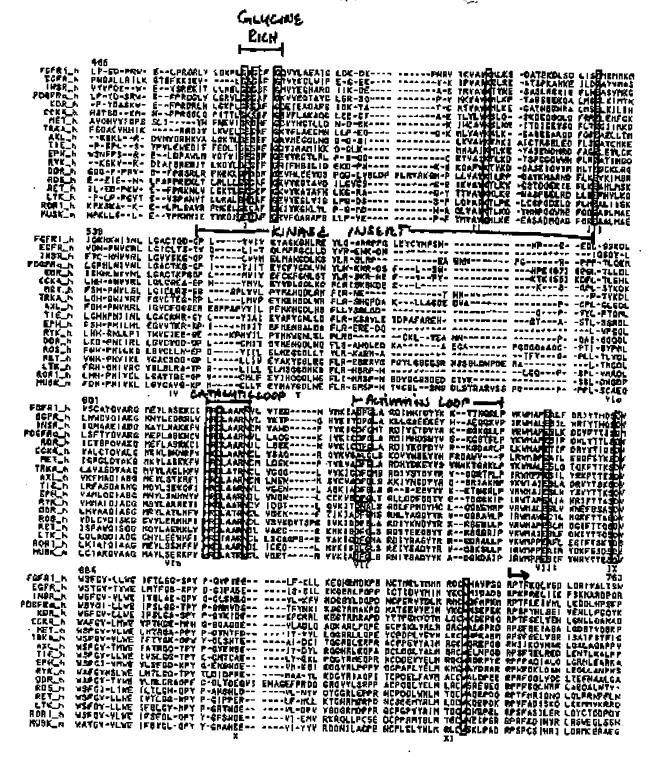


FIGURE 6A

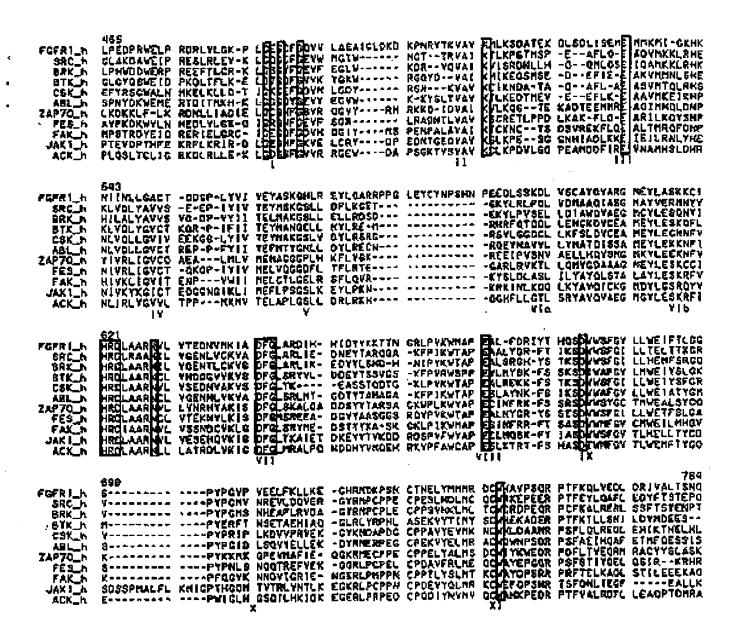


FIGURE 6B

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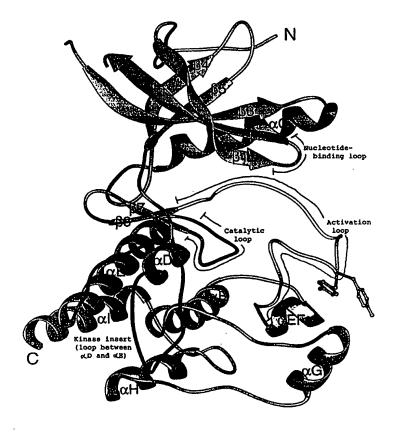
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(57) Abstract

The present invention relates to the three-dimensional structures of a protein tyrosine kinase optionally complexed with one or more compounds. The atomic coordinates that define the structures of the protein tyrosine kinase and any of the compounds bound to it are pertinent to methods for determining the three-dimensional structures of protein tyrosine kinases with unknown structure and to methods that identify modulators of protein tyrosine kinase functions.

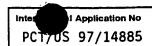


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DE Germany LI Liechtenstein SD Sudan DK Denmark LK Sri Lanka SE Sweden EE Estonia LR Liberia SG Singapore

INTERNATIONAL SEARCH REPORT



A. CLASSIFICATION OF SUBJECT MATTER IPC 6 C12N15/54 C07K14/71 C12Q1/48 G01N33/68

CO7K14/705 C07D209/34 C12N9/12 A61K31/40 C12N15/12

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

Category °	Citation of document, with indication, where appropriate, of the relevant passages	. Relevant to claim No.		
X	S. R. HUBBARD ET AL: "Crystal structure of the Tyrosine kinase domain of the human insulin receptor" NATURE., vol. 372, 22 December 1994, LONDON GB, pages 746-754, XP002061072 cited in the application see the whole document	1,2,6, 24,25,30		
X	LEI WEI ET AL: "Expression, characterization, and crystallization of the catalytic core of the human insulin receptor protein-tyrosine kinase domain" JOURNAL OF BIOLOGICAL CHEMISTRY., vol. 270, no. 14, 1995, MD US, pages 8122-8130, XP002061073 see page 8129, last paragraph - page 8130	1,2,24, 25,30		

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X Further documents are listed in the continuation of box C.	Patent family members are listed in annex.
"A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art. "&" document member of the same patent family
Date of the actual completion of the international search	Date of mailing of the international search report
17 April 1998	2 7 07 1998
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer LE CORNEC N.D.R.

INTERNATIONAL SEARCH REPORT

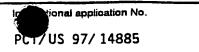
PCT/US 97/14885

Category °	Citation of document, with indication, where appropriate, of the relevant passages	 Relevant to claim No.
A	WO 92 13870 A (THE REGENTS OF THE UNIVERSITY OF CALIFORNIA) 20 August 1992 see claims 26-28	24,25,27
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Form PCT/ISA/210 (continuation of second sheet) (July 1992)





Box I Observations where certain claims were f und unsearchabl (Continuation of item 1 first sheet)	
This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons	:
Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:	
2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:	
Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).	
Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)	
This International Searching Authority found multiple inventions in this international application, as follows:	
As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.	
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.	
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:	
4. X No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:	
subject 1 (Please see Extra sheet)	
Remark on Protest The additional search fees were accompanied by the applicant's protest No protest accompanied the payment of additional search fees.	t.

Form PCT/ISA/210 (continuation of first sheet (1)) (July 1992)

FURTHER INFORMATION CONTINUED FROM PCT/ISA/

1. Claims: 1-3, 6, 24-25, 27, 30 all partially

Crystalline form of a polypeptide corresponding to the catalytic domain of a receptor protein tyrosine kinase: PDGF-R. The polypeptide and the method used to form the crystal.

2. Claims: 1-3, 6, 24-25, 27, 30 all partially .

Crystalline form of a polypeptide corresponding to the catalytic domain of a receptor protein tyrosine kinase:FLK/KDR. The polypeptide and the method used to form the crystal.

3. Claims: 1-3, 6, 24-25, 27, 30 all partially

Crystalline form of a polypeptide corresponding to the catalytic domain of a receptor protein tyrosine kinase: CCK4. The polypeptide and the method used to form the crystal.

4. Claims: 1-3, 6, 24-25, 27, 30 all partially

Crystalline form of a polypeptide corresponding to the catalytic domain of a receptor protein tyrosine kinase: MET. The polypeptide and the method used to form the crystal.

5. Claims: 1-3, 6, 24-25, 27, 30 all partially

Crystalline form of a polypeptide corresponding to the catalytic domain of a receptor protein tyrosine kinase: TRKA. The polypeptide and the method used to form the crystal.

6. Claims: 1-3, 6, 24-25, 27, 30 all partially

Crystalline form of a polypeptide corresponding to the catalytic domain of a receptor protein tyrosine kinase: AXL. The polypeptide and the method used to form the crystal.

7. Claims: 1-3, 6, 24-25, 27, 30 all partially

Crystalline form of a polypeptide corresponding to the catalytic domain of a receptor protein tyrosine kinase: TIE. The polypeptide and the method used to form the crystal.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/

8. Claims: 1-3, 6, 24-25, 27, 30 all partially

Crystalline form of a polypeptide corresponding to the catalytic domain of a receptor protein tyrosine kinase: EPH. The polypeptide and the method used to form the crystal.

9. Claims: 1-3, 6, 24-25, 27, 30 all partially

Crystalline form of a polypeptide corresponding to the catalytic domain of a receptor protein tyrosine kinase: RYK. The polypeptide and the method used to form the crystal.

10. Claims: 1-3, 6, 24-25, 27, 30 all partially

Crystalline form of a polypeptide corresponding to the catalytic domain of a receptor protein tyrosine kinase: DDR. The polypeptide and the method used to form the crystal.

11. Claims: 1-3, 6, 24-25, 27, 30 all partially

Crystalline form of a polypeptide corresponding to the catalytic domain of a receptor protein tyrosine kinase: ROS. The polypeptide and the method used to form the crystal.

12. Claims: 1-3, 6, 24-25, 27, 30 all partially

Crystalline form of a polypeptide corresponding to the catalytic domain of a protein tyrosine kinase receptor: RET. The polypeptide and the method used to form the crystal.

13. Claims: 1-3, 6, 24-25, 27, 30 all partially

Crystalline form of a polypeptide corresponding to the catalytic domain of a receptor protein tyrosine kinase: LTK. The polypeptide and the method used to form the crystal.

14. Claims: 1-3, 6, 24-25, 27, 30 all partially

Crystalline form of a polypeptide corresponding to the catalytic domain of a receptor protein tyrosine kinase: ROR1. The polypeptide and the method used to form the crystal.

15. Claims: 1-3, 6, 24-25, 27, 30 all partially

Crystalline form of a polypeptide corresponding to the catalytic domain of a receptor protein tyrosine kinase: MUSK. The polypeptide and the method used to form the crystal.



- 16. Claims: 1,4-6, 24, 26, 28, 30 all partially.

 Crystalline form of a polypeptide corresponding to the catalytic domain of a non-receptor protein tyrosine kinase:

 SRC. The polypeptide and the method used to form the crystal.
- 17. Claims: 1,4-6, 24, 26, 28, 30 all partially.

Crystalline form of a polypeptide corresponding to the catalytic domain of a non-receptor protein tyrosine kinase: BRK. The polypeptide and the method used to form the crystal.

18. Claims: 1,4-6, 24, 26, 28, 30 all partially.

Crystalline form of a polypeptide corresponding to the catalytic domain of a non-receptor protein tyrosine kinase: BTK. The polypeptide and the method used to form the crystal.

19. Claims: 1,4-6, 24, 26, 28, 30 all partially.

Crystalline form of a polypeptide corresponding to the catalytic domain of a non-receptor protein tyrosine kinase: CSK. The polypeptide and the method used to form the crystal.

20. Claims: 1,4-6, 24, 26, 28, 30 all partially.

Crystalline form of a polypeptide corresponding to the catalytic domain of a non-receptor protein tyrosine kinase: ABL. The polypeptide and the method used to form the crystal.

21. Claims: 1,4-6, 24, 26, 28, 30 all partially.

Crystalline form of a polypeptide corresponding to the catalytic domain of a non-receptor protein tyrosine kinase: ZAP70. The polypeptide and the method used to form the crystal.

22. Claims: 1,4-6, 24, 26, 28, 30 all partially.

Crystalline form of a polypeptide corresponding to the catalytic domain of a non-receptor protein tyrosine kinase: FES. The polypeptide and the method used to form the crystal.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/

23. Claims: 1,4-6, 24, 26, 28, 30 all partially.

Crystalline form of a polypeptide corresponding to the catalytic domain of a non-receptor protein tyrosine kinase: FAK. The polypeptide and the method used to form the crystal.

24. Claims: 1,4-6, 24, 26, 28, 30 all partially.

Crystalline form of a polypeptide corresponding to the catalytic domain of a non-receptor protein tyrosine kinase:

JAK. The polypeptide and the method used to form the crystal.

25. Claims: 1,4-6, 24, 26, 28, 30 all partially.

Crystalline form of a polypeptide corresponding to the catalytic domain of a non-receptor protein tyrosine kinase: ACK. The polypeptide and the method used to form the crystal.

26. Claims: 1, 24-25, 27, 30 all partially and 7-23, 29, 31-34 all completely.

Crystalline form of a polypeptide corresponding to the catalytic domain of a FGF receptor protein tyrosine kinase which is complexed or not with a compound. The polypeptide (cDNA encoding it) and the method used to form the crystal. The cDNA encoding FGFR tyrosine kinase as in seq ID. no 5.

27. Claims: 35-42 completely

Method to determine the three dimensional structure of receptor and/or non-receptor tyrosine kinases.

28. Claims: 43-50

Method of identifying a potential modulator of protein tyrosine kinase function by using a three dimensional computer representation.

29. Claims: 51-54, 57 all completely and 58-61 all partially

A modulator of protein tyrosine kinase function and its use in a method of treating a disease.



FURTHER INFORMATION CONTINUED FROM PCT/ISA/

30. Claims: 55 completely and 58-61 all partially

Method of identifying a potential modulator of protein tyrosine kinase by comparing the level of protein kinase phosphorylation between cells not administered the potential modulator and cells administered said potential modulator.

31. Claims: 56 completely and 58-61 all partially

Method of identifying a potential modulator of protein tyrosine kinase by comparing the rate of cell growth between cells not administered the modulator and cells administered the modulator.

INTERNATIONAL SEARCH REPORT

Information on patent family members

Into all Application No
PC17US 97/14885

Patent document	Publication date	Patent family	Publication		
cited in search report		member(s)	date		
WO 9213870 A	20-08-1992	AU 669328 B AU 1346792 A CA 2101632 A EP 0572505 A EP 0811685 A EP 0811686 A JP 6505629 T NZ 241479 A	06-06-1996 07-09-1992 01-08-1992 08-12-1993 10-12-1997 10-12-1997 30-06-1994 27-09-1994		

Form PCT/ISA/210 (patent family annex) (July 1992)

